

[illegible]

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 1 (bases 1 to 6513)  
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 Wang, P. and Warneke, J.W.  
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DEFINITION Sequence 7 from patent US 5688917.  
ACCESSION 174672  
VERSION 174672.1 GI:3010813  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 6513)  
AUTHORS Arena, J.P., Peng, G., Hall, L.M., Liu, K., Van Der Ploeg, L.H.T.,  
Wang, P. and Wamke, J.W.  
TITLE Process for functional expression of the para cation channel  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1509	TCTTCCTTAGGTCAATTCATCTGTGAAATTTGATTTTGGCCATTGTTGCCATGTCCGTA	1568
QY	1321	ACGAATTGCCAAGGAGGCGCGAAGAAAGAGGCTGCGAAGAGGAGCGGATACGCTGAAG	1380
Db	1569	ACGAATTGCCAAGGAGGCGCGAAGAAAGAGGCTGCGAAGAGGAGCGGATACGCTGAAG	1628
QY	1381	CGAAGAAAGCTGCGCGCCGCAAAAGCGGCGCAAGCTGAGAGAGCGGCGCAATGCGAGCTC	1440
Db	1629	CGAAGAAAGCTGCGCGCCGCAAAAGCGGCGCAAGCTGAGAGAGCGGCGCAATGCGAGCTC	1688
QY	1441	AGGCAAGCAGCGGATGCGGCTGCGCGGAAAGGCTGCACTGCAATCCGGAATTTGGCCAGA	1500
Db	1689	AGGCAAGCAGCGGATGCGGCTGCGCGGAAAGGCTGCACTGCAATCCGGAATTTGGCCAGA	1748
QY	1501	GTCGCGCATATTCCTTGCACTAGACTATGAGCTATTTGTTGGCGGCGGAGAAAGGCAACATG	1560
Db	1749	GTCGCGCATATTCCTTGCACTAGACTATGAGCTATTTGTTGGCGGCGGAGAAAGGCAACATG	1808
QY	1561	ACAACAAACAAAGAGAAGATGTCATTTCGAGAGGTCGAGGTGAGAGTCGAGTCCGATGACG	1620
Db	1809	ACAACAAACAAAGAGAAGATGTCATTTCGAGAGGTCGAGGTGAGAGTCGAGTCCGATGACG	1868
QY	1621	TTATTCAAAGACAAACAGACCTTACACAGCACACCAAGCTACCAAGTTGGTAAAGTGA	1680
Db	1869	TTATTCAAAGACAAACAGACCTTACACAGCACACCAAGCTACCAAGTTGGTAAAGTGA	1928
QY	1681	GAAGAGCATCTTATCTTATCTTACCTGGTTACCGGTTTAAATTCATACGAGGGAGATCAAGTACTT	1740
Db	1929	GAAGAGCATCTTATCTTATCTTACCTGGTTACCGGTTTAAATTCATACGAGGGAGATCAAGTACTT	1988
QY	1741	CTCACAAAGTACAGTAACGGAACGAGCGTGGCCGTTTGGTATACCCTGGTACGATCCGTA	1800
Db	1989	CTCACAAAGTACAGTAACGGAACGAGCGTGGCCGTTTGGTATACCCTGGTACGATCCGTA	2048
QY	1801	AGCCTTGGTATTTGTCACATATCAGATATGCCAGACAGCTTGCGCTTATGCTCCGACACT	1860
Db	2049	AGCCTTGGTATTTGTCACATATCAGATATGCCAGACAGCTTGCGCTTATGCTCCGACACT	2108
QY	1861	CGAATGCGGTACCCCGATGTGCCGAAGAAATGGGGCCATATAGTGGCCGCTGATCTATG	1920
Db	2109	CGAATGCGGTACCCCGATGTGCCGAAGAAATGGGGCCATATAGTGGCCGCTGATCTATG	2168
QY	1921	GCAATCTTAGGCTCCCGACATCTATCTGTATCCTCGCATCAAGTCCGGAATATCTATACCT	1980

Db	2169	GCACATCTAGGCTCCCGACACCTCATGGTATACCTCGCATAGTCCCGAATATCGTATACCT	2228
Qy	1981	CACATGAGCGATCTACTCGGCGGCATAGCCGTCATGAGGCGCTCAGACAAATGACCAAGAGA	2040
Db	2229	CACATGGCGATTTACTCGGCGGCATAGCCGTCATGAGGCGCTCAGACAAATGACCAAGAGA	2288
Qy	2041	GCACATTTGGCAACCGCAACACACGCAATCAATCAATGAGGCGCCACCAATGCGGCA	2100
Db	2289	GCAATTTGGCAACCGCAACACGCAATCAATCAATGAGGCGCCACCAATGCGGCA	2348
Qy	2101	CCTGTCTGGAACCAATCAAGAGCTCGATTCATCGGCACTAACGAAATTTGGCGTGGAGTGA	2160
Db	2349	CCTGTCTGGAACCAATCAAGAGCTCGATTCATCGGCACTAACGAAATTTGGCGTGGAGTGA	2408
Qy	2161	CGGACGAAGCTGGCAAGATTTAAACATCATGACAAATCTTTTATCGAGCCGCTCAGACAC	2220
Db	2409	CGGACGAAGCTGGCAAGATTTAAACATCATGACAAATCTTTTATCGAGCCGCTCAGACAC	2468
Qy	2221	AAACGGTGGTGAATATGAAGATGTGATGCTCTGAATGACATCATGAAACAGCGCGCTG	2280
Db	2469	AAACGGTGGTGAATATGAAGATGTGATGCTCTGAATGACATCATGAAACAGCGCGCTG	2528
Qy	2281	GTCGGCAACATCGGGCAAGCCATTCGCGGTGTCTCGCTTACTATTTTCCCAACAGAGACG	2340
Db	2529	GTCGGCAACATCGGGCAAGCCATTCGCGGTGTCTCGCTTACTATTTTCCCAACAGAGACG	2588
Qy	2341	ATGACGAGATGGGCGACAGCTTCAAGACAGGCACTCGAAGTACCTTCAAGGCAATCG	2400
Db	2589	ATGACGAGATGGGCGACAGCTTCAAGACAGGCACTCGAAGTACCTTCAAGGCAATCG	2648
Qy	2401	ATGTGTTTTGTGTGTGGGACTGTGTGCGGTTTGTGTGAATTTCAAGAGTGGGTATCGC	2460
Db	2649	ATGTGTTTTGTGTGTGGGACTGTGTGCGGTTTGTGTGAATTTCAAGAGTGGGTATCGC	2708
Qy	2461	TCATGCTTTCGATCCCTTCGTGAGCTTTTCATCACGCTGTGACATTTGTGTCAACGA	2520
Db	2709	TCATGCTTTCGATCCCTTCGTGAGCTTTTCATCACGCTGTGACATTTGTGTCAACGA	2768
Qy	2521	TGTTCATGGCAATGATATCCACGATATGAACAGAGATGGAACGCGTCTCAAGAGTG	2580
Db	2769	TGTTCATGGCAATGATATCCACGATATGAACAGAGATGGAACGCGTCTCAAGAGTG	2828
Qy	2581	GCAACTATTTCTTCAACCGCACTTTGCCATCGAGGCAACATGAAGCTAATGCGCATGA	2640
Db	2829	GCAACTATTTCTTCAACCGCACTTTGCCATCGAGGCAACATGAAGCTAATGCGCATGA	2888
Qy	2641	GCCCAAGTACTATTTCCAGAGGCGTGGACATCTTGCACTTATTCGTGGCCCTAT	2700
Db	2889	GCCCAAGTACTATTTCCAGAGGCGTGGACATCTTGCACTTATTCGTGGCCCTAT	2948
Qy	2701	CGCATTTGGAATCGGGAACTCGAGGGGTGTCAGAGGTCGTCGCAATGTCGCTTCTTCGAT	2760
Db	2949	CGCATTTGGAATCGGGAACTCGAGGGGTGTCAGAGGTCGTCGCAATGTCGCTTCTTCGAT	3008
Qy	2761	TGCTCGTGTATTTCAAACTGCGCAAGCTTTGGCCCACTTAATTTACTATTTTCGATTA	2820
Db	3009	TGCTCGTGTATTTCAAACTGCGCAAGCTTTGGCCCACTTAATTTACTATTTTCGATTA	3068
Qy	2821	TGGAGCGCAACATGAGGCGCTTTGGGTATCTGACATTTGTACTTTGCAATTAATCTTCA	2880
Db	3069	TGGAGCGCAACATGAGGCGCTTTGGGTATCTGACATTTGTACTTTGCAATTAATCTTCA	3128
Qy	2881	TCTTTGCGGTGATGAGGAATGCAACGTTGCGGAAAGAAATTAATCAATGATCAAGACCGCT	2940
Db	3129	TCTTTGCGGTGATGAGGAATGCAACGTTGCGGAAAGAAATTAATCAATGATCAAGACCGCT	3188
Qy	2941	TTCCGGAATGCGACCTGCGCGCTGGAACTTTCACCGACTTTATATGCAACAGCTTCATGTCG	3000
Db	3189	TTCCGGAATGCGACCTGCGCGCTGGAACTTTCACCGACTTTATATGCAACAGCTTCATGTCG	3248
Qy	3001	TGTTCCGAGTGTCTTGCGGAGATGATGAGTCCATGTTGGGACTGCAATGATGTCGTGGCGG	3060

D	3249	TGTTCCGGGAGTCTCTCGGAGAAATGATTCGATGTCATGTGAGCACTGCATGTACGTGGGCG	3308
Q	3061	ATGTCCTGTGCATTTCCCTTCTTCTTGGCCACCGTTGTCAATCGCAATCTTGTGGTACTTA	3120
D	3309	ATGTCGTGTGATTTCCCTTCTTCTTGGCCACCGTTGTCAATCGCAATCTTGTGGTACTTA	3368
Q	3121	ACCTTTCTTAGCCTTGCTTTTGTCAAATTTGGCTCATCTAGCTTATCAGGCGCCGACTG	3180
D	3369	ACCTTTCTTAGCCTTGCTTTTGTCAAATTTGGCTCATCTAGCTTATCAGGCGCCGACTG	3428
Q	3181	CCGATTAACGATACGAATAAATATAGCCGAGGCTTCAATCGAATTGGCCGATTTAAAGTT	3240
D	3429	CCGATTAACGATACGAATAAATATAGCCGAGGCTTCAATCGAATTGGCCGATTTAAAGTT	3488
Q	3241	GGGTTTAAGCCTTAATTTTGTCTGATTTGTTTCAAGTTAATACGTAACAAATTTGACAAATCAA	3300
D	3489	GGGTTTAAGCCTTAATTTTGTCTGATTTGTTTCAAGTTAATACGTAACAAATTTGACAAATCAA	3548
Q	3301	TAAATGATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTTGAGCGA-----	3355
D	3549	TAAATGATCAACCATCAGGTGAGAGGACCAACAGATCAGTTGGATTTGAGCGA-----	3608
Q	3356	-----AAGACATGCTGACAAAGCACTGAGCTGGGCGACG	3390
D	3609	AAGCGTTTGTGTTGTATATCTGCAGAGCATGTGTGCAAGCAACTGAGCTGGGCGACG	3668
Q	3391	ACGAGATCTCGCCGACGGCCTCATCAAGAGGGGATTCAGAGACAGCAACGCAATCTGAGG	3450
D	3669	ACGAGATCTCGCCGACGGCCTCATCAAGAGGGGATTCAGAGACAGCAACGCAATCTGAGG	3728
Q	3451	TGGCCATCGGGAGATCGATGGAATTCACGATACACGGCCGACTGAAAGAACAAACGCGCA	3510
D	3729	TGGCCATCGGGAGATCGATGGAATTCACGATACACGGCCGACTGAAAGAACAAACGCGCA	3788
Q	3511	AGAAATCCAAATATATTAATTAACGCAACGATGATTGGCACTCAATTAAACCAACAAACA	3570
D	3789	AGAAATCCAAATATATTAATTAACGCAACGATGATTGGCACTCAATTAAACCAACAAACA	3816
Q	3571	ATAGACTGGAACACGAGCTAAACCATAGAGGTTGTCTTACAGAGACGACGACCTGCCA	3630
D	3817	-----GGACGACGACACTGCCA	3833
Q	3631	GCATTAACTCATATGTGTAGCCATTAAGATTCGACCAATTCGAAGAGAGGCCACAAGGGCA	3690
D	3834	GCATTAACTCATATGTGTAGCCATTAAGATTCGACCAATTCGAAGAGAGGCCACAAGGGCA	3893
Q	3691	GCGCCGAGACGATGAGAGGGCGAGAGGACGCGACGCCAGCAAGAGAGATTAGGCTCG	3750
D	3894	GCGCCGAGACGATGAGAGGGCGAGAGGACGCGACGCCAGCAAGAGAGATTAGGCTCG	3953
Q	3751	ACGAGGAACCTGACGAGAGGGCGCAATGCGAGAGAGGGCCGCTGACCGGTATATCATTA	3810
D	3954	ACGAGGAACCTGACGAGAGGGCGCAATGCGAGAGAGGGCCGCTGACCGGTATATCATTA	4013
Q	3811	TTTCATGCAACGACGAGATTAATCTCGATGATATTCGACTGATTTGCTGCCCCGACTTGT	3870
D	4014	TTTCATGCAACGACGAGATTAATCTCGATGATATTCGACTGATTTGCTGCCCCGACTTGT	4073
Q	3871	ACTATAGAAATTTCCGATCTTAGCCCGGTGACGATGACTCGCCGTTCTGGCAAGATGGG	3930
D	4074	ACTATAGAAATTTCCGATCTTAGCCCGGTGACGATGACTCGCCGTTCTGGCAAGATGGG	4133
Q	3931	GGAAATTTAGACGTGAAAATTTTTCGAATTAATTGAATAAATAATTTTGAACAAGCTGTTA	3990
D	4134	GGAAATTTAGACGTGAAAATTTTTCGAATTAATTGAATAAATAATTTTGAACAAGCTGTTA	4193
Q	3991	TCACTATGATTTTAAATGAGTACCTTAGCCTTGGCATTAAGAGATGTACATCTGCCACAA	4056
D	4194	TCACTATGATTTTAAATGAGTACCTTAGCCTTGGCATTAAGAGATGTACATCTGCCACAA	4253
Q	4051	GACCCATCTCGACGATATTTTATATCTATATATGACAGAAATATTTACGGTTATATCTCT	4110
D	4254	GACCCATCTCGACGATATTTTATATCTATATATGACAGAAATATTTACGGTTATATCTCT	4313

QY	4111	TGGAATGTTAATCAAGTGGTGGCGTGGCTTCAAAAGTGAAGCTTCAACCAAGCGGCT	41.77
Db	4314	TGGAAAAGTTAATCAAGTGGTGGCGTGGCTTCAAAAGTGAAGCTTCAACCAAGCGGCT	43.73
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Db	4374	GTTGGCTCGAATTCGATGTCATGCTATCGCTTATCAACTTCGTTGCTTCACTGTTG	44.33
QY	4231	GAGCTGGTGTAATTCAGGCTTCAAGCTATGCGAAGCTTAAAGCACTAAGCCACTAC	42.90
Db	4434	GAGCTGGTGTAATTCAGGCTTCAAGCTATGCGAAGCTTAAAGCACTAAGCCACTAC	44.93
QY	4291	GTCGCATGTCCCGATCAGAGGCGATGAGGGTCGCTTAATGCGCTGGTCAAGCTATAC	43.50
Db	4494	GTCGCATGTCCCGATCAGAGGCGATGAGGGTCGCTTAATGCGCTGGTCAAGCTATAC	45.53
QY	4351	CGTCCATCTTCATATGTCATATGCTATGCTAATATTTTGGCTAATTTTGGCTAATG	44.10
Db	4554	CGTCCATCTTCATATGCTATGCTATGCTAATATTTTGGCTAATTTTGGCTAATG	46.13
QY	4411	GTTGAACGCTTTTGTGCTGGAATAATTTTAAAGTCGAGGACATGAATGGCACGACTCA	44.70
Db	4614	GTTGAACGCTTTTGTGCTGGAATAATTTTAAAGTCGAGGACATGAATGGCACGACTCA	46.73
QY	4471	GCCACGAGATCATACAAATCGCAATCGCTCGAGACGAGAACTACACGTGGTGAAAT	45.30
Db	4674	GCCACGAGATCATACAAATCGCAATCGCTCGAGACGAGAACTACACGTGGTGAAAT	47.33
QY	4531	CAGCAATGAATTTTGATCATTAGTAAAGCGTATCTGTGCTTTCCAAATGGCCACT	45.90
Db	4734	CAGCAATGAATTTTGATCATTAGTAAAGCGTATCTGTGCTTTCCAAATGGCCACT	47.93
QY	4591	TCAAAGCTGATACAAATCATGAACGATGCTATCGATTCCAGAGGTGACAAAGAAC	46.50
Db	4794	TCAAAGCTGATACAAATCATGAACGATGCTATCGATTCCAGAGGTGACAAAGAAC	48.53
QY	4651	CAATTCGTGAACCGAACATCTACATGTAATTTTGTGATTTCTTCACTCATATTTGGAT	47.10
Db	4854	CAATTCGTGAACCGAACATCTACATGTAATTTTGTGATTTCTTCACTCATATTTGGAT	49.13
QY	4711	CGTTTTCACCTCAATCTGTCACTGGTGTGTTATCATTTGAATTTTAAATGAGCAAAAGA	47.70
Db	4914	CATTTTTCACCTCAATCTGTCACTGGTGTGTTATCATTTGAATTTTAAATGAGCAAAAGA	49.73
QY	4771	AAAAAGCAGTGGATCATTAAGAAATGTTCATGACAGAAATCAGAAAAAGTACTATATG	48.30
Db	4974	AAAAAGCAGTGGATCATTAAGAAATGTTCATGACAGAAATCAGAAAAAGTACTATATG	50.33
QY	4831	CTATGAAAAAATGGGCTCTAAAAAACATTTAAAGCAATCCAAAGCACAAGGTGGCGAC	48.90
Db	5034	CTATGAAAAAATGGGCTCTAAAAAACATTTAAAGCAATCCAAAGCACAAGGTGGCGAC	50.93
QY	4891	CACAAGCAATAGTCTTTGAAATAGTAAACGATTAAGAAATTCGATTAATCATTTATGTTAT	49.56
Db	5094	CACAAGCAATAGTCTTTGAAATAGTAAACGATTAAGAAATTCGATTAATCATTTATGTTAT	51.53
QY	4951	TGATTTGCTGAACATGTTCAACAGAACCCCTCGATTCGTTAGAGCGCGGAGACAGTATA	50.10
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QY	5011	ACGCGGCTCTAGACATCTCAATGCGAATTCGTATGTTATTTTCAGTTCGAAATGCTAT	50.70
Db	5214	ACGCGGCTCTAGACATCTCAATGCGAATTCGTATGTTATTTTCAGTTCGAAATGCTAT	52.73
QY	5071	TAAAAATATCGCTTTAGCATATCACTATTTTATGAGCCATGAAATTTATTTATGATGAG	51.33
Db	5274	TAAAAATATCGCTTTAGCATATCACTATTTTATGAGCCATGAAATTTATTTATGATGAG	53.33
QY	5131	TAGTTGTCAATTTTAAACATCTTAAGGCTTGTAACCTAAGGAAATTAATCGAAGATCTTCG	51.90
Db	5334	TAGTTGTCAATTTTAAACATCTTAAGGCTTGTAACCTAAGGAAATTAATCGAAGATCTTCG	53.93

QY	5191	TCGTCCCGA	CCTGCTCGG	AGTGGTGGTGGCGTATGGCGA	AAAGTGGGCGCTGCTCTTGATCGTGG	5250
Db	5394	TGTCGCCCA	CCCTGTCTCGG	AGTGGTGGTGGCGA	AAAGTGGGCGCTGCTCTTGATCGTGG	5453
QY	5251	TGAAGGAGC	CAAGGGCA	TTGGGA	CACTGCTTGGCGGTGGCCANTGTCGTCGCGGACC	5310
Db	5454	TGAAGGAGC	CAAGGGCA	TTGGGA	CACTGCTTGGCGGTGGCCANTGTCGTCGCGGACC	5513
QY	5311	TGTTCAAC	ATCTGCTGCTGTCTGTTCTCTG	ATCATTTGATCTTTTGGCA	ATTTTTCGGCATGT	5370
Db	5514	TGTTCAAC	ATCTGCTGCTGTCTGTTCTCTG	ATCATTTGATCTTTTGGCA	ATTTTTCGGCATGT	5573
QY	5371	CGTTCTTCA	TGCACTGA	AGGAGGAAGCGGCA	TTTAAACGCTTCAACATTCAAGACT	5430
Db	5574	CGTTCTTCA	TGCACTGA	AGGAGGAAGCGGCA	TTTAAACGCTTCAACATTCAAGACT	5633
QY	5431	TTGGCACA	GACATGATCCTGCTCTTTTCA	ATGTGCACTCAACGCGGTTGGGATGGTGTAC		5490
Db	5634	TTGGCACA	GACATGATCCTGCTCTTTTCA	ATGTGCACTCAACGCGGTTGGGATGGTGTAC		5693
QY	5491	TGGA	CGCATTATCATATG	AGGAGGATCGATCCACC	CGACAGCGACAAGAGGCTTTCGG	5550
Db	5694	TGGA	CGCATTATCATATG	AGGAGGATCGATCCACC	CGACAGCGACAAGAGGCTTTCGG	5753
QY	5551	GCAATTTG	TGTTCACCGACCGTTGG	AATPACGTTTCTCTCTCATACCTAGTTATACCT		5610
Db	5754	GCAATTTG	TGTTCACCGACCGTTGG	AATPACGTTTCTCTCTCATACCTAGTTATACCT		5813
QY	5611	TTTTGAT	TGTTATTAATATG	TATCATTTGCTGTCACTTCTGGAA	ACTATAGTCAAGCCACCG	5670
Db	5814	TTTTGAT	TGTTATTAATATG	TATCATTTGCTGTCACTTCTGGAA	ACTATAGTCAAGCCACCG	5873
QY	5671	AGGACGT	CAAGAGGGGTCTAAC	CCGACGACGACTACGATGATCTATAGATCTTGGCAGC		5730
Db	5874	AGGACGT	CAAGAGGGGTCTAAC	CCGACGACGACTACGATGATCTATAGATCTTGGCAGC		5933
QY	5731	AATTGAT	TCGGAGGGCA	CCCAAGTACATACGCTATGATCAGCTGTCCGAATTCCTGACG		5790
Db	5934	AATTGAT	TCGGAGGGCA	CCCAAGTACATACGCTATGATCAGCTGTCCGAATTCCTGACG		5993
QY	5791	TACTGGA	ACCCCGCTG	CAGATCCCAACCGA	AAAGTACATATTCATGATGACA	5850
Db	5994	TACTGGA	ACCCCGCTG	CAGATCCCAACCGA	AAAGTACATATTCATGATGACA	6053
QY	5851	TACCAT	CTGTGCGG	GTGACCTCATGTGTCGATCCTGTGAGCGCCCTTACGAAG		5910
Db	6054	TACCAT	CTGTGCGG	GTGACCTCATGTGTCGATCCTGTGAGCGCCCTTACGAAG		6113
QY	5911	ACTTCTT	TGCGCGGAAGGCA	ATCCGATAGAGAGACGGGTGAGATTGGTAGATAGACGG		5970
Db	6114	ACTTCTT	TGCGCGGAAGGCA	ATCCGATAGAGAGACGGGTGAGATTGGTAGATAGACGG		6173
QY	5971	CCCGC	CCGGAATACGAGAGGCTTACGAGCCGCTCTCATCA	CGCTGTGCGCTGACGCTGAGG		6030
Db	6174	CCCGC	CCGGAATACGAGAGGCTTACGAGCCGCTCTCATCA	CGCTGTGCGCTGACGCTGAGG		6233
QY	6031	AGTACTG	GCCCGGTATTCACAGACG	CTGCGGAACACAAAGCGCGCGACGAGAG		6090
Db	6234	AGTACTG	GCCCGGTATTCACAGACG	CTGCGGAACACAAAGCGCGCGACGAGAG		6293
QY	6091	GTGGGT	CTTTTGAAGCGCGATACGATCATATG	AGCGGTGATTCGGGATCCGCGGAC		6150
Db	6294	GTGGGT	CTTTTGAAGCGCGATACGATCATATG	AGCGGTGATTCGGGATCCGCGGAC		6353
QY	6151	CGGCGCC	CGGATGAAACGACGCGCGATGCGCCCGCTGTGAGATGGTATGTTAACG			6210
Db	6354	CGGCGCC	CGGATGAAACGACGCGCGATGCGCCCGCTGTGAGATGGTATGTTAACG			6413
QY	6211	GTA	CTGCAAGAGAGCTGCGATGCGATGAGATGTAATATGATCCGGGTAGAGATG			6270
Db	6414	GTA	CTGCAAGAGAGCTGCGATGCGATGAGATGTAATATGATCCGGGTAGAGATG			6473
QY	6271	CAGCGCG	CGCGACAGACAGACGACGCGCGCGCGCGCGGACGACGACGCGCGGAA			6330

DB	6474	CAGCGCCGCGCGCAGACAGACAGAGAGCGCGCGCGAGCAGCAGCGCGGAA	6533
Qy	6331	GTCCCGAGCGGGGTAGCGCGCGGAGCAGACGCGCGTTCTCTGCGAGAGCGAGGGTTGC	6390
Db	6534	GTCCCGAGCGGGTAGCGCGCGGAGCAGACCGCGCTTCTCTGAGAGCGACCGGGTTGC	65933
Qy	6391	TGACGAGAACCGCGCCACAGAGGTGTGATCACTCGCGATCGCCGAGCATCACTCGCGCA	6450
Db	6594	TGACGAGAACCGCGCCACAGAGGTGTGATCACTCGCGATCGCCGAGCATCACTCGCGCA	66533
Qy	6451	CGGCGGATGTCTGAGCCAGCGCTTGCCCCCTTCGAAGATGCAACGAGATTAAGTCT	6510
Db	6654	CGGCGGATGTCTGAGCCAGCGCTTGCCCCCTTCGAAGATGCAACGAGATTAAGATG	6713
Qy	6511	AG 6512	
Db	6714	AG 6715	
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ACCESSION	CO593262		
VERSION	CO593262.1	GI:41650821	
KEYWORDS			
SOURCE			
ORGANISM			
	Drosophila sp.		
	Drosophila sp.		
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
	Ephydroidea; Drosophilidae; Drosophila.		
REFERENCE			
AUTHORS	1		
TITLE	Venter,J.C., Adams,M., Li,P.W. and Myers,B.W.		
JOURNAL	Detection kits, such as nucleic acid arrays, for detecting the		
	expression of 10,000 or more Drosophila genes and uses thereof		
	Patent: WO 0171042-A 21020 27-SEP-2001;		
	PE Corporation (NY) (US)		
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	/db_xref="taxon:7242"		
ORIGIN			
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Best Local Similarity	97.9%; Pred. No. 0;		
Matches 6355; Conservative	0; Mismatches 34; Indels 105; Gaps 2;		
Qy	1	TC TAGACGTTGGCGGCATAGCAATGACAGAAAGTTCCGACTCGATATCTGAGAGAAAC	60
Db	109	TCTCATCTGTGGCGCGATAGACATGACAGAAAGTTCCGACTCGATATCTGAGAGAAAC	168
Qy	61	GCAGTTGTTCCGTCCTTTACCGCGCAATGATGTGGCAATGAGCAACAGCATTTGCCG	120
Db	169	GCAAGTTGTTCCGTCCTTTACCGCGCAATATTTGTGCAATGAGCAACAGCATTTGCCG	228
Qy	121	CTGAACATGAAAACAGAGAGCTGGAAAAGAAAGAGAGCGGAGGAGGTGCCGAT	180
Db	229	CTGAACATGAAAACAGAGAGCTGGAAAAGAAAGAGAGCGGAGGAGGTGTTAATCT	288
Qy	181	ATGATCGCAGAAAAAACAAAAAGAAATCCGATATGATGACGAGACGAGATTAAGTC	240
Db	289	ATTGTTGCCCAACCATTTCTGTGAGATCCGATATGATGACGAGACGAGATTAAGTC	348
Qy	241	CACAACCGGATCTACACTTGAACAGAGGTGCAATAACCTGTTGATTCAGAGGACGCT	300
Db	349	CACAACCGGATCTACACTTGAACAGAGGTGCAATAACCTGTTGATTCAGAGGACGCT	408
Qy	301	TCCGCGCGGAATTGGCTCTCACTCTTCGAGATATGATCCCTACTACAGCAATGAC	360
Db	409	TCCGCGCGGAATTGGCTCTCACTCTTCGAGATATGATCCCTACTACAGCAATGAC	468

QY 361 TGACATTCGATGTTGTAAGCAAGAAAGATATTTTCCTTTCTGCATCAAAAGCA 420  
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Db 469 TGACATTCGATGTTGTAAGCAAGAAAGATATTTTCCTTTCTGCATCAAAAGCA 528  
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QY 421 TGTGATGCTGCATTCATTCATCCGATACGTGTGTGGCCATTACATTTAGTCATC 480  
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QY 481 CATTAATTTCCCATTCATCATCACCAATTCCTGCTCACTGATCTGATGATATC 540  
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Db 589 CATTAATTTCCCATTCATCATCACCAATTCCTGCTCACTGATCTGATGATATC 648  
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QY 541 CGACAAAGCCCAAGCTTGAATGCACTGAGGTGATATTCACCGAATCTACATTTGAAT 600  
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QY 661 CAGGAAATGGCTGATCTGATGATATAGCTTTAGCTTATGTACCATGGTATAGATT 720  
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QY 721 TAGGTAATCTAGCAAGCCCTGCGAAAGTTTAAAGGCTGCGAGGCTTTAAACCGTAGCCA 780  
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Db 829 TAGGTAATCTAGCAAGCCCTGCGAAAGTTTAAAGGCTGCGAGGCTTTAAACCGTAGCCA 888  
| | | | |  
QY 781 TTGGGCAAGGCTTGAAGAACATGTCGGGCGCCGTCATGCAATCGTGAAGATCTGCGCG 840  
| | | | |  
Db 889 TTGGGCAAGGCTTGAAGAACATGTCGGGCGCCGTCATGCAATCGTGAAGATCTGCGCG 948  
| | | | |  
QY 841 ATGTGATTAATCTGACCAATGTTCTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900  
| | | | |  
Db 949 ATGTGATTAATCTGACCAATGTTCTCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1008  
| | | | |  
QY 901 ATATGAGCGGTCTCAACCGAAGATGCAATCAAGAGTTCCCGCTGGAAGGTTCCGCGGCGCA 960  
| | | | |  
Db 1009 ATATGAGCGGTCTCAACCGAAGATGCAATCAAGAGTTCCCGCTGGAAGGTTCCGCGGCGCA 1068  
| | | | |  
QY 961 ATTCGACCGAAGAACTGGGACTATCAATCGCAATAGCTCCCAATTTGGTATTTCCGAGG 1020  
| | | | |  
Db 1069 ATTCGACCGAAGAACTGGGACTATCAATCGCAATAGCTCCCAATTTGGTATTTCCGAGG 1128  
| | | | |  
QY 1021 ACGAGGCGATCTCAATTCCTGATGCGCAATATATTCGGTGTGGGCGCAATGCGACACG 1080  
| | | | |  
Db 1129 ACGAGGCGATCTCAATTCCTGATGCGCAATATATTCGGTGTGGGCGCAATGCGACACG 1188  
| | | | |  
QY 1081 ATTACGTGTGCTGACAGGGGTTTGTGCGAATCGGAATTAATGCTACACAGCTTCGATT 1140  
| | | | |  
Db 1189 ATTACGTGTGCTGACAGGGGTTTGTGCGAATCGGAATTAATGCTACACAGCTTCGATT 1248  
| | | | |  
QY 1141 CGTTGCGATGAGGCTTTCTGTCCGCTTCGCGCTGATGACACAGAGCTTTCTGGAGATC 1200  
| | | | |  
Db 1249 CGTTGCGATGAGGCTTTCTGTCCGCTTCGCGCTGATGACACAGAGCTTTCTGGAGATC 1308  
| | | | |  
QY 1201 TGTACCAAGCTGTGTGTGGGCGCGCGCGACATGCGACATGCTGTCTTTATATCTATCA 1260  
| | | | |  
Db 1309 TGTACCAAGCTGTGTGTGGGCGCGCGCGACATGCGACATGCTGTCTTTATATCTATCA 1368  
| | | | |  
QY 1261 TCTTCCTAAGTTCATTTCTATCTGTGAAATTTGATTTTGGCCATTTGTCATGTCTATG 1320  
| | | | |  
Db 1369 TCTTCCTAAGTTCATTTCTATCTGTGAAATTTGATTTTGGCCATTTGTCATGTCTATG 1428  
| | | | |  
QY 1321 ACGAATTCGAAAGAGGCGCGAAGAAAGAGGCTGCGAAGAGAGGCGATACGTGAG 1380  
| | | | |  
Db 1429 ACGAATTCGAAAGAGGCGCGAAGAAAGAGGCTGCGAAGAGAGGCGATACGTGAG 1488  
| | | | |  
QY 1381 CGGAAGAGCTGCGCGCGCGAAGAGGCGCGAAGAGGCGCGAAGAGGCGCGAAGGCTC 1440  
| | | | |  
Db 1489 CGGAAGAGCTGCGCGCGCGAAGAGGCGCGAAGAGGCGCGAAGAGGCGCGAAGGCTC 1548  
| | | | |  
QY 1441 AGGACGACGCGATGCGGCTGCGCGCGAAGAGGCTGACATCCGGAATGCGCAAGA 1500  
| | | | |

Db 1549 AGGACGACGCGATGCGGCTGCGCGCGAAGAGGCTGACATCCGGAATGCGCAAGA 1608  
| | | | |  
QY 1501 GTCCGACGTAATCTTCATCAGCTATGAGCTATTTGTTGGCGGAGAAAGGCGCAACGATG 1560  
| | | | |  
Db 1609 GTCCGACGTAATCTTCATCAGCTATGAGCTATTTGTTGGCGGCGAAGAGGCGCAACGATG 1668  
| | | | |  
QY 1561 ACAACAAAGAAAGAAATGTCATTTCCGAGCGTCCGAGTGGAGTCCGAGTCCGAGCG 1620  
| | | | |  
Db 1669 ACAACAAAGAAAGAAATGTCATTTCCGAGCGTCCGAGTGGAGTCCGAGTCCGAGCG 1728  
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QY 1621 TTATCAAAAGCAACAGACCTTACACAGACACCAAGCTAACAAAGTTGTAAGTGA 1680  
| | | | |  
Db 1729 TTATCAAAAGCAACAGACCTTACACAGACACCAAGCTAACAAAGTTGTAAGTGA 1788  
| | | | |  
QY 1681 GCACGACATCTTATCTTACCTGCTTCAACGTTTAAATACATGCGAGGGATACGTAAT 1740  
| | | | |  
Db 1789 GCACGACATCTTATCTTACCTGCTTCAACGTTTAAATACATGCGAGGGATACGTAAT 1848  
| | | | |  
QY 1741 CTCACAGTACAGATACGGAACGGAAGTGGCGCTTGTATACCGGATAGCGATCGTA 1800  
| | | | |  
Db 1849 CTCACAGTACAGATACGGAACGGAAGTGGCGCTTGTATACCGGATAGCGATCGTA 1908  
| | | | |  
QY 1801 AGCCATTTGATTTGTCACATATACAGATGCCCCAGACACTTGGCTTATGCGGACGACT 1860  
| | | | |  
Db 1909 AGCCATTTGATTTGTCACATATACAGATGCCCCAGACACTTGGCTTATGCGGACGACT 1968  
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QY 1861 CGAATGCGCTCACCCGATGTCGGAAGAAATGGGGCCATCTATGCCCCGTTACTATG 1920  
| | | | |  
Db 1969 CGAATGCGCTCACCCGATGTCGGAAGAAATGGGGCCATCTATGCCCCGTTACTATG 2028  
| | | | |  
QY 1921 GCAATGAGCTCCGACACCTCATGATACCTGCGATGATCCGGAATATGCTATACCT 1980  
| | | | |  
Db 2029 GCAATGAGCTCCGACACCTCATGATACCTGCGATGATCCGGAATATGCTATACCT 2088  
| | | | |  
QY 1981 CACATGCGATCTACTGCGGCGATGCGGCTGATGAGGCTGACACATGACCAAGAGA 2040  
| | | | |  
Db 2089 CACATGCGATCTACTGCGGCGATGCGGCTGATGAGGCTGACACATGACCAAGAGA 2148  
| | | | |  
QY 2041 GCAATTTGGCGAACCGGCAACACGCAATCAATCAATGAGGCGCGCAATGAGCGGACCA 2100  
| | | | |  
Db 2149 GCAATTTGGCGAACCGGCAACACGCAATCAATCAATGAGGCGCGCAATGAGCGGACCA 2208  
| | | | |  
QY 2101 CCTGTGACACCAATCAACAGCTGATCATGCGACTACGAAATTTGGCTGTGATGCA 2160  
| | | | |  
Db 2209 CCTGTGACACCAATCAACAGCTGATCATGCGACTACGAAATTTGGCTGTGATGCA 2268  
| | | | |  
QY 2161 CGGACGAAGCTGCGAAGATTTAAATCATGACATCTTTTATCGAGCCGCTCCAGAC 2220  
| | | | |  
Db 2269 CGGACGAAGCTGCGAAGATTTAAATCATGACATCTTTTATCGAGCCGCTCCAGAC 2328  
| | | | |  
QY 2221 AAACGGTGTGATTAAGAAAGATGATGATGCTGCTGAAATGACATCATGCAAGAGCGCTG 2280  
| | | | |  
Db 2329 AAACGGTGTGATTAAGAAAGATGATGATGCTGCTGAAATGACATCATGCAAGAGCGCTG 2388  
| | | | |  
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| | | | |  
Db 2389 GTGCGACAGTCCGGCAAGGATGCGGCTGTCTCCGTTACTATTTTCCCAACAGAGACG 2448  
| | | | |  
QY 2341 ATGACAGATGAGGCGGACGTTCAAAAGCAAGGACATCGAAGATCTCAAAAGGATCG 2400  
| | | | |  
Db 2449 ATGACAGATGAGGCGGACGTTCAAAAGCAAGGACATCGAAGATCTCAAAAGGATCG 2508  
| | | | |  
QY 2401 ATGAGTTTGTGTGAGGACTGTTGCTGGGTTTGTGAAATTTCAAGAGTGGATTCG 2460  
| | | | |  
Db 2509 ATGAGTTTGTGTGAGGACTGTTGCTGGGTTTGTGAAATTTCAAGAGTGGATTCG 2568  
| | | | |  
QY 2461 TCAATGCTTCATCCCTTGTGAGCTTTCATCAAGCTGTGATTTGTGTAACACGA 2520  
| | | | |  
Db 2569 TCAATGCTTCATCCCTTGTGAGCTTTCATCAAGCTGTGATTTGTGTAACACGA 2628  
| | | | |  
QY 2521 TGTTCATGGAATGATCAACAGATATGAACAAAGGATGGAACGGGTGCTCAAGATG 2580  
| | | | |

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 Db 2689 GCAACTATTTCTTCCCGCCACCTTTGCCATCGAGGCCACCATGAAGCTAATGGCCATGA 2748  
 Qy 2641 GCCCAAGTACTATTTCCAGAGGGGCTGAAACATTTGACCTTCAATTACGTCGAGCCCTAT 2700  
 Db 2749 GCCCAAGTACTATTTCCAGAGGGGCTGAAACATTTGACCTTCAATTACGTCGAGCCCTAT 2808  
 Qy 2701 CGCTATTGGAACCTGGGACTCGAGGGGTGTCAGGGGTCTGTCCGATTTGGCTTCTTCCAT 2760  
 Db 2809 CGCTATTGGAACCTGGGACTCGAGGGGTGTCAGGGGTCTGTCCGATTTGGCTTCTTCCAT 2868  
 Qy 2761 TGTGCGGTGATTTCAAACTGGCCAAAGTCTTGGCCCACTTAATTACTCATTTGATTA 2820  
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 Qy 2821 TGGGACGACCAATGGGGGCTTTGGGTAACTGACATTTGTACTTGTGCAATTATCATCTTCA 2880  
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 Qy 3001 TGTTCGCGGTGCTCGGGGAAATGAGTCGATCATGAGGACGTCATGACGTCGAGCG 3060  
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 Qy 3061 ATGTCTCGTGAATCCCTTCTTCTTGGCCACCGTGTGATCGGCAATCTGTGACTTA 3120  
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 Qy 3121 ACCTTTTCTTACGCTTGTCTTGTTCGAATTTGGCTCATGACTTATGAGCGCCGACTG 3180  
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 Db 3289 CCGATTAACGATACGAATAAATAGCCGAGGCTTCAATCGAATGGCCGATTTAAAGTT 3348  
 Qy 3241 GGGTTAAGCGTAATATGCTGATTTGTTCAAGTTAATGTAACAATTTGAACAATCAA 3300  
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 Qy 3301 TAAAGTATCAACCATCAGGTGAGAGACCAACCATGATCACTTGGATTGGAGCGA---- 3355  
 Db 3409 TAAAGTATCAACCATCAGGTGAGAGACCAACCATGATCACTTGGATTGGAGCGA 3468  
 Qy 3356 -----AGAGCATGTGACAAAGCAACTGGAGCTGGGCGCAG 3390  
 Db 3469 AAGGCGTTTGTGCTTTATCTGCAAGACATGTGCAACGAACTGGAGCTGGGCGCAG 3528  
 Qy 3391 ACGAGATCTCGCCGACGCGCTCATCAAGAAAGGGATCAAGAGCAGACGCACTGGAG 3450  
 Db 3529 ACGAGATCTCGCCGACGCGCTCATCAAGAAAGGGATCAAGAGCAGACGCACTGGAG 3588  
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 Db 3589 TGGCCATCGGGGATCGATGGAATTCAGATACACGCGCAGCATGAAGAAACAAGCCGA 3648  
 Qy 3511 AGAATCCAAATATCTAATAACGAAGATTTGCACTTAACCAACAAGACA 3570  
 Db 3649 AGAATCCAAATATCTAATAACGAAGATTTGCACTTAACCAACAAGACA 3676  
 Qy 3571 ATAGACTGGAACACGAGCTAAACCATAGAGGTTGTCTTACAGAGCAGACACTGCGCA 3630  
 Db 3677 -----GGACGACGACACTGCGCA 3693

Qy 3631 GCATTAAGTCAATGTTAGCCATTAAGATCGAACCATTTCAAGAGACGAGCCCAAGGCA 3690  
 Db 3694 GCATTAAGTCAATGTTAGCCATTAAGATCGAACCATTTCAAGAGACGAGCCCAAGGCA 3753  
 Qy 3691 GCGCCGAGACGATGAGAGGGGAGAGAAAGCCGACGCGCAGCAAGAGAGATTTAGGTCG 3750  
 Db 3754 GCGCCGAGACGATGAGAGGGGAGAGAAAGCCGACGCGCAGCAAGAGAGATTTAGGTCG 3813  
 Qy 3751 ACGAGAACTGACGAGAGGGGCGAATGCGAGAGGGCGCGCTCGACGCTGATATCATTA 3810  
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 Qy 3811 TTCAATGCAACGACGAGATATATCTCCATGAAATATCCAGCTGATTTGCTGCCCCGATTCG 3870  
 Db 3874 TTCAATGCAACGACGAGATATATCTCCATGAAATATCCAGCTGATTTGCTGCCCCGATTCG 3933  
 Qy 3871 ACTAATGAAGAAATTTCCGATCTTACCGGTGACGATGATCGCCGCTTGGCAAGATGG 3930  
 Db 3934 ACTAATGAAGAAATTTCCGATCTTACCGGTGACGATGATCGCCGCTTGGCAAGATGG 3993  
 Qy 3931 GCAATTTACGACTGAAAATTTTCAATTAATGAAAATTAATTTTGAACAGCTGTTA 3990  
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 Qy 3991 TCACTATGATTTTAATGATGATGCTTACGCTTGGCATTAAGAGATGATCTGCGACAAA 4050  
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 Qy 4051 GACCATATGACGAGATATTTTATTAATGATGATGATGATGATGATGATGATGATGATGAT 4110  
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 Qy 4111 TGAATATGTTAATCAAGTGTGAGCGCTCGGCTTCAAGTGTGATTCACAAAGCGTGT 4170  
 Db 4174 TGAATATGTTAATCAAGTGTGAGCGCTCGGCTTCAAGTGTGATTCACAAAGCGTGT 4233  
 Qy 4171 GTTGGCTGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4230  
 Db 4234 GTTGGCTGATTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4293  
 Qy 4231 GAGCTGTGTGATTTCAAGCTTCAAGACTATGCGAAGCTTAAGAGACTGAGACCACTAC 4290  
 Db 4294 GAGCTGTGTGATTTCAAGCTTCAAGACTATGCGAAGCTTAAGAGACTGAGACCACTAC 4353  
 Qy 4291 GTGCGATGTCGCTATGAGGGCATGAGGGTGTGTTAATGCGCTGCTGTAACGCTATAC 4350  
 Db 4354 GTGCGATGTCGCTATGAGGGCATGAGGGTGTGTTAATGCGCTGCTGTAACGCTATAC 4413  
 Qy 4351 CGTCCATCTTCAATGCTGATTTGCTGATTAATTTTGGCTAATTTTGGCTAATTTTGG 4410  
 Db 4414 CGTCCATCTTCAATGCTGATTTGCTGATTAATTTTGGCTAATTTTGGCTAATTTTGG 4473  
 Qy 4411 GTGTACAGCTTTTGTGGAATAATTTTAAGTCCGAGACATGAATGGCAGAGCTCA 4470  
 Db 4474 GTGTACAGCTTTTGTGGAATAATTTTAAGTCCGAGACATGAATGGCAGAGCTCA 4533  
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 Db 4534 GCCACGAGATCATCAAAATGCAATGCTGCGAGAGCGAGAACTACAAGTGGTAAT 4593  
 Qy 4531 CAGCAATGAATTTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4590  
 Db 4594 CAGCAATGAATTTGATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4653  
 Qy 4591 TCAAGGCTGATCAATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4650  
 Db 4654 TCAAGGCTGATCAATATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4713  
 Qy 4651 CAATTCGTGAACGAAATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4710  
 Db 4714 CAATTCGTGAACGAAATCTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4773



[illegible]

Db	5854	TACTGAGAGCCCGGCTGCGATCCACAAACCGAAGTACAGATCATATCATGTGACACA	5913
QY	5851	TACCCATCTGTCCGGGTGACCTATGTATCTGTGCTCGACATCTCTCGACGCCCTTAACGAAG	5910
Db	5914	TACCCATCTGTCCCGGTGACCTCATGTATCTGACCTTCACATCTTCGACGCCCTTAACGAAG	5973
QY	5911	ACTTCTTTGGCGGGAAGGGCAATCCGATAGAGAGAAGCGGTGATGTGTGAGATAGCGG	5970
Db	5974	ACTTCTTTGGCGGGAAGGGCAATCCGATAGAGAGAAGCGGTGATGTGTGAGATAGCGG	6033
QY	5971	CCGCGCCGATATACGAGAGGCTACGAGGCCGTCTCATCAACGCTGTGGCGTCAAGCTGAGG	6030
Db	6034	CCGCGCCGATATACGAGAGGCTACGAGGCCGTCTCATCAACGCTGTGGCGTCAAGCTGAGG	6093
QY	6031	AGTACTGCGCCCGGCTATATCCAGACAGCTCTGGCGAAAGCACAAAGCGCGCGGAGAGGAG	6090
Db	6094	AGTACTGCGCCCGGCTATATCCAGACAGCTCTGGCGAAAGCACAAAGCGCGCGGAGAGGAG	6153
QY	6091	GTGGTTCCTTTGAGCCGCGATACGGATATGGCGCATGGCGGATGCCGATGCCGAGGAGCC	6150
Db	6154	GTGGTTCCTTTGAGCCGCGATACGGATATGGCGCATGGCGGATGCCGATGCCGAGGAGCC	6213
QY	6151	CGGCGCCCGATGAGACCAACGCAACGCGCATGCCGCCCTGTGTGAGATGTAGTGTAAAC	6210
Db	6214	CGGCGCCCGATGAGACCAACGCAACGCGCATGCCGCCCTGTGTGAGATGTAGTGTAAAC	6273
QY	6211	GTACTGCAAGAAAGAGCTGCCGATGCCGATGAGATTAATGTAAATATGTCGCGGTGAGGATG	6270
Db	6274	GTACTGCAAGAAAGAGCTGCCGATGCCGATGAGATTAATGTAAATATGTCGCGGTGAGGATG	6333
QY	6271	CAGCGCGCGCGGCGACGACAGCAGCAGCGCGCGCGCGCGGACCAACGACGCGGGA	6330
Db	6334	CAGCGCGCGCGGCGACGACGACGACGACGACGCGCGCGCGGACCAACGACGCGGGA	6393
QY	6331	GTCCCGGAGCGGGGTAGCGCGCGCGGACAGACCGCGCTTCTGTGTGAGAGCGACGGTTTCG	6390
Db	6394	GTCCCGGAGCGGGGTAGCGCGCGCGGACAGACCGCGCTTCTGTGTGAGAGCGACGGTTTCG	6453
QY	6391	TGACGAGAAACGCGCACAAAGGTGTATCCATCTGGCGATGGCGAGATCAACGTCCGCGCA	6450
Db	6454	TGACGAGAAACGCGCACAAAGGTGTATCCATCTGGCGATGGCGAGATCAACGTCCGCGCA	6513
QY	6451	CGGCGGATGTCTGA 6464	
Db	6514	CGGCGGATGTCTGA 6527	
RESULT 6			
LOCUS	AR028545	6519 bp	DNA
DEFINITION	Sequence 24 from patent US 5858713.		linear
ACCESSION	AR028545		
VERSION	AR028545.1		GI:5940518
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 6519)		
AUTHORS	Soderlund,D.M. and Ingles,P.J.		
TITLE	Calcium permeable insect sodium channels and use thereof		
JOURNAL	Patent: US 5858713-A 24 12-JAN-1999;		
FEATURES	Location/Qualifiers		
source	1..6519		
ORIGIN	/organism="unknown" /mol_type="unassigned DNA"		
Query Match	94.6%;	Score 6163.8;	DB 6; Length 6519;
Best Local Similarity	97.7%;	Pred. No. 0;	
Matches 6339;	Conservative	0; Mismatches	12; Indels 138; Gaps 3
QY	24	ATGACGAAGAAATTCGCAGCTCATATCTGAGAGAAACGACAGTTGTTCCTCCCTTTAAC	83



Db 1 ATGAGAGAAAGATTCGAGCTCGATATCTGAGAGAAACGAGATTGTCCGTCCCTTAC 60  
Qy 84 CGCGATCATTTGGTGCAGAAATCGAACAGCATTCGCCCTGAAACATGAAAGAGAGAG 143  
Db 61 CGCGAATCATTTGGTGCAGAAATCGAACAGCATTCGCCCTGAAACATGAAAGAGAGAG 120  
Qy 144 CTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203  
Db 121 CTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
Qy 204 GAAATCCGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
Db 181 GAAATCCGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240  
Qy 264 CAGGCTGCGCAATACCTGTTGATTCGATTCGAGGAGAGAGAGAGAGAGAGAGAGAG 323  
Db 241 CAGGCTGCGCAATACCTGTTGATTCGATTCGAGGAGAGAGAGAGAGAGAGAGAGAG 300  
Qy 324 CCTCTCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 383  
Db 301 CCTCTCGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360  
Qy 384 GGAAGAGATATTTTTCGCTTTTCGATCAAAAGAGATGAGATGAGATGAGATGAGATG 443  
Db 361 GGAAGAGATATTTTTCGCTTTTCGATCAAAAGAGATGAGATGAGATGAGATGAGATG 420  
Qy 444 CGGATACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 503  
Db 421 CGGATACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 480  
Qy 504 ACCCAATTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 563  
Db 481 ACCCAATTCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 540  
Qy 564 ACTGAGGATATTCACCGGAGATCTACACATTTGATGAGATGAGATGAGATGAGATG 623  
Db 541 ACTGAGGATATTCACCGGAGATCTACACATTTGATGAGATGAGATGAGATGAGATG 600  
Qy 624 GGTTCATTTATATGCGGCTTACGATCTTATGAGATGAGATGAGATGAGATGAGATG 683  
Db 601 GGTTCATTTATATGCGGCTTACGATCTTATGAGATGAGATGAGATGAGATGAGATG 660  
Qy 684 GTAATAGCTTATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 743  
Db 661 GTAATAGCTTATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
Qy 744 ACGTTAGGAGTGTGTCGAGCGCTTAAACCGTAGCCATTTGCGAGGCTTGAAGACATC 803  
Db 721 ACGTTAGGAGTGTGTCGAGCGCTTAAACCGTAGCCATTTGCGAGGCTTGAAGACATC 780  
Qy 804 GTGCGCGCGCTCATCGATCGGTGAGAGATCTGCGCATGATGATGATGATGATGATG 863  
Db 781 GTGCGCGCGCTCATCGATCGGTGAGAGATCTGCGCATGATGATGATGATGATGATG 840  
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Db 841 TCCCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTCGCTGTC 900  
Qy 924 TGCATCAAGAGATTCGCGCTGAGCGGTTCTTGCGGCAATCTGACGAGAACTGGGAC 983  
Db 901 TGCATCAAGAGATTCGCGCTGAGCGGTTCTTGCGGCAATCTGACGAGAACTGGGAC 960  
Qy 984 TATCAATCGCAATAGCTCAATTTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1043  
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Qy 1044 TGCGGCAATATATCGCGTGGCGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1103  
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Qy 1104 GGTTCGATCGCAATATATGCTGACACGAGCTTCGATTCGATGAGAGAGAGAGAGAG 1163

Db 1081 GGTTCGATCGCAATATATGCTGACACGAGCTTCGATTCGATGAGAGAGAGAGAGAG 1140  
Qy 1164 GGTTCGCGCTGATGACACAGAGATTCGAGAGATCTGATACAGCTGTGTTGCGGCC 1223  
Db 1141 GCTTCGCGCTGATGACACAGAGATTCGAGAGATCTGATACAGCTGTGTTGCGGCC 1200  
Qy 1224 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1283  
Db 1201 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260  
Qy 1284 GTGAATTTGATTTTGGCATTGTTGCAATGCTGATGATGATGATGATGATGATGATGAT 1343  
Db 1261 GTGAATTTGATTTTGGCATTGTTGCAATGCTGATGATGATGATGATGATGATGATGAT 1320  
Qy 1344 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403  
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Qy 1404 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463  
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Qy 1524 TATGAGCTATTTGTTGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583  
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Qy 1704 GGTTCACCGTTTAAATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1763  
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RESULT 7  
MDPARA

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voltage-sensitive sodium channel.  
KEYWORDS Musca domestica (house fly)  
SOURCE Musca domestica  
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Muscoidea; Muscidae; Musca.  
REFERENCE  
AUTHORS Williams M.S., Martinez-Torres D., Hick C.A. and Devonshire A.L.  
TITLE Identification of mutations in the housefly para-type sodium  
channel gene associated with knockdown resistance (kdr) to  
pyrethroid insecticides  
Mol. Gen. Genet. 252 (1-2), 51-60 (1996)  
JOURNAL  
MEDLINE 8804403  
PubMed 96397509  
2 (bases 1 to 6899)  
REFERENCE  
AUTHORS Williams M.S.  
TITLE Direct Submission  
Submitted (15-MAR-1996) M.S. Williams, IACR-Rothamsted,  
Department of Biological & Ecological Chemistry, Harpenden,  
Hertfordshire, AL5 2JQ, UK  
location/Qualifiers  
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## ORIGIN

Query Match 69.2%; Score 4508.2; DB 3; Length 6899;  
Best Local Similarity 82.3%; Pred. No. 0;  
Matches 5360; Conservative 0; Mismatches 1003; Indels 150; Gaps 10;

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 Musca domestica  
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 house fly strains  
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 96245434  
 8814780  
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 Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.  
 Direct Submission  
 Submitted (17-OCT-1995) Dave M. Soderlund, Entomology, New York  
 State Agricultural Experiment Station, Cornell University, Castle  
 Street, Geneva, NY 14456, USA  
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 Ingles,P.J., Adams,P.M., Knipple,D.C. and Soderlund,D.M.  
 Direct Submission  
 Submitted (15-JUN-1997) Dave M. Soderlund, Entomology, New York  
 State Agricultural Experiment Station, Cornell University, Castle  
 Street, Geneva, NY 14456, USA  
 Nucleotide and protein update by submitter  
 On Jan 18, 1997 this sequence version replaced gi:1304398.  
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## ORIGIN

Query Match 68.3%; Score 4447.8; DB 3; Length 6318;  
 Best Local Similarity 82.0%; Pred. No. 0;  
 Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;

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ACCESSION AR028529  
VERSION AR028529.1 GI:5940502  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6318)  
AUTHORS Soderlund, D.M. and Ingles, P.J.  
TITLE Calcium permeable insect sodium channels and use thereof  
JOURNAL Patent: US 5858713-A 1 12-JAN-1999;  
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ORIGIN  
Query Match 68.3%; Score 4447.8; DB 6; Length 6318;  
Best Local Similarity 82.0%; Pred. No. 0;  
Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;

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Best Local Similarity 81.8%; Pred. No. 0;  
Matches 5284; Conservative 0; Mismatches 1013; Indels 162; Gaps 8;

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Db 1 ATGACAAAGATTCGACCTCGATATCTGAGAGAAACGCGATTGTTCCGTCCTTTACC 60
Qy 84 CGCGAATCATTTGGTCAATCGAACACGATTCGCGTGAACATGAAAGAGAGAG 143
Db 61 CGCGAATCATTTGGTCAATCGAACACGATTCGCGTGAACATGAAAGAGAG 117
Qy 144 CTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203
Db 118 CTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148
Qy 204 GAATCCGATATGATGACGAGAGACGAGATGAGAGAGAGAGAGAGAGAGAGAG 263
Db 149 -AGATACATATGATGACGAGAGACGAGATGAGAGAGAGAGAGAGAGAGAG 207
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DB 2281 GATGCTCCACATTCACAGACATCGCCCTCGAATATCTTAAAGGACATGAAATCTTT 2340  
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QY 2529 GCAATGATCAACAAGATATGAACAAAGAGATGAAACGCTGCTCAAGAGTGCATAT 2588  
DB 2461 GCAATGATCATCAACAAGATATCCGAAATTTGAGAGAGTGTGAAAGTGTGATAT 2520  
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DB 2641 GAATTTGGGCTGAGGGGTCTCAGAGGCTGTCTGATTTGAGAGTGTCTGCTGCT 2700  
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QY 2949 GGGACCTGCGCGCTGGAACTTCAACGACCTTATGACAGCTTCATGATGCTTCCG 3008  
DB 2881 CATGATTTACCGCGCTGGAACTTCAACGACCTTATGACAGCTTCATGATGCTTCCG 2940  
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QY 3249 CGTATATTGCTGATTTGTTCAAGTTAATACCTAACAATTTGACAAATCAATTAAGTAT 3308  
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QY 4026 TTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4085  
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DB 4162 ACATGCGCGCGCTTAAGGCAATGCGTGTCTGTAGAGGAGGCTATGAAAGTTGCT 4221  
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Oy	4446	GAGGCATGAATGGACAGAAAGTCACGACAGATCATACCAATTCGAATGCTCGAG	4505
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Oy	4506	AGCGGAATCTACAGTGGGTGAATTCAGCAATGAAATTTCCATCATGTAGTAAAGCGTAT	4565
Db	4402	AGTGAACCTACACCTGGGAAATTCGGCAATGAACCTTCGATCACTGTAGTAAATGCCAT	4461
Oy	4566	CTGTGCTCTTTTCCAAATGGCCACCTTCAAAAGGCTGATACAAATCATGAAGATCTATC	4625
Db	4462	CTGTGCTAATTTCCAAATGGCCACCTTTAAAGGCTGATTCGAATTTAAAGATGCCATT	4521
Oy	4626	GATTCACGAGAGTGGACAAAGCAACCAATTCGTGAAGCAACATCTACATGATTTATAT	4685
Db	4522	GATTCACGAGAGTGGACAAAGCAGCCGATCCGAAACCAATATCTACATGATTTATAT	4581
Oy	4686	TTCCGATTCCTCATATATTTTGGATTCCTTTTCACTCAATCTGTTCATTTGGTATTC	4745
Db	4582	TTCCGATTCCTCATATATTTTGGATTCATTTTTCACATCAATCTGTTCATTTGGTATTC	4641
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Oy	4926	AAATTCGATTAATCATATATGTTATCTAATGGTCTGAACATGTTCAACATGACCTCGAT	4985
Db	4822	AAATTCGATTAATCATATATGTTATCTAATGGTCTGAACATGTTCAACATGACCTCGAT	4881
Oy	4986	CGTTACGATGCGTGGACACGATTAACCGCGTCTTAGACTATCTCAATGCCATATTGCTA	5045
Db	4882	CGTTACGATGCGTGGACACCAAGATGTCCTGCAAAATCTCAATGGGATATTGCTA	4941
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Db	4942	GTATATTTCAAGTTCGGAATGTCATTAATAAATTTCCGTTACGATATCACTATTTCAA	5001
Oy	5106	GAGGCATGGAATTTATTTGAATGATGATGATGCAATTTATTCACATTAAGTCTGTACTT	5165
Db	5002	GAGGCATGGAATTTATTTGAATGATGATGATGCAATTTATTCACATTAAGTCTGTACTT	5061
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Db	5062	AGCGATATTAATCGAAGATTAAGTGTGCGCGACCTCTCTCCGAGTGTGAGAGTGGCC	5121
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Db	5122	AAAGTGGGCGGTGCTCTGCTGTTTATGTCAAAGGATGTCAAAGGATTCGGAAGCTGCTGTC	5181
Oy	5286	GCGTTGGCGAATGTCGTCGCGCGGCGCTGTTCAACATGCGCGTGCCTGTCCTGTATG	5345
Db	5182	GCGTTGGCGAATGTCGTCGCGCGCTCTTATTAACAATGTGTCGTGTCGTTTGTGTATG	5241
Oy	5346	TTCAATCTTTGGCAATTTTGGGATGTCGTTCTTCAATGACGTAAGAGAAAGCGGCAAT	5405
Db	5242	TTCAATCTTTGGCAATTTTGGGATGTCCTTTCTTAATGATATCAAGAAAGAGCGGCAAT	5301
Oy	5406	AAAGATGTCATCAACTTCAAGACTTTTGGCAAGATGATCTGCTCTTCAAGATGTCG	5465

Db	5302	AATGCTGTCTAATTTTAAGA	CAATTGGCCAAAGTATGATATTGCTGTTCCAGATGCT	5368	
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Db	5362	AACCTAGCCGGTTGGAGTGT	GTGTGTAGATCCCATTTATCATATGAGAAAGATTGGGATCCA	5421	
QY	5526	CCCGACACCGACAAGGCTAT	CCGCGCAATTGTGGTTACGCGACCGTTGGAAATAACGTTT	5585	
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QY	5586	CTCCCTCATATCCATGATTAT	AGCTTTTGTATGATTTATATATGATCATTTGCGTCAAT	5645	
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Db	5662	GACCAAGCTGTCCGAGTTCT	TGGAGCGTGTGGAGCCCGCTGCGAGATCCACAACCCGAC	5721	
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Db	5722	AAGTACAAGATCATATCGAT	GGAATACGCGATATGTGCGGCGCAGATGATATATCTGTGT	5781	
QY	5886	GACATCTCTGACGCGCTTA	CGAAGACTTCTTTGCGCGGAAGGGCAATCCGATATGAGAG	5945	
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QY	5946	ACGGGTGAGATTGTGTGAG	ATGACGCGCCCGCCCGGATATCGAGAGGCTACAGAGCCGCTCTCA	6005	
Db	5842	ACGGGTGAAATTTGTGTGAG	ATTTGTCGCGCGACCGGACCCGAGGGCTATGATCTCGGTGTGC	5901	
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QY	6066	AAGCACAAGCGCGCGCGG	CGAGGAGGTGTCTTTGAGCCCGATACGGATCATGGCGAT	6125	
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QY	6126	GCGCGGTATCCGGAATGCC	CGGAGGACC	CGCGATGTAAGCAACGACGCGGATGCCGCC	6185
Db	5977	CCACCCCGAGGGGTGTAT	GAGGCGGAGGCGGCTGTGTGCGCAAGATGTGTGCTGAAGGCGGT	6036	
QY	6186	GCTGTGTGAGATGTGTATG	TTAAACGTTATCTGCATACAAAGAGAGTGTGCGGATGTAGAGT	6245	
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QY	6246	AATGTAAATATCTCCGGG	TGAGAGATGACGCGCGCGCGACGACGACGACGACGACGCGCGC	6305	
Db	6097	GGAGCGACATACCCCAAG	ATCCAGATGCCGCGGCAACAGATGTGTGCGACGCGCGCAAT	6156	
QY	6306	GCGCGCGGCGACGACGAG	CGGCGGAATGCCGAGCGGGTATGCGCGCGCGCGACAGACGCGC	6365	
Db	6157	GGTGTGCGGCGCCCTT	AGTCTGAGTGTGTATAGTGTGCGCGAGTAAATGTGCGCGCAACCGGCG	6216	
QY	6366	GTTCTGTGTGAGAGAGCG	AGGGTTGTGTACGAGAAAGGCGCACAGATGATGATCATCATCTG	6425	
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RESULT 11  
AR028530

LOCUS AR028530 6315 bp DNA linear PAT 29-SEP-1999  
DEFINITION Sequence 2 from patent US 5858713.  
ACCESSION AR028530  
VERSION AR028530.1 GI:5940503  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 6315)  
Soderlund, D. M. and Ingles, P. J.  
TITLE Calcium permeable insect sodium channels and use thereof  
JOURNAL Patent: US 5858713-A 2 12-JAN-1999;  
FEATURES  
location/Qualifiers  
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/organism="unknown"  
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Best Local Similarity 81.8%; Pred. No. 0;  
Matches 5284; Conservative 0; Mismatches 1013; Indels 162; Gaps 8;  
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QY 84 CGCGAATCATTTGTCGAATCGAACGCAATTCGCGCTGAACATGAAAAGCAAGAG 143  
DB 61 CGGAAATCATTTGTCGAATCGAACGCAATTCGCGCTGAACATGAAAAGAG 117  
QY 144 CTGGAAGAAAGAGAGCGGAGAGAGAGTCCCGGATATGCTGCGAAGAAAACAAA 203  
DB 118 CTGGAAGAAAGAGAGCGGAGAGAGTCCCGGATATGCTGCGAAGAAAACAAA 148  
QY 204 GAAATCCGATATGATGAGAGAGAGAGATGAGAGTCCACACCGATCTTACCTTGA 263  
DB 149 -AGATACGATATGATGAGAGAGAGATGAGAGTCCACACCGATCTTACCTTGA 207  
QY 264 CAGGCTGCGCAATACCTGTTGATTCGAGGAGGCTTCCCGCGGAATTGGCTCCACT 323  
DB 208 CAGGCTGCGCAATACCTGTTGATTCGAGGAGGCTTCCCGCGGAATTGGCTCCACT 267  
QY 324 CCTCTGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383  
DB 268 CCTCTGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327  
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QY 444 CGGATAGCTGCTGAGGCAATTAATTCATGATGATGATGATGATGATGATGATGATG 503  
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QY 1824 CAGGATCCGAGAGACCTTGCCTATGCGAGATGATGATGATGATGATGATGATGATGATGAT 1883  
DB 1765 CAGGATCCGAGAGACCTTGCCTATGCGAGATGATGATGATGATGATGATGATGATGATGAT 1824

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Db	1825	GAAAGAAATGGGGCCATTAATAGTACCAACCTTACTATTTAAATTTAAGTTCTTAGACATTTCT	18844
QY	1944	TCGTATACCTCGCATCAGTCCCGAATATCGTATACCTCACATGGCGATCTACTCGCGGC	20033
Db	1885	TCATATACCTCGCATCAATCAAGATCTCGTATACATCATGTGGATTTATTTGGGTGGC	19444
QY	2004	ATGGCGTCAATGGGCGTGAACAATGACCAAGAGAGCAAAATTTGGCAACCGCAACACA	20633
Db	1945	ATGGCGGCATATGGGTGGCCAGCAACAATGACCAAAAGAGCAAAATTTGGCAGTCCGCAACACA	20044
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Db	2005	CGCAATCAATCAATGGGTGGTGGCAACCAATGGTGGCAATAGTATACGGCGGTGGTGGTAT	20644
QY	2134	CTCGAT-----CATCGGCACTACGAAAATTTGGCTGGATGGACGGACGAA	2166
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QY	2169	GCTGGCAAGATTTAAACATCATGACCAATCTTTTATCGACCCGTCAGACACAACAACGCTG	2228
Db	2125	GCTGGCAAAATTAACACCAACGACATCTTTTATCGAGCCGTCACAACTCAAAACAGTG	2184
QY	2229	GTTGATATGAAGAATGTGATGGTCTGTAATGACATCATCGAACAGCCGCTGGTCGAC	2288
Db	2185	GTAGACATGAAGAAGTTATGGTCTTAATGATATCATTTGAACAAGCCGCTGGTCGCAAT	2244
QY	2289	AGTCGGGGAAGGATCGGGGTGTCTCCGTTTACTATTTCCACAGAGAGATGACGAG	2348
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Db	2461	GCGATGATATCATACGACATGATATCCGGAATTTGAGAAAGGTGCTGAAGAAGTGTATCTAT	2520
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RESULT 12  
AY663385 6317 bp mRNA linear INV 14-JUL-2004  
LOCUS Aedes aegypti voltage-dependent para-like sodium channel mRNA,  
DEFINITION partial cds, alternatively spliced.  
ACCESSION AY663385  
VERSION AY663385.1 GI:50080865  
KEYWORDS  
SOURCE Aedes aegypti (yellow fever mosquito)  
ORGANISM Aedes aegypti  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes;  
Stegomyia.  
1 (bases 1 to 6317)  
Wu, J.-H. and Zhao, T.-Y.  
Direct Submission  
Submitted (21-May-2004) Department of Vector Biology and Control,  
Microbiology and Epidemiology Institute, 20 Dongda Street, Fengtai  
District, Beijing 100071, China  
Location/Qualifiers  
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FEATURES  
SOURCE

CDS

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ORIGIN

Query Match 54.3%; Score 3536.4; DB 3; Length 6317;  
Best Local Similarity 74.0%; Pred. No. 0; Mismatches 1561; Indels 72; Gaps 11;  
Matches 4655; Conservative 0;

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1873 CAGCGAGACTTGTATATGCTCAAGACTGTACAGAGCAAGTGTGCGCAAAATTAACACAC 1932  
QY 2190 GACATCTCTTTATGAGCCCGCTCAGACACAAAGTGTGTAATGAAGTGTGAT 2249  
Db 1933 GACATCTCTTTATGAGCCCGCTCAGACACAAAGTGTGTAATGAAGTGTGAT 1992  
QY 2250 GTCTGATGATGATGATGAGAGAGGCGGCTGAGGAGCAAGTGTGAGGAGGAGGAGGAGGAG 2309  
Db 1993 GTGTTAAAGATATGATGAGAGAGGCGGCTGAGGAGCAAGTGTGAGGAGGAGGAGGAGGAG 2052  
QY 2310 GTCTGATGATGATGATGAGAGAGGCGGCTGAGGAGCAAGTGTGAGGAGGAGGAGGAGGAG 2369  
Db 2053 GTCTGATGATGATGATGAGAGAGGCGGCTGAGGAGCAAGTGTGAGGAGGAGGAGGAGGAG 2112  
QY 2370 AAGGCACTGAGAGTGTGATGAGAGGAGGCGGCTGAGGAGCAAGTGTGAGGAGGAGGAGGAG 2429  
Db 2113 AAGGCACTGAGAGTGTGATGAGAGGAGGCGGCTGAGGAGCAAGTGTGAGGAGGAGGAGGAG 2172  
QY 2430 GTTGGTTGAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2489  
Db 2173 GTTGGTTGAATTTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2232  
QY 2490 TTATATCAGCTGTGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2549  
Db 2233 TTATATCAGCTGTGATGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2292  
QY 2550 AACAGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2609  
Db 2293 GACCCGAGATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2352  
QY 2610 ATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2669  
Db 2353 ATGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2412  
QY 2670 AACATCTGATCTTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2729  
Db 2413 AACATCTGATCTTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2472  
QY 2730 CAGGCTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2789  
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QY 2790 TGCCCACTTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2849  
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QY 2850 CTGACATTTGATCTTATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2909  
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QY 2910 GGAAGAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2969  
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QY 2970 TTGACGATTTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3029  
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QY 3030 GAGTGTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3089  
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QY 3210 GCGTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3269  
Db 2953 GCGTTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 3012

QY 3270 AAGTTAATCGTAACAAATTGACAAATCAATTAAGTATCAACCATCGATGAGAGACC 3329  
Db 3013 AAGTTGCGAAAAAACAAGTTAAACAAGCCAGATTGGCTCCGTCCGACCCGACG-----GC 3066  
QY 3330 AACGATCAGTTGGATTGGAGCGAAGAGCATGGTGAACAACGAACTGAGCTGGAGCCAC 3389  
Db 3067 AAAGGGTATGTCATGATATCTCTGCAAGCATGGTGAATAATGACTGGAATTAATCTCA 3126  
QY 3390 GACGAGATCTTCGCGACGCGCTCATCAAGAGGGGATCAAGAGCAGACGCACTGAG 3449  
Db 3127 GATGACATACGCGCGAGCGGGCTGCTCAAGAAAGGCGTCAAGAGACACAAACAGCTGAG 3186  
QY 3450 GTGGCATCGGGGATCGGATGGAATTCACGATACCGCGCATGAAGAACAACAGCCG 3509  
Db 3187 GTGGCATCGCGAGCGGATGGAATTCACGATACCGCGCATGAAGAACAAGGCGCAAG 3246  
QY 3510 AAGAAATCCAATATCTAAATPACGAACGATGATTGGCAACTCAAT---TAACCAACA 3566  
Db 3247 AAGAAACAACAGCTGATGAACAATTCGAAGTGATAGGCAATTTCTAATGATATCA 3306  
QY 3567 GACAATAGACTGGAACACAGACTAAACCATAGAGGTTGTCTTACAGACGACGACACT 3626  
Db 3307 GATATAATTAAGACACGAACGATCATAGAGGCAATGCTTTCAGAGACGATGATCT 3366  
QY 3627 GCCGACATTAATCTCATATGATAGCAATGAAGATGCAACCATTCAGAGACGACGACAG 3686  
Db 3367 GCCGATTAATGAAGTCTTATGAGAGTCAACAAGATCCCGCTTCAGAGAGAAAGCCACA 3426  
QY 3687 GCGACGCGCGAGACGATGAGAGGCGAGAGAGAACGCGACGCGAGAGAGGATTTAGT 3746  
Db 3427 GCGACGCGCGAGACGATGAGAGGCGAGAGAGAACGCGACGCGAGAGAGGATTTAGT 3486  
QY 3747 CTGACGAGAACTGAGACGAGAGGCGAGATGCGAGAGGCGCGCTGACGCGATATC 3806  
Db 3487 ATTGATGAAGAGCTAGACGATGAGCGATGCGAGAGGCGCGCTGATGAGCGAACTG 3546  
QY 3807 ATTATTCATGACACGAGAGATPACTCGATGAATTCAGAGCTATTTGCTCCCGCAT 3866  
Db 3547 ATATTCACGCGCGAGAGAGAGATGATGAAGACTCAACGAGCGAGCTGTTGTCGAGC 3606  
QY 3867 TCGACTATAAGAAATTTCCGATCTTAGCCGTCAGATGACTCGCCGCTTTCGCAAGA 3926  
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QY 3927 TGGGCAATTTACGACTGAAAACTTTCAATTAATTAATTAATTTTGAACAGCT 3986  
Db 3667 TGGGCAATTTGCGACTGAAAACTTTCAAGCTCATCGAACAAGTACTTTGAGACGCGC 3726  
QY 3987 GTATCACTATGATTTTAATGATGACTTAGCTTTGCAATTAAGAGATGATCTGCGA 4046  
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QY 4047 CAAGAACCCTACTGACGAGATATTTTACTATATAGACAGAAATTTTACGTTATATTC 4106  
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QY 4107 TTTCTTGAATGTTAATCAAGTGTGGCGCTCGGCTTCAAGTGTACTTCAACAACGCG 4166  
Db 3847 TTTCTTGAATGTTAATCAAGTGTGGCGCTCGGCTTCAAGTGTACTTCAACAACGCG 3906  
QY 4167 TGTGTTGCTGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTT 4226  
Db 3907 TGTGTTGCTGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTT 3966  
QY 4227 GTTGAAGCTGTTGATTTCAAGCTTCAAGACTATGCAAGCTTAAAGACGACTGAGACA 4286  
Db 3967 TGTGAAGCTGTTGATTTCAAGACTTCAAGACTATGCAAGCTTAAAGACGACTGAGACA 4026  
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Db 4027 CTACGTCATGTCCTCGTATGCAAGGCTGCTGTTAATGCGCTGATGCTGATGCTGATGCT 4086

QY 4347 ATACGTCATCTTCAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4406  
Db 4087 ATACGTCATCTTCAATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4146  
QY 4407 ATGGGTGACAGCTTTTGTGCTGAAAAATTTTAAGTGCAGAGACGATGATGCGACAG 4466  
Db 4147 ATGGGTGACAGCTTTTGTGCTGAAAAATTTTAAGTGCAGAGACGATGATGCGACAG 4206  
QY 4467 CTCAGCAGAGATCATCAAAATCGCAATCCCTGCGAGAGCGAGAACTACAGTGGTG 4526  
Db 4207 CTGTGCGACGAGATCATCTCCGATGATGAACCGTGGCGCTGAGAACTACAGTGGTG 4266  
QY 4527 AATTCAAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4586  
Db 4267 AACTGCGATGAACTTGCACAGTGGAGAGGCGTACCTGTGTCTGTTCCAGTGGCA 4326  
QY 4587 ACTTCAAGAGGCTGATCAATCATGATGACGATCTGATTCAGACGAGAGTGGCAAG 4646  
Db 4327 ACGTTCAAGGCTGATTCAGATCATGACGACGCACTGCGGAGAGTGGGAAAG 4386  
QY 4647 CAACCAATTCGTGAACGACATCTACATGATTTAATTTGATTTCTTCAATATTT 4706  
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QY 4707 GGATCCTTTTACACTCATCTGTTCAATGCTGATGATGATGATGATGATGATGATGAT 4766  
Db 4447 GGATCCTTTTACACTCATCTGTTCAATGCTGATGATGATGATGATGATGATGATGAT 4506  
QY 4767 AAGAAAAAGCAGGTGATCATTAAGAAATGTTCAATGACAGAAATGCAAGAAAGTACT 4826  
Db 4507 AAGAAAAAGCAGGTGATCATTAAGAAATGTTCAATGACAGAAATGCAAGAAAGTACT 4566  
QY 4827 AATGCTATGAAAAATGAGGCTCTAATAAACATTAAGCAATTCAGACCAAGTGG 4886  
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Db 4627 CGACCAAGAGATGATCTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 4686  
QY 4947 TTATTCATGCTGACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5006  
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QY 5007 TATAAGCGGCTCTAAGATCTCAATGATGATGATGATGATGATGATGATGATGATGAT 5066  
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QY 5187 TTGCTGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5246  
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QY 5247 CTGATGAAGAGGAGCAAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 5306  
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QY 5307 GCCCTGTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5366  
Db 5047 GCGCTGTTCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5106  
QY 5367 ATGCTGTTCTTATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5426  
Db 5107 ATGCTGTTCTTATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5166  
QY 5427 ACCTTTGGCAGAGCATGATCTGCTTTCAAGATGCGAGTACGCGGTTGGAGTGT 5486



Db 6 AATCGAGAGAGCATCCGCGATGCGAGCAAAACAGCGGAAATTGAAAGAAACGAGC 65  
 Qy 161 CGAGGAGAGGTGCCGATATGTCGCAAGAAAAAAGAAATCCGATATGATGA 220  
 Db 66 CGAGGAGAGAG---CTGGTATTTGGTCGGAAGAAAAAGAAATCCGATACAGCA 122  
 Qy 221 CGAGGAGAGAGATGAGGTTCACAAACGGGATCTTCACTTGAACAGGGGTGGCAATAC 280  
 Db 123 TGAAGATGAGATGAGGTTCACAGCCGAGACTCCACACTCGAGAGGGAGTCCAAATCC 182  
 Qy 281 TGTTCATGTCAGGAGAGCTTCCGCGCGAAATGGCTTCACCTCTCGAGATATGA 340  
 Db 183 GGTTCGATGTCAGGAGAGCTTCCGCGGAAATGGCTTCACAGCTCTCGAGATATGA 242  
 Qy 341 TCCCTACTACAGCAATGATCTGACATTTGATGTTGAAGCAAGAGAAATATTTTCG 400  
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 Qy 401 CTTTTCGATCAAAAGCAATGAGATGTCGATCCATTCATCCGATACGTCGTGGC 460  
 Db 303 TTTCTCCGCAACAAATGATATATATGATCTGATCCGTTCAATCCATACGTCGTGGC 362  
 Qy 461 CATTTACATTTAGTGCATCCATTAATTTCCCTATTCATCAACAATTCCTGTCGA 520  
 Db 363 TATTTATATTTAGTGCATCCATTCATTTTATTTATATTAACAACATTTCTTACCA 422  
 Qy 521 CTGCATCTGATGATATATGCGCAACGCGGATGATGTCACCTGAGTATATTCAC 580  
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 Qy 581 CGGAACTACACATTTGAATGAGCTGTTAAGTGAAGGACAGAGTTTCAATTTATGCCC 640  
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 Qy 641 GTTTACGATCTTGAAGTGCATGGAATGGCTGAGCTCTAGTAAATAGCTTTAGCTTA 700  
 Db 543 GTTTACTTATTTAGATGATGATGGAATGGTGGACTTCTGATATATGATATAGATA 602  
 Qy 701 TGTACCATGGGATATGATTTAGTAAATCTAGCAGCCCTGCAACGTTAGGGTGTGCG 760  
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 Qy 821 ATCCGTGAGAAATCTGCGCATGATATCTGACCATGTTCTCCCTGCGTGTTCGC 880  
 Db 723 GTCCGTTAAGATCTCAGAGATGATATTTTAAACAATGTTTCTGTTATCGGTGTTCG 782  
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 Qy 1121 TGGCTACACAGCTTCGATTCGATGAGGCTTTCGTCGCGCTTCGCGCGATGATGAC 1180  
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 Qy 1181 ACAGAGATTTCTGGAGATCTGTACAGCTGTGTGCGCGCGCGAGCAATGAGCAAT 1240  
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Qy 1241 GCTGTCTTATATGATCATCTTCTAGGTTCAATCTATCTTGATTTGATTTGGC 1300  
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 Db 1316 -----AGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347  
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 Db 1467 ACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1524  
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 Db 1584 TCTTGTAGAGAGATCTAGAGATCACATGATTAACATGATAGAGAGAGAGAGAGAGAG 1643  
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 Db 1644 GGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703  
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 Db 1704 AGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1761  
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 Db 1762 -----GTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1787  
 Qy 1955 GCATCATGCGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2014  
 Db 1788 GCATCATGCGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1841  
 Qy 2015 GAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2074  
 Db 1842 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1901  
 Qy 2075 AGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2134  
 Db 1902 GCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1958  
 Qy 2135 GAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2194  
 Db 1959 AGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2018  
 Qy 2195 TCTTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2254  
 Db 2019 TCTTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2078  
 Qy 2255 GAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2314  
 Db 2079 AAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2138

QY	2315	CGTTTACTATTTTCCCAACAAGACCATGACACAGATGGGCCGACGTTTCAAAACAAGGC	2374
Db	2139	TGTTTACTACTTCCCAACAAGACCGACGACGAGAGCGGTCAACGTTCAAGACAAGGC	2198
QY	2375	ACTCGAAGTATCCTCAAGGACATCGATGATGTTTGTGTGGGACTGTGTCTGGGTTTG	2434
Db	2199	CTTGAGCTTCCGCATGGCGATGAGTACATCTTCTGTGTGGGACGTGCTGGGTTGTG	2258
QY	2435	GTTGAAATTTCCAGAGTGGGGTATCGCTCATGCTCTTTCGATCCCTTGGTCAAGCTCTTTCAT	2494
Db	2259	GCTCAAGTCTCAGGAGTGGGTTTCATTCATCGTTCGTTTGCACCCGTTGCTCAAGCTGTTTCAT	2318
QY	2495	CAGCCTGGCATTTGGTGCACAACGATGTTCAATGGCAATGATCAACACATATGACAACAA	2554
Db	2319	CACCTTGTCATCGTGGTCAACACGCTGTTCAATGAGCCCTGATACCAACATATGAGACC	2378
QY	2555	GGAGATGGAAACGCGTGTCTCAAGATGGCAACTATATTTCTTACCGCGACCTTTGGCATGCA	2614
Db	2379	GGACATGGAGGCGGCCCTCAAGAGTGGTAATCTATTTTTCACCGCGACCTTTCCGCAATGCA	2438
QY	2615	GGCCACCATGAAAGTAAATGGCCATGAGACCCCAATACTATTTTCCAGAGAGGCTGGAAAT	2674
Db	2439	AGCAACAGATGAAGCTGATAGCGATGAGTCCCAATGACTACTTCCAAAGAGGCTGGAAAT	2498
QY	2675	CTTGACACTTCAATTAATCGTGCCCTATGCGCTATTTGAACTGGGACTCGAGGGGTGTCCAGG	2734
Db	2499	TTTGATTTTCAATCATGTCGTGGCCCTGTGCTGCTGAGATGGGCGCTGGAAAGGTGTTCAAGG	2558
QY	2735	TCTGTCCGTAATTTGGTTCCTTTGCATTTGCTGCTGCTGATTCAAATATGGCCAAAGCTTTGGCC	2794
Db	2559	ATTGTCAGATATTAAGGTTTCAATTCGTTGCTTCAGGTGTTCAACTATGAGAAATGTAGCC	2618
QY	2795	CACACTTAATTTACTCATTTTCGATTTATGGAAGCAGACCATGGGCGCTTTGGGTAATCTGAC	2854
Db	2619	GACGCTGAATTTAATCTCATTTTCATCATGAGGTGCAGAACATGGGTGCGTTAGGTAATCTGAC	2678
QY	2855	AATTTGACTTTTGCAATTAATCATTTCTCATTTTGGCGGTGATGGGAATGCACTGTTCCGAAA	2914
Db	2679	GTTTGTGCTCTGCATTAATCATTTCTCATTTTGGCGGTGATGGGAATGCAAGCTGTGCGGCA	2738
QY	2915	GAATTAATCATATCAACAAGACCGCTTCCGAGATGCGACCTGCGCGCTGGAACTTTCAC	2974
Db	2739	GACATCAATGACACATGATGATCGCTTCCGGAACAAGACCTGACCGGTGGAATCTTAC	2798
QY	2975	CGACTTAATGCAACAGCTTCATGATGCTGTTCGGGGTCTCTGCGGAGAAATGATTCGATGCT	3034
Db	2799	CGACTTAATGCACTGCTTCATGATGCTGTTCGGGGTCTCTGCGGAGAAATGATTCGATGCT	2858
QY	3035	CATGAGGACATGCAATGTAAGTGGGAGATGTCTGCGCAATTCCTTCTTCTGGCCACCGT	3094
Db	2859	CATGAGGACATGCAATGCTGCTGCGGAGATGTCTGCGCAATTCCTTCTTCTGGCCACCGT	2918
QY	3095	TGTCATCGGCATCTTGTGTGATCTTAACCTTTTCTTACCTTGTGCTTTGTGCCAATTTTGG	3154
Db	2919	AGTATAGGAATCTAGTATCTTAACCTTTTCTTACCTTGTGCTTTGTGCCAATTTTGG	2978
QY	3155	CTCATCTAGCTTAATCAAGCGCGGACCTGCGGATGACATGCAATGAATAAATAGCGAGGCTT	3214
Db	2979	TTTCATCTGCTGCTGCGGACCGACGCGCGCAACAACAAACAAACAAAGATCGCGAGGCGTT	3038
QY	3215	CAATGCAATTTGGCCGATTTTAAAGTTGGGTTAAGGTAATATTTGCTGATTTGTTTCAAGTT	3274
Db	3039	CAACCGGATATGCGCGCTTTTCCAACTGATGATCAAGTCAACATCGCCAAACGCGCTCAAGTT	3098
QY	3275	AATACGTAACAATGACAAATCAATAATAGTATCAACATCAGGTGAGAGACCAACA	3334
Db	3099	CGTGAATAACAAGTTTACA-----AGCA	3122
QY	3335	GATCAGTTTGAATTTGGAGGGAAGACATGTTGACACAGAACTGAGCTGGGCAACGACA	3394
Db	3123	GATTCGCTCCGTGCGACCCCGCAGAGATGTGTAATAATAGCTGGAATTTAATCTCCAGATGA	3182
QY	3395	GATCTCTCGCAACGCGCTCATACAGAGGGGATCAAGAGCAGACGCACTGGAGGTGGC	3454

Db	3183	CATACGCGCGACGGCGTCTCAAGAAAGCGCTCAAGAGACACACCAAGCTTGAGGTGGC	3242
Oy	3445	CATCGGGGATCGGATGGAATTCCAGATACACGGCGCATGAAACAACAAGCCGAAGAA	3514
Db	3243	CATCGGAGCGGGATGGAGTTCAAGATACACGGCGACCTGAAGAACAAAGGCAAGAAAGAA	3302
Oy	3515	ATCCAAATATCTAATATACCGAACGATGATTGGCACTCAATTAACCAACAACAATAG	3574
Db	3303	CAAAACGCTGATGAAACAATCGAACA-----	3328
Oy	3575	ACTGAAACACAGCGTAAACCATAGAGGTTGTCTTACAGAGACGACGACCTGCCAGAT	3634
Db	3329	-----AGAGCGATGATCTGCCAGTAT	3350
Oy	3635	TAAGCTATATGTAGCCATTAAGAAATGCAACCATTCACAGACGAGAGCCACAAGGCGACGC	3694
Db	3351	AAATGCTTAATGGCAGTCAACAAGATCCCGCTTCAAGAGAGAAAGCCACAAGGCAAGCGC	3410
Oy	3695	CGAAGCATAGAGGGCGAGAGAGAGAGCGCGACGCGAGCAAGAGATTTAGGTCTCGACGA	3754
Db	3411	CGAAACCATGAGAGCGCAAGAGAGAGAGCGTGAACGTACAGAAAGAGACCTTAGAATTGATGA	3470
Oy	3755	GGAACCTGACGAGAGAGGCGCAATGCGAGAGAGGCGCGCTGACGCGTGAATCATTAATCA	3814
Db	3471	AGAGTTGGATGACGAGTGGCGACGCGCGAGGAAGGTCCACTGGAACGCGCAACATGATTAATCA	3530
Oy	3815	TGCACATGACGAGGATATATCTCGATGAAATATCCAGCTGATTTGCTGCGCCGATTCGTACTA	3874
Db	3531	CGCGACGAGAGACAAAGTGAATGAGAGATTACCGGCGGACCTGCTGTCCGACCAATTGCTA	3590
Oy	3875	TAAGAAATTTCCGATCTTACCGGTGAACGATGACTGCGCGTCTGGCAAGATGGGCGAA	3934
Db	3591	CAAAAAGTTCCGGTCTCGGACGAGGAGACGACGAAGCCCGTCTGCGACGAGCTGGGCGAA	3650
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REFERENCE  
AUTHORS  
TITLE  
Blattellidae; Blattellinae; Blattella.  
1 (bases 1 to 6096)  
Dong, K.  
A single amino acid change in the para sodium channel protein is associated with knockdown-resistance (kdr) to pyrethroid insecticides in German cockroach  
Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)

JOURNAL  
MEDLINE  
97218696  
606120  
2 (bases 1 to 6096)  
Dong, K.  
Submission  
Direct  
Submitted (07-OCT-1996) Entomology, Michigan State University, East Lansing, MI 48824, USA

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RESULT 15  
BGU73583 6096 bp mRNA linear INV 19-MAR-1997  
LOCUS Blatella germanica para sodium channel mRNA, complete cds.  
DEFINITION U73583  
ACCESSION U73583.1 GI:1657983  
VERSION  
KEYWORDS  
SOURCE Blatella germanica (German cockroach)  
ORGANISM Blatella germanica  
Eubacteria; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blatelloidea; Blattellidae; Blattellinae; Blattella.  
REFERENCE 1 (bases 1 to 6096)  
Dong, K.  
A single amino acid change in the para sodium channel protein is associated with knockdown-resistance (kdr) to pyrethroid insecticides in German cockroach  
Insect Biochem. Mol. Biol. 27 (2), 93-100 (1997)  
JOURNAL MEDLINE 9066120  
PUBMED 92718696  
REFERENCE 2 (bases 1 to 6096)  
Dong, K.  
Direct Submission  
JOURNAL TITLE Submitted (07-OCT-1996) Entomology, Michigan State University, East Lansing, MI 48824, USA  
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ORIGIN

Query Match	44.6%	Score 2904.2	DB 3	Length 6096
Best Local Similarity	69.0%	Pred. No. 0		
Matches 4245	Conservative 0	Mismatches 1738	Indels 168	Gaps 13

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Qy	2481	GT	CAAGCTT	TCATACCGCT	GTGATTTGT	GTCAACAGTTCATGAGCA	2540
Db	2350	G	TGAGTGT	TCATACCCCTT	TGCAATGTGTGT	CAATACGTTCATGAGCC	2409
Qy	2541	CAC	GATATGA	CAAGAGATG	GAACGCGT	CTCAAGATG	2600



D	2410	CACGACATGATTAAGACATGATAGCTCTCAAGAGTGGCACAATTCTTCACAGCG	2465
O	2601	ACCTTTGCCATCGAGGCCACATGAAGCTAATGGCCATGAGCCCCAAGTACTATTTCCAG	2666
D	2470	ACCTTTGCCATTTAGAGGCCAGCGCTCAAGTTGATAGCAATGAGCCCTAAGTACTACTTCCAG	2529
O	2661	GAGGGCTGGAACTTTTGCATCTTATTCGTGGCCCTATGGCTATTGGAACTGGGACTTC	2722
D	2530	GAGGATGGAACATTTTGTATTTCACTATGTGTGACATTTCTTCCCTGGAAATGGGTCTT	2589
O	2721	GAGGGTGTCCAGGGGTCTGCGGATTTGGGTTCCCTTGATTTGCTGCGGTATTCAACTG	2780
D	2550	GAGGTGTCCAGAGTGCTGTCCGTCTCGGATTCGTTCAATTTGTTAGAGTCTTCAACTT	2649
O	2781	GCCAAAGTCTTGCGCCACACTTAATTTACTATTCGATTTATGGAAGCAGCACATGGCGCT	2840
D	2650	GCGAAGTCTTGCGCCAGCGCTGAATCTGCTCATTTCCATCATGAGGGATGAACGTGGTGT	2709
O	2841	TTGGGTATCTGACATTTGTACTTTGCATTTATCATCTTCACTTTTCCGCTGATGGGAATG	2900
D	2710	CTGGGTAACTCGACCTTTGTGTGTGTATATTCATTTTCACTTTTCCGCTATGGGTATG	2765
O	2901	CAACGTTCGGAAAAGATATATCATGATCAAGACCGCTTCCGGATGGGGACCTGCG	2966
D	2770	CAACTCTTTGGCAAAATTTATATATATATGTGAACCTTTCCCTGACGGGGATATGCG	2829
O	2961	CGCTGGAACCTTACCGCACTTTATATGACAGCTTCATGATCGTGTCCGGGTCTCTCGGA	3020
D	2830	AGATGGAACTTTAGGACTTATGCACTCATTCATGATTTGTGTCCAGTGTGTGGCGG	2889
O	3021	GAATGATCGAGTCCATGTGGACTGCATGTAAGTGGCGATGTCTCGTCAATTCCTTC	3080
D	2890	GAGTGAATAGAGTCTATGTGGGATTTGTATGTCTGTTGAGAGCTGGTCTCGATCCCGTTC	2949
O	3081	TTCTTTGGCAACGGTGTGATCGGCACTCTTGGAACCTTAACCTTTTACGCTGTGTT	3140
D	2950	TTCTTTGGCACTGTGCTATTTGAAGAACTTGTGTGTGAACCTTCTTGGCTGTGCT	3009
O	3141	TTGTTCATTTTGGCTCATCTTACGTTTATCAGCGCGCATGGCCGATACGATACGATTA	3200
D	3010	CTCAGCAACTTTGGTTCATCCATCTGTCAAGCCCAACAGCTGACATAGAAACCAACAG	3055
O	3201	ATAGCCGAGCCTTTCATCGAATGTGGCCGATTTAAAGTTGGGTTAAGCGTAAATTTGCT	3260
D	3070	ATTGCTGAGGATTTGAGCGGTTTCTCAAGATTTCTTAACGTAAATACGTAGCGGCTA	3129
O	3261	GATGTGTTCAAGTTAATACGTAAACAAATTTGACAAATCAATATGATTCACATCAGT	3320
D	3130	AACGTGGCAAAATGTGTGCGTCCAAATTAACATATCGAATTCGATCAAGCCGCAAT	3189
O	3321	GAGAGGACCAACAGATCAGTTGATTTTGAAGCGAAGACATGGTGAACAAGAACTGGAG	3380
D	3190	GCCC-----ATGAGCGTGAACGGAACCTTGAC	3216
O	3381	CTGGGCCACGACGAGATCTCGCGACGCGCTCAT-----CAAGAGGGGATCAAG	3431
D	3217	CTCACAGCGAGTGAATCTCGCGAGTGAATCTGTATAGAGCAAGAAAGTCCAAAG	3276
O	3432	GAGCAGATGCACTGAGAGTGGCCATCGGGGATGGGATGGAATTCAGATACAGCGGAC	3491
D	3277	GAGCAGATGCACTTGGAGTGGCGATAGGAATGGAATGAGGATTCACATCTCATGTGAGAT	3336
O	3492	ATGAAGAACAACAAGCCGAGAAATCCAAATATCTAAATTAACGACAGATATTGGCAAC	3551
D	3337	CTGAAAAACAAAGCTGAAAGAGGACAAGCTGATGATGAACAGACGAGAGGTATCGCAAT	3396
O	3552	TCAATTAAACAACAAGCAATTAAGCTGGAACAAGACTAAACATAGAGGTTTGTCTTA	3611
D	3397	TCTTTGATTCATTAAGAACAATCGGATAGAAAGTGTGCTATTCACAAATCGG-----	3450
O	3612	CAGACACGACGACTGCGACGATTAATCTCATATGTGTAGCCCTTAAGATCGACATTCAG	3671
D	3451	CAGACGAGGATCTTTAGACACAGGGTCAATGTGAAGTCACAAAACCGTCTCATACAG	3510

QY	3672	GACGAGAGCCCA	CAGGGGAGCGCCGAGACCAT	TGAGGGCCAGAGAAACGGCAGCCACG	3733
Db	3511	GATGACACCCAT	TAAGGGAAGTGACAGAGCAT	TATGATGGGAGGAAAGAAAGATGCAAG	3570
QY	3732	AAGGAGATTTAT	AGGCTTCGACGAGAACT	GTGACAGAGGGCGCAATGCGAGAGGCCG	3791
Db	3571	AAAGAAAGATCT	CGATCAGAAGAGGAAAGGTGAA	AGAAATGGAAGAGGAAAGCACTCTG	3633
QY	3792	CTCGACGGTAT	ATCATTAATTCATGCACA	CGACGAGATATATCTGATGAATATTCACCT	3851
Db	3631	GAGGAGGACAT	AGTATGGATGTCAGAGGCACT	GAGACGTCAGATGTCAGAAATATCCGCA	3690
QY	3852	GATTGCTGCCCC	GAATTTGCTATTAAGAAATTTTCGAT	CTTAAGCCGGGAGAGATGACCTGC	3911
Db	3651	GATTCGTCTTG	ATCACTGCTATTAAGCGCTTCCCTTC	CTTGCTCGAGAGCAAGACCTCT	3750
QY	3912	CCGTTCTGGCA	AGGATGGGCAATTTACGCTGAAA	CTTTTCATTAATTTGAAATATA	3971
Db	3751	CTTTCTTGCA	AGGCGTGGGCAACCTCGAC	CTGAAAACCTTCAACATCATTTAGAACAA	3810
QY	3972	TATTTTGA	AACGCTGTATATCATATGATTTTA	TGAGTACCTTAGCTTTGGCAATTAGA	4031
Db	3811	TACTTTGAA	AGGCGTGTATACCATATCTGTTAG	CACTTCGCACTGGCCCTTGAG	3870
QY	4032	GATGTACATCT	GCACAAGAACCAATCACTGAGAGAT	ATTTATATCTATATGACAGATA	4091
Db	3871	GATGTACATCT	GCCTCACTGACACCAATTCGAGAG	CAACTTATATATCATGATCTGATC	3930
QY	4092	TTTACGGTAT	ATATCTTTGGAAATGTAAATCA	AGTGTGGCGCTTCGCTCAAGTG	4151
Db	3931	TTTACGTGAT	CACTCTTATTTGAATGTGATCA	AGGTGGCGCCCTTGCTTCAAAAA	3990
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QY	4272	AGAGCACTG	AGACCACTACGTCGATCCCGTAT	TGACAGGGCATGAGAGGTCTGTATAT	4331
Db	4111	AGGCGCCCT	TAAAGCCCTTAATGTCTA	GAATGAGGGAGTGAAGGTGTGTAAAC	4170
QY	4332	GGCGTGTGA	CAAGCTATACCGTCATCTTCA	ATGTGCTATATGTTTGG	4391
Db	4171	GCTTTGTG	CAAGCAATCCCAATATCTTCA	ATGTGCTCTCCGTGTGTCTCATCTTCTGC	4230
QY	4392	CTAAATTTTG	CCATATGGGTGTACAGCTTTT	TGCTGAAAATATTTTAAGTCGAGAC	4451
Db	4231	CTCATCTTTG	CCATCATGAGGTGTGACGCTG	TTTCTGAAAATATCTAATATGTGTGAT	4290
QY	4452	ATGAATGGC	ACAAGAGCTCAAGCACAAGATCA	TACCAATGSCATGTGCTGAGAGGAG	4511
Db	4291	TCCAACTT	CAACCTTAGGCAAGAAATCAT	CTTGACAAAATGTCTGATTCGTA	4350
QY	4512	AACCTACA	CGTGGGTGAATTCAGCAATGA	ATTTCGATCATGTAGGTAAACGCTATCTGTGC	4571
Db	4351	AACTACAT	GATGGAGAACTGGCCAAATGA	ATTTTATCACGTCCGCAAAAGCTTATCTCTGC	4410
QY	4572	CTTTTCCA	GTGGCCACTTTCAAAGCGCTGA	TACAAATCATGAAACGATGCTATGATTTCA	4631
Db	4411	CTCTTCCA	AGTGGCCACTTTCAAAGATTT	TAGATCATGAATGACGCTATAGACTCT	4470
QY	4632	CGAAGGTGA	CAAGCAACAATTCGTAACCA	ATCTTACATGATATTTATATTTGCTA	4691
Db	4471	AGAGAGCT	CCAATAAGCAAGCAATCAGGAA	AAACGAATCTTACATGTAACCTCTACTTTGTG	4530
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 DB 4591 AACTTTAATGACAAAAGAAAAGACGAGAGGGTGGCTAGATGTTTATGACTGAAGAT 4650  
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 DB 4651 CAGAAAAGTACTATATGCTATGAAAAGATGGGCTCTAAAACCATTAAGCATT 4710  
 QY 4872 CCAAGACCAAGGAGGAGACCAAGCAATAGTCTTGAATAGTAAACCAATGAATTC 4931  
 DB 4711 CCCAGGCCAAGTGGAGACCGACGGCCATTGTTGAAATCTGCACACAAAGAAATTT 4770  
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 DB 4771 GACATATCATATGTTGTTTCATTTGCTTAAACATGTAACATGACTGATGATCAT 4830  
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 DB 4831 CAAACAGTCGAAGAGTTCAGCCGAGTTCGATTACTTGAACATGATCTTCATGCTATC 4890  
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 DB 5071 GATGAGTCCGCTGCTGTAAGGAGTCTAAGGATTCGACATTCGCTGCTGCTTG 5130  
 QY 5292 GCCATGCTGCTGCTGCTGCTTCAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5351  
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 DB 5968 CCGAGCTTCAGACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5998

Search completed: May 9, 2005, 12:19:12  
 Job time : 2688 secs

CC putative Drosophila VASC beta subunit. The para VASC cDNA clone was obt.

from 3 overlapping regions of para cDNA isolated by PCR amplification.  
CC using primers (see also AAT18987-92) based on a published para sequence.  
CC Recombinant host cells (E.coli, yeast mammalian or insect) expressing the  
CC Drosophila para VASC can be used to isolate para VASC in biologically  
CC active form. Antisense constructs can block expression of the gene

XX Sequence 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 U; 0 Other;

Query Match 100.0%; Score 6513; DB 2; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 TCTAGACGTTGGCGCATAGACATGACAGAAATTCGACTCGATATCTGAGAAAGAAC 60
Db 1 TCTAGACGTTGGCGCATAGACATGACAGAAATTCGACTCGATATCTGAGAAAGAAC 60
Qy 1 TCTAGACGTTGGCGCATAGACATGACAGAAATTCGACTCGATATCTGAGAAAGAAC 60
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Qy 1621 TTATACAAAGACACAGACCTTACACAGACACACAGACACCAAGTTCGTAAGTGA 1680
Db 1621 TTATACAAAGACACAGACCTTACACAGACACACAGACACCAAGTTCGTAAGTGA 1680
Qy 1621 TTATACAAAGACACAGACCTTACACAGACACACAGACACCAAGTTCGTAAGTGA 1680
Db 1621 TTATACAAAGACACAGACCTTACACAGACACACAGACACCAAGTTCGTAAGTGA 1680
Qy 1681 GCACGACATCCTTATCCTTACCTGATGACGTTTAACTAACAGCAGAGGATCACGTAGT 1740
Db 1681 GCACGACATCCTTATCCTTACCTGATGACGTTTAACTAACAGCAGAGGATCACGTAGT 1740
Qy 1681 GCACGACATCCTTATCCTTACCTGATGACGTTTAACTAACAGCAGAGGATCACGTAGT 1740
Db 1681 GCACGACATCCTTATCCTTACCTGATGACGTTTAACTAACAGCAGAGGATCACGTAGT 1740
Qy 1741 CTCACAGTACAGATACGAGACGAGACGTGCGCTTTGGTATATCCCGTAGCGATGTA 1800
Db 1741 CTCACAGTACAGATACGAGACGAGACGTGCGCTTTGGTATATCCCGTAGCGATGTA 1800
Qy 1741 CTCACAGTACAGATACGAGACGAGACGTGCGCTTTGGTATATCCCGTAGCGATGTA 1800
Db 1741 CTCACAGTACAGATACGAGACGAGACGTGCGCTTTGGTATATCCCGTAGCGATGTA 1800
Qy 1801 AGCCATTGTATTTGATCACTATTCAGAGATGCCAGAGACCTTGCCCTATGCGAGACT 1860
Db 1801 AGCCATTGTATTTGATCACTATTCAGAGATGCCAGAGACCTTGCCCTATGCGAGACT 1860
Qy 1801 AGCCATTGTATTTGATCACTATTCAGAGATGCCAGAGACCTTGCCCTATGCGAGACT 1860
Db 1801 AGCCATTGTATTTGATCACTATTCAGAGATGCCAGAGACCTTGCCCTATGCGAGACT 1860
Qy 1861 CCAATGCGGTCACCCCGATGCGGAAGAGATGGGCGCATATAGTCCCGTGTACTATG 1920
Db 1861 CCAATGCGGTCACCCCGATGCGGAAGAGATGGGCGCATATAGTCCCGTGTACTATG 1920
Qy 1861 CCAATGCGGTCACCCCGATGCGGAAGAGATGGGCGCATATAGTCCCGTGTACTATG 1920
Db 1861 CCAATGCGGTCACCCCGATGCGGAAGAGATGGGCGCATATAGTCCCGTGTACTATG 1920
Qy 1921 GCAATCTAGGCTCCCGACACTCATCTGATATCTTGCATCATGTCGCAATATCTGATCT 1980
Db 1921 GCAATCTAGGCTCCCGACACTCATCTGATATCTTGCATCATGTCGCAATATCTGATCT 1980
Qy 1921 GCAATCTAGGCTCCCGACACTCATCTGATATCTTGCATCATGTCGCAATATCTGATCT 1980
Db 1921 GCAATCTAGGCTCCCGACACTCATCTGATATCTTGCATCATGTCGCAATATCTGATCT 1980
Qy 1981 CAGATGGGATCTTACTGCGGCGCATGCGCGTCAATGGCGCTCAGAGCAATACCAAGAGA 2040
Db 1981 CAGATGGGATCTTACTGCGGCGCATGCGCGTCAATGGCGCTCAGAGCAATACCAAGAGA 2040
Qy 1981 CAGATGGGATCTTACTGCGGCGCATGCGCGTCAATGGCGCTCAGAGCAATACCAAGAGA 2040
Db 1981 CAGATGGGATCTTACTGCGGCGCATGCGCGTCAATGGCGCTCAGAGCAATACCAAGAGA 2040
```

Db	1991	CACATGGCGATTACTCGGCGCGCATGGCCGCTCATGGCGCTGACGACCAATTGACCAAGAGA	2040
Qy	2041	GCAAAATTGCGCAACCGGCAACACACGCCAAATCAATCAGTGGGCGCCCAATGGCGGACCA	2100
Db	2041	GCAAAATTGCGCAACCGGCAACACACGCCAAATCAATCAGTGGGCGCCCAATGGCGGACCA	2100
Qy	2101	CCTGTCGTGGACACCAATCAACAAGCTGCATCATCGGACTTAGAATTTGGCTGGAGTSCA	2160
Db	2101	CCTGTCGTGGACACCAATCAACAAGCTGCATCATCGGACTTAGAATTTGGCTGGAGTSCA	2160
Qy	2161	CGGACGAAGCTGGCAAGATTTAAACATCATGACAAATCCTTTTATCGAGCCGCGCAGACAC	2220
Db	2161	CGGACGAAGCTGGCAAGATTTAAACATCATGACAAATCCTTTTATCGAGCCGCGCAGACAC	2220
Qy	2221	AAACGGTGGTGTATATGAAAGATGTGATGCTCTGAATGACATCATTCGAAACAGGCCGCTG	2280
Db	2221	AAACGGTGGTGTATATGAAAGATGTGATGCTCTGAATGACATCATTCGAAACAGGCCGCTG	2280
Qy	2281	GTCCGACACATCGGGCAAGCCATCGCGGTGTCTCCGTTACTATTTCGCAACAGAGACG	2340
Db	2281	GTCCGACACATCGGGCAAGCCATCGCGGTGTCTCCGTTACTATTTCGCAACAGAGACG	2340
Qy	2341	ATGACGAGATATGGGCGCGAGCTTTCAAAAGCAAGGCACTCGAAGTATCCTCAAAAGGACG	2400
Db	2341	ATGACGAGATATGGGCGCGAGCTTTCAAAAGCAAGGCACTCGAAGTATCCTCAAAAGGACG	2400
Qy	2401	ATGTGTATTTGTGTGGGACGTGTGCTGGGTGTGGTGAATAATTCAGAGAGTGGTATCGC	2460
Db	2401	ATGTGTATTTGTGTGGGACGTGTGCTGGGTGTGGTGAATAATTCAGAGAGTGGTATCGC	2460
Qy	2461	TCATGTCTTGATTCCTTTGCTGAGCTCTTTCATACACGCTGCAATTTGGTCAACAGA	2520
Db	2461	TCATGTCTTGATTCCTTTGCTGAGCTCTTTCATACACGCTGCAATTTGGTCAACAGA	2520
Qy	2521	TGTTCAATGGCAATGGATACCAACGATATGAAACAAGGAAATGGAAACGCTGCTCAAGAGTG	2580
Db	2521	TGTTCAATGGCAATGGATACCAACGATATGAAACAAGGAAATGGAAACGCTGCTCAAGAGTG	2580
Qy	2581	GCAACTAATTTCTTCAACCGCCACCTTTGGCATCGAGGCGCACCATGAGAGGTATGGCCATGA	2640
Db	2581	GCAACTAATTTCTTCAACCGCCACCTTTGGCATCGAGGCGCACCATGAGAGGTATGGCCATGA	2640
Qy	2641	GCCCCAAGTACTAATTTCAAGAGGCGCTGGAACATCTTGACTTCATTATCGTGGGCCCTAT	2700
Db	2641	GCCCCAAGTACTAATTTCAAGAGGCGCTGGAACATCTTGACTTCATTATCGTGGGCCCTAT	2700
Qy	2701	CGCTAATTGGAATCGGGAATCGAGAGGTGTCCAGGCGTCTCGGTATTTGGTCTCTTGAT	2760
Db	2701	CGCTAATTGGAATCGGGAATCGAGAGGTGTCCAGGCGTCTCGGTATTTGGTCTCTTGAT	2760
Qy	2761	TGTCGCGGTATTTCAAACTGGCCAAAGTCTTGAGCCACACTTAATTACTCATTTGCAATTA	2820
Db	2761	TGTCGCGGTATTTCAAACTGGCCAAAGTCTTGAGCCACACTTAATTACTCATTTGCAATTA	2820
Qy	2821	TGGACGCAACATGGGCGCTTTGGGTATCTGACATTTGTACTTTGCAATTCATCTTCA	2880
Db	2821	TGGACGCAACATGGGCGCTTTGGGTATCTGACATTTGTACTTTGCAATTCATCTTCA	2880
Qy	2881	TCTTTTGGCGTATATGGGAATGCAACGTTCGGAAGAAATTAATCAAGATCACAGGACCGCT	2940
Db	2881	TCTTTTGGCGTATATGGGAATGCAACGTTCGGAAGAAATTAATCAAGATCACAGGACCGCT	2940
Qy	2941	TTCCGGAATGGGCACTTCGCGCGCTGGAACTTCAACGCACTTTATATGACAAGCTTCAATGAC	3000
Db	2941	TTCCGGAATGGGCACTTCGCGCGCTGGAACTTCAACGCACTTTATATGACAAGCTTCAATGAC	3000
Qy	3001	TGTTCCGCGTGTCTTCGCGGAAGATGGAATGCAATGCAATGGGCACTGATACGTACGTGGCG	3060
Db	3001	TGTTCCGCGTGTCTTCGCGGAAGATGGAATGCAATGCAATGGGCACTGATACGTACGTGGCG	3060
Qy	3061	ATGTCTGTGTGATTCCTTTCTTTCTTGCGCAACCGTTGTGATATGGCAATCTTGTGTACTTA	3120
Db	3061	ATGTCTGTGTGATTCCTTTCTTTCTTGCGCAACCGTTGTGATATGGCAATCTTGTGTACTTA	3120

QY	3121	ACCTTTCTTAGCCTTGCTTTTGTCACATTTTGGCTCATCTAGCTTATCAGCCGCACTG	3180
Db	3121	ACCTTTCTTAGCCTTGCTTTTGTCACATTTTGGCTCATCTAGCTTATCAGCCGCACTG	3180
QY	3181	CGATTAACGATACGATTAATAATAGCCGCGCTTCAATCGAATTGGCCGATTTTAAAGTT	3240
Db	3181	CGATTAACGATACGATTAATAATAGCCGCGCTTCAATCGAATTGGCCGATTTTAAAGTT	3240
QY	3241	GGGTTAAGCGTATATTTGCTGATTTGTTCAAGTTATATCGTAAACAATTGCAAAATCAA	3300
Db	3241	GGGTTAAGCGTATATTTGCTGATTTGTTCAAGTTATATCGTAAACAATTGCAAAATCAA	3300
QY	3301	TAAAGATCAACAATCAGGTAGAGGAACAACAAGATAGTTGGATTTTGGACGAAGC	3360
Db	3301	TAAAGATCAACAATCAGGTAGAGGAACAACAAGATAGTTGGATTTTGGACGAAGC	3360
QY	3361	ATGTGTACAAACGAACTGGAGCTGGGCCCAACAAGATCTTGGCCGACGGCTCATCAAGA	3420
Db	3361	ATGTGTACAAACGAACTGGAGCTGGGCCCAACAAGATCTTGGCCGACGGCTCATCAAGA	3420
QY	3421	AGGGGATCAAGAGACGACGCACTGGAGGGTGGCCATCGGGAAATCGATGGAAATTCACGA	3480
Db	3421	AGGGGATCAAGAGACGACGCACTGGAGGGTGGCCATCGGGAAATCGATGGAAATTCACGA	3480
QY	3481	TACACGGCGCATGTAAGAACAAACAAGCCGAAGAATCCAATATCTTAATAATAACCAACA	3540
Db	3481	TACACGGCGCATGTAAGAACAAACAAGCCGAAGAATCCAATATCTTAATAATAACCAACA	3540
QY	3541	TGATTTGGCACTCAATTAACCAACAAGCAATTAAGCTGGAAACAGAGCTAAACCATAGAG	3600
Db	3541	TGATTTGGCACTCAATTAACCAACAAGCAATTAAGCTGGAAACAGAGCTAAACCATAGAG	3600
QY	3601	GTTTGTCTTACAGGACGACACTGACACATTAATCTATATGTAAGCATTAAGATC	3660
Db	3601	GTTTGTCTTACAGGACGACACTGACACATTAATCTATATGTAAGCATTAAGATC	3660
QY	3661	GACCAATTCAGAGACGAGACCAACAAGGCGACGCGCAGACGATGAGGGCGAGAGAAC	3720
Db	3661	GACCAATTCAGAGACGAGACCAACAAGGCGACGCGCAGACGATGAGGGCGAGAGAAC	3720
QY	3721	CGACGCCGACAGAGAGATTTAGTCTTCCACAGAGAACTGACAGAGAGGGCGAATGCG	3780
Db	3721	CGACGCCGACAGAGAGATTTAGTCTTCCACAGAGAACTGACAGAGAGGGCGAATGCG	3780
QY	3781	AGAGAGGCGCCCTCGACGCGTATTCATTTATTCAGACAGAGAGATATCTCATG	3840
Db	3781	AGAGAGGCGCCCTCGACGCGTATTCATTTATTCAGACAGAGAGATATCTCATG	3840
QY	3841	AATATCCAGCTGATTTGCTGCCCGCATTCGTATTAAGAAATTTCCGATCTTACCCGCTG	3900
Db	3841	AATATCCAGCTGATTTGCTGCCCGCATTCGTATTAAGAAATTTCCGATCTTACCCGCTG	3900
QY	3901	ACGATGAATGCGCGTTTCGCGCAAGAGAGGGGCAATTTACGCTGAACACTTTCAATTA	3960
Db	3901	ACGATGAATGCGCGTTTCGCGCAAGAGAGGGGCAATTTACGCTGAACACTTTCAATTA	3960
QY	3961	TTGAATAATTAATTTTGAACAAGCTGTATTCATCTATGATTTTATGATAGCTTACCTT	4020
Db	3961	TTGAATAATTAATTTTGAACAAGCTGTATTCATCTATGATTTTATGATAGCTTACCTT	4020
QY	4021	TGCGATTTGAAGATGTACATCTGGCACAAAGACCATCTGCAAGATATTTTATATCTATA	4080
Db	4021	TGCGATTTGAAGATGTACATCTGGCACAAAGACCATCTGCAAGATATTTTATATCTATA	4080
QY	4081	TGCAACAGAAATTTACGGTATATATCTCTCTGTGAAGATGTTAATCAATGGTGGCGCTCG	4140
Db	4081	TGCAACAGAAATTTACGGTATATATCTCTCTGTGAAGATGTTAATCAATGGTGGCGCTCG	4140
QY	4141	GCTTCAAAAGTACTTCAACAAGCGGTGGTGGCTGCAATTCGTGATTTGTCATGGTAT	4200
Db	4141	GCTTCAAAAGTACTTCAACAAGCGGTGGTGGCTGCAATTCGTGATTTGTCATGGTAT	4200

QY 4201 CGCTTAACTTCGTTGCTTCACTTTGAGCTGCTGATTCAGCCTTCAAGACTA 4260  
Db 4201 CGCTTAACTTCGTTGCTTCACTTTGAGCTGCTGATTCAGCCTTCAAGACTA 4260  
QY 4261 TCGGAACGTTAAGAGCACTGAGACCACTACGTCCTGATCCCGATGACGAGG 4320  
Db 4261 TCGGAACGTTAAGAGCACTGAGACCACTACGTCCTGATCCCGATGACGAGG 4320  
QY 4321 TCGTGGTAAAGCACTGAGACCACTACGTCCTGATCCCGATGACGAGG 4380  
Db 4321 TCGTGGTAAAGCACTGAGACCACTACGTCCTGATCCCGATGACGAGG 4380  
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Db 4381 TAAATTTTGGCTAATTTTGGCCATTAAGGCTGACCTTTTGTGCAAAATTTTA 4440  
QY 4441 AGTGGAGCACTGAATGGAACGACCTGACGACGACGACGACGACGACGACGAC 4500  
Db 4441 AGTGGAGCACTGAATGGAACGACCTGACGACGACGACGACGACGACGACGAC 4500  
QY 4501 GCGAGAGCGAGACTACACGTCGGTGAATTCAGCAATGAATTTTCATGATGATGACG 4560  
Db 4501 GCGAGAGCGAGACTACACGTCGGTGAATTCAGCAATGAATTTTCATGATGATGACG 4560  
QY 4561 CGTATCTGCTCTTTTCAAGTGGCCACTTCAAGGCTGGATTCGAATTCAGATGACG 4620  
Db 4561 CGTATCTGCTCTTTTCAAGTGGCCACTTCAAGGCTGGATTCGAATTCAGATGACG 4620  
QY 4621 CTATCGATTCAGAGAGTGGACCAAGCAACCAATTCGTGAACGAACTTCATGATGAT 4680  
Db 4621 CTATCGATTCAGAGAGTGGACCAAGCAACCAATTCGTGAACGAACTTCATGATGAT 4680  
QY 4681 TAAATTTTGGCTAATTTTGGCCATTAAGGCTGACCTTTTGTGCAAAATTTTA 4740  
Db 4681 TAAATTTTGGCTAATTTTGGCCATTAAGGCTGACCTTTTGTGCAAAATTTTA 4740  
QY 4741 TTAATTTTGGCTAATTTTGGCCATTAAGGCTGACCTTTTGTGCAAAATTTTA 4800  
Db 4741 TTAATTTTGGCTAATTTTGGCCATTAAGGCTGACCTTTTGTGCAAAATTTTA 4800  
QY 4801 TGAAGAGAGTCAAGAAAGTACTATATGCTATGAAGAAAGTGGCTTAAAGCAAT 4860  
Db 4801 TGAAGAGAGTCAAGAAAGTACTATATGCTATGAAGAAAGTGGCTTAAAGCAAT 4860  
QY 4861 TAAAGCCATTCAGAACCAAGTGGGCAACCAAGCAATGCTTGAAGTGAACG 4920  
Db 4861 TAAAGCCATTCAGAACCAAGTGGGCAACCAAGCAATGCTTGAAGTGAACG 4920  
QY 4921 AATAAGAAATTCGATATATCATATGATGATCATTTGGCTGAACATGTCACATGACC 4980  
Db 4921 AATAAGAAATTCGATATATCATATGATGATCATTTGGCTGAACATGTCACATGACC 4980  
QY 4981 TCGATCGTTAGATGCGTGGACAGTAAACGCGGCTGATGATCATTCATTCATGAT 5040  
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Db 5041 TCGATGATTTTCAAGTCCGAATGCTATTAAGAAATTTTGGCTTGAAGTGAACAT 5100  
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Db 5221 TGGGCAAGTGGGCGGCTGCTTGAAGTGAAGGAGCAAGGCAATTCAGACATGAC 5280  
QY 5281 TCTTGGCGTGGCACTGCTGCGGCGCTGCTTCAACATCTGCTGCTGCTGCTG 5340

Db 5281 TCTTGGCGTGGCACTGCTGCGGCGCTGCTTCAACATCTGCTGCTGCTGCTGCTG 5340  
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Db 5341 TCAATGATCTTTTGGCAATTTTGGCAATGCTGCTTCAATGCACTGAGAGAGAGAGC 5400  
QY 5401 GCATTAACGAGTGTACAACTTCAAGACCTTTGGCCAGAGATGATCTGCTTTCAGA 5460  
Db 5401 GCATTAACGAGTGTACAACTTCAAGACCTTTGGCCAGAGATGATCTGCTTTCAGA 5460  
QY 5461 TGTGACGCTGAGCGGCTGGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
Db 5461 TGTGACGCTGAGCGGCTGGATGATGATGATGATGATGATGATGATGATGATGATG 5520  
QY 5521 ATCCACCGAGCAGCAGCAAGGCTATCCGGCAATTTGGCTTCAAGACCTTTTCAGA 5580  
Db 5521 ATCCACCGAGCAGCAGCAAGGCTATCCGGCAATTTGGCTTCAAGACCTTTTCAGA 5580  
QY 5581 CGTTCTCTCTCATACCTAGTTAAGCTTTTGAATGATTAATTAATGATGATGATGATG 5640  
Db 5581 CGTTCTCTCTCATACCTAGTTAAGCTTTTGAATGATTAATTAATGATGATGATGATG 5640  
QY 5641 TCATTTCTGAGAACTATAGTCAAGCCAGGAGAGCTGCAAGAGGCTTAAACCGAGAGC 5700  
Db 5641 TCATTTCTGAGAACTATAGTCAAGCCAGGAGAGCTGCAAGAGGCTTAAACCGAGAGC 5700  
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Db 5701 ACTAGACATGATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
QY 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
Db 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
QY 5821 CGAACAAGTCAAGATCATATGATGATGATGATGATGATGATGATGATGATGATG 5880  
Db 5821 CGAACAAGTCAAGATCATATGATGATGATGATGATGATGATGATGATGATGATG 5880  
QY 5881 GGTGCAATTCCTGAGCGCTTCAAGAAAGCTTTCAGAAAGCTTTCAGAAAGCTTTCAG 5940  
Db 5881 GGTGCAATTCCTGAGCGCTTCAAGAAAGCTTTCAGAAAGCTTTCAGAAAGCTTTCAG 5940  
QY 5941 AGGAGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
Db 5941 AGGAGAGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
QY 6001 TCTCATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6060  
Db 6001 TCTCATCAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6060  
QY 6061 GCGGAGAGCAAGAGCGCGCGGAGAGGAGTGGCTCTTTGAGCCGATGATGATGATG 6120  
Db 6061 GCGGAGAGCAAGAGCGCGCGGAGAGGAGTGGCTCTTTGAGCCGATGATGATGATG 6120  
QY 6121 GCGATGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6180  
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QY 6241 AGAGTATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
Db 6241 AGAGTATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
QY 6301 CGCGCGGCGGAGCAAGAGCGCGGAGAGTCCGGAAGGCTGAGCGCGGAGCAAG 6360  
Db 6301 CGCGCGGCGGAGCAAGAGCGCGGAGAGTCCGGAAGGCTGAGCGCGGAGCAAG 6360  
QY 6361 CGCGCGGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6420



Db 6361 CCGCGTTCGTGTGAGAGCGAGCGGTTCTGTGACGAGAACCGGCCAAGAGTGTCATCC 6420  
Qy 6421 ACTGCGATCGCCGAGCATCAGTCGCGGACGCGGATGTCTGAGCAGGCGCTGCGCC 6480  
Db 6421 ACTGCGATCGCCGAGCATCAGTCGCGGACGCGGATGTCTGAGCAGGCGCTGCGCC 6480  
Qy 6481 CCTTCAGAGTGCACGCGAGTATTAGCTCTAGA 6513  
Db 6481 CCTTCAGAGTGCACGCGAGTATTAGCTCTAGA 6513  
RESULT 2  
AAT33238  
ID AAT33238 standard; cDNA; 6513 BP.  
XX  
AC AAT33238;  
XX  
DT 15-OCT-1996 (first entry)  
XX  
DE Drosophila para voltage-activated sodium channel cDNA.  
XX  
KW Para voltage-activated sodium channel; cation channel; insecticide;  
KW archinicide; pesticide; neuroprotective; ischaemia; antagonist; therapy;  
KM monoclonal antibody; ss.  
XX  
OS Drosophila melanogaster.  
XX  
PN MO9614860-A1.  
XX  
PD 23-MAY-1996.  
XX  
PF 06-NOV-1995; 95WO-US014262.  
XX  
PR 10-NOV-1994; 94US-00338702.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Van Der Ploeg LHT, Warmke JW;  
XX  
DR WPI; 1996-259563/26.  
XX  
XX Mono-specific antibodies to voltage-activated cation channel - also new  
PT cation channel DNA, useful for identifying channel modulators,  
XX potentially useful partic. as insecticide and neuroprotective agents.  
XX  
PS Claim 17, Page 39-43; 55pp; English.  
XX  
XX A full-length cDNA clone (AAT33238) codes for the Drosophila para voltage  
CC -activated sodium channel (VASC), a protein responsible for the fast  
CC depolarising phase of the action potential that underlies electrical  
CC signalling in neurons, muscles, etc. The cDNA clone was obtd. from 3  
CC overlapping regions of para cDNA isolated by PCR amplification using  
CC primers (see also AAT33239-44) based on a published para sequence.  
CC Recombinant host cells (E.coli, yeast mammalian or insect) expressing the  
CC Drosophila para VASC can be used to identify modulators of insect VAScs,  
CC useful as insecticides and archinicides. VASC antagonists can be used as  
CC neuroprotective agents for treatment of ischaemia in humans  
XX  
SQ Sequence 6513 BP; 1681 A; 1548 C; 1702 G; 1582 T; 0 U; 0 Other;  
Query Match 100.0%; Score 6513; DB 2; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 121 CTGAACATGAAAGAGAGAGCTGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAT 180  
Qy 181 ATGTGCGAAGAAAAAAGAAAAAAGAAATCCGATATGATGACAGAGAGAGAGATGAGATC 240  
Db 181 ATGTGCGAAGAAAAAAGAAAAAAGAAATCCGATATGATGAGAGAGAGAGATGAGATC 240  
Qy 241 CACAACCGGATCTTCACTTGAACAGAGGTGAGCAATTCCTGTTGATGAGAGGACACT 300  
Db 241 CACAACCGGATCTTCACTTGAACAGAGGTGAGCAATTCCTGTTGATGAGAGGACACT 300  
Qy 301 TCCCGCGGAAATGAGCTCCACTCTCGAGATATGATCCCTACTACAGCAATGTAC 360  
Db 301 TCCCGCGGAAATGAGCTCCACTCTCGAGATATGATCCCTACTACAGCAATGTAC 360  
Qy 361 TGAATTCGTAGTTGTAAGCAAGAAAGATATTTTTCCTTTCTGATCAAAAGCA 420  
Db 361 TGAATTCGTAGTTGTAAGCAAGAAAGATATTTTTCCTTTCTGATCAAAAGCA 420  
Qy 421 TGTGAGTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 480  
Db 421 TGTGAGTGTGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTCGATTC 480  
Qy 481 CATTAATTTCCCTATTCATCATCAACCAATTCCTGTCATCGATCCCTGATGATATGC 540  
Db 481 CATTAATTTCCCTATTCATCATCAACCAATTCCTGTCATCGATCCCTGATGATATGC 540  
Qy 541 CGACAGGCCCAAGGTTGAGTCCAGTGAAGTATTCACCGGAATCTACATTTGAT 600  
Db 541 CGACAGGCCCAAGGTTGAGTCCAGTGAAGTATTCACCGGAATCTACATTTGAT 600  
Qy 601 CAGCTGTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660  
Db 601 CAGCTGTTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 660  
Qy 661 CATGGAATTTGCTGAGCTCTGATTAATAGCTTATAGTATGATGATGATGATGATGAT 720  
Db 661 CATGGAATTTGCTGAGCTCTGATTAATAGCTTATAGTATGATGATGATGATGATGAT 720  
Qy 721 TAGGTAATCTAGACAGCCCTGAGAGCTTTAGAGGTGTCGAGAGCGCTTAAACCGTAGCA 780  
Db 721 TAGGTAATCTAGACAGCCCTGAGAGCTTTAGAGGTGTCGAGAGCGCTTAAACCGTAGCA 780  
Qy 781 TTGTGCGAGGTTGAAGAACCATGCTGCGCCCGCTCATGGAATGATGATGATGATGATG 840  
Db 781 TTGTGCGAGGTTGAAGAACCATGCTGCGCCCGCTCATGGAATGATGATGATGATGATG 840  
Qy 841 ATGTGATTTATCTGACCATGATTTCTCCTGTGCGGTTCGCGGTGATGATGATGATGATG 900  
Db 841 ATGTGATTTATCTGACCATGATTTCTCCTGTGCGGTTCGCGGTGATGATGATGATGATG 900  
Qy 901 ATATGAGCGGTGCTCAGCAGAGAGTGCATCAAGAGTTCCGCTGAGCGTTCTTGAGGCA 960  
Db 901 ATATGAGCGGTGCTCAGCAGAGAGTGCATCAAGAGTTCCGCTGAGCGTTCTTGAGGCA 960  
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Db 1021 ACGAGGCGATCTCATTTCCGTTATGCGGCAATATATCCGATGCGGCAATGCGAGCAAG 1080  
Qy 1081 ATTAAGTGTGCTGACAGAGGTTTGTGTCGAATCGAATTAATGCTACACAGCTTGAT 1140  
Db 1081 ATTAAGTGTGCTGACAGAGGTTTGTGTCGAATCGAATTAATGCTACACAGCTTGAT 1140  
Qy 1141 CGTTGCGATGAGGCTTTCTGCTCCGCTTCGCGGTGATGACACAGACTTTGAGAGATC 1200  
Db 1141 CGTTGCGATGAGGCTTTCTGCTCCGCTTCGCGGTGATGACACAGACTTTGAGAGATC 1200  
Qy 1201 TGTACAGCTGTGTTGTGCGCGCGGACATGAGCAATGCTGTTCTTATAGTATCA 1260  
Db 1201 TGTACAGCTGTGTTGTGCGCGCGGACATGAGCAATGCTGTTCTTATAGTATCA 1260

Db 1201 TGTACCAAGCTGGTGTGGCGCGCCGACCATGACATGCTGTCTTTATAGTCATCA 1260  
QY 1261 TCTTCCAGGTTCAATCTATCTTTGAAATTTTGGCCATTTGTCATGCTGATG 1320  
Db 1261 TCTTCCAGGTTCAATCTATCTTTGAAATTTTGGCCATTTGTCATGCTGATG 1320  
QY 1321 ACGAATTTGCAAGAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
Db 1321 ACGAATTTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380  
QY 1381 CGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
Db 1381 CGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440  
QY 1441 AGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
Db 1441 AGGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500  
QY 1501 GTCCGAGATTTCTTCATGAGCTATGCTATTTGTTGGCGGAGAGAGAGAGAG 1560  
Db 1501 GTCCGAGATTTCTTCATGAGCTATGCTATTTGTTGGCGGAGAGAGAGAGAG 1560  
QY 1561 ACAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
Db 1561 ACAACAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1620  
QY 1621 TTATACAAAGACACAGACACCTTACACAGACACCAAGCTACCAAGTTCGAAAGTGA 1680  
Db 1621 TTATACAAAGACACAGACACCTTACACAGACACCAAGCTACCAAGTTCGAAAGTGA 1680  
QY 1681 GCAAGCATCTTATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
Db 1681 GCAAGCATCTTATCTTATCTTACCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1740  
QY 1741 CTCACAAGTACAGATACGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
Db 1741 CTCACAAGTACAGATACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1800  
QY 1801 AGCCATTTGATTTGTCAACATATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
Db 1801 AGCCATTTGATTTGTCAACATATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1860  
QY 1861 AGCCATTTGATTTGTCAACATATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
Db 1861 AGCCATTTGATTTGTCAACATATCAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1920  
QY 1921 GCAATCTAGGCTCCGACACTCATCTGATATCTTCCGATCAGTCCGATATCTGATATCT 1980  
Db 1921 GCAATCTAGGCTCCGACACTCATCTGATATCTTCCGATCAGTCCGATATCTGATATCT 1980  
QY 1981 CAGATGGCGATCTATCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040  
Db 1981 CAGATGGCGATCTATCTGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2040  
QY 2041 GCAAAATTTGCGCAACCGGACACAGCAATCATGAGAGAGAGAGAGAGAGAGAG 2100  
Db 2041 GCAAAATTTGCGCAACCGGACACAGCAATCATGAGAGAGAGAGAGAGAGAGAG 2100  
QY 2101 CTTGTCTGACACCAATCACAAGCTGATCTGCGATCTGCAAAATTTGCTGAGAGTGA 2160  
Db 2101 CTTGTCTGACACCAATCACAAGCTGATCTGCGATCTGCAAAATTTGCTGAGAGTGA 2160  
QY 2161 CGGACGAAAGCTGGCAAGATTTAAATCATGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
Db 2161 CGGACGAAAGCTGGCAAGATTTAAATCATGAGAGAGAGAGAGAGAGAGAGAGAG 2220  
QY 2221 AAAAGGATTTGATATGAAAGATGATGCTGATGATGATGATGATGATGATGATGATG 2280  
Db 2221 AAAAGGATTTGATATGAAAGATGATGATGATGATGATGATGATGATGATGATG 2280  
QY 2281 GTGCGGACAGTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
Db 2281 GTGCGGACAGTGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340

QY 2341 ATGACGAGAGATGGGCGGACGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
Db 2341 ATGACGAGAGATGGGCGGACGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400  
QY 2401 AATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460  
Db 2401 AATGATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2460  
QY 2461 TCAATGCTTTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2520  
Db 2461 TCAATGCTTTGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2520  
QY 2521 TGTTCATGCAATGATATCAACAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
Db 2521 TGTTCATGCAATGATATCAACAGATATGAGAGAGAGAGAGAGAGAGAGAGAGAG 2580  
QY 2581 GCAACTAATTTCTTCAACGACCTTTGCGATGAGAGAGAGAGAGAGAGAGAGAGAG 2640  
Db 2581 GCAACTAATTTCTTCAACGACCTTTGCGATGAGAGAGAGAGAGAGAGAGAGAGAG 2640  
QY 2641 GCGCCAAAGTATTTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
Db 2641 GCGCCAAAGTATTTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2700  
QY 2701 CGCTATTTGGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
Db 2701 CGCTATTTGGAACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2760  
QY 2761 TGTGCTGATTTTCAAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
Db 2761 TGTGCTGATTTTCAAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2820  
QY 2821 TGGGACGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880  
Db 2821 TGGGACGACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2880  
QY 2881 TCTTTGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940  
Db 2881 TCTTTGCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2940  
QY 2941 TTTCCGATGGCGACCTGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000  
Db 2941 TTTCCGATGGCGACCTGCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3000  
QY 3001 TGTTCGCGGATGCTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060  
Db 3001 TGTTCGCGGATGCTGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3060  
QY 3061 ATGCTCGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3120  
Db 3061 ATGCTCGGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3120  
QY 3121 ACCCTTTCTTGAAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3180  
Db 3121 ACCCTTTCTTGAAGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 3180  
QY 3181 CCGATTAACGATATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240  
Db 3181 CCGATTAACGATATGAGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3240  
QY 3241 GGGTTAAGCGATATTTGCTGATTTGTTCAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA 3300  
Db 3241 GGGTTAAGCGATATTTGCTGATTTGTTCAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA 3300  
QY 3301 TAAAGTAAACCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
Db 3301 TAAAGTAAACCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3360  
QY 3361 AATGATTAACCAACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420  
Db 3361 AATGATTAACCAACATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3420

QY	3421	AGGGGATCAAGGAGGAGCGCACTGGAGTGGCCATGGGGATGGATGGAATTCA	3480
Db	3421	AGGGGATCAAGGAGGAGCGCACTGGAGTGGCCATGGGGATGGATGGAATTCA	3480
QY	3481	TACAGCGGCACATGGAAGAACCAAGCGCAAAATCCAAATATCTTAATTAACGACGA	3540
Db	3481	TACACGGGCACATGGAAGAACCAAGCGCAAAATCCAAATATCTTAATTAACGACGA	3540
QY	3541	TGATTGGCAACTCAATTAAACAACAAGCAATAGA CTGGAACACGAGCTAAACATAG	3600
Db	3541	TGATTGGCAACTCAATTAAACAACAAGCAATAGA CTGGAACACGAGCTAAACATAG	3600
QY	3601	GTTTTCTCTTAACAGACGACACTGCCAGATTAACTCATATGTGTCCATAAATC	3660
Db	3601	GTTTTCTCTTAACAGACGACACTGCCAGATTAACTCATATGTGTCCATAAATC	3660
QY	3661	GACCAATTCAAGGACGAGGCCAAGGGAGCGCGAGACGATGAGGCGACGAGAAC	3720
Db	3661	GACCAATTCAAGGACGAGGCCAAGGGAGCGCGAGACGATGAGGCGACGAGAAC	3720
QY	3721	GCGAGCGCCAGCAAGAGGATTTAGTCTTCACGAGAACTGACACGAGAGGGCGAATCG	3780
Db	3721	GCGAGCGCCAGCAAGAGGATTTAGTCTTCACGAGAACTGACACGAGAGGGCGAATCG	3780
QY	3781	AGGAGGGCCCGCTCGACGGTGATCATTTATTCATGCAACGACGAGATATCTCGATG	3840
Db	3781	AGGAGGGCCCGCTCGACGGTGATCATTTATTCATGCAACGACGAGATATCTCGATG	3840
QY	3841	AATATCCAGCTGATGTGCTGCCCCGAGTTGTAATATAAGAAATTCGATCTTAAGCCGCTG	3900
Db	3841	AATATCCAGCTGATGTGCTGCCCCGAGTTGTAATATAAGAAATTCGATCTTAAGCCGCTG	3900
QY	3901	ACGATGACTCGCGCTGTTCGCGCAGGATGGGCAATTTACACTGAAACTTTTCAATTA	3960
Db	3901	ACGATGACTCGCGCTGTTCGCGCAGGATGGGCAATTTACACTGAAACTTTTCAATTA	3960
QY	3961	TTGAAATTAATATTTTGAACAAGCTGTATATCATATGATTTTAATGATAGTACGTT	4020
Db	3961	TTGAAATTAATATTTTGAACAAGCTGTATATCATATGATTTTAATGATAGTACGTT	4020
QY	4021	TGGCAATTGAAGATGATACATCGCCACAAGGCCATCTCAGAGATTTTATATCTTA	4080
Db	4021	TGGCAATTGAAGATGATACATCGCCACAAGGCCATCTCAGAGATTTTATATCTTA	4080
QY	4081	TGACAGAAATTTTACGGTTATATCTTCTTGGAAATGTATATCAAGTGTGGCGCTCG	4140
Db	4081	TGACAGAAATTTTACGGTTATATCTTCTTGGAAATGTATATCAAGTGTGGCGCTCG	4140
QY	4141	GCTTCAAAAGTATCTTCAACAACGGGTGTGTGGCTCGATTTGCTGATGTATCTAT	4200
Db	4141	GCTTCAAAAGTATCTTCAACAACGGGTGTGTGGCTCGATTTGCTGATGTATCTAT	4200
QY	4201	CGCTTATCAACTTGGTGTCTTCACTTGTGAGCTGTGTGTATCAAGCTTCAAGACTA	4260
Db	4201	CGCTTATCAACTTGGTGTCTTCACTTGTGAGCTGTGTGTATCAAGCTTCAAGACTA	4260
QY	4261	TGCGAAGCTTAAAGACACTGAGACCACTACGAGCAATGCCGATGAGAGGGCATGAGG	4320
Db	4261	TGCGAAGCTTAAAGACACTGAGACCACTACGAGCAATGCCGATGAGAGGGCATGAGG	4320
QY	4321	TGCTGTATTAATGCGCTGTGTACAAAGCTATACGCTTCATTAATGTGTCTATTTG	4380
Db	4321	TGCTGTATTAATGCGCTGTGTACAAAGCTATACGCTTCATTAATGTGTCTATTTG	4380
QY	4381	TAAATTTTGGCTAATTTTGGCATATAGGGTGTACAGCTTTTGGCTGAAAAATTTTA	4440
Db	4381	TAAATTTTGGCTAATTTTGGCATATAGGGTGTACAGCTTTTGGCTGAAAAATTTTA	4440
QY	4441	AGTGGAGGACATGATGGGACGAAGAGCTCAGCAGAGATATACAAATGCGCAATGCT	4500
Db	4441	AGTGGAGGACATGATGGGACGAAGAGCTCAGCAGAGATATACAAATGCGCAATGCT	4500
QY	4501	GCGAAGCGAGAACTACAGTGGGTGAATTCAGCAATGAATTTGATCANTAGATGAC	4560

Db	4501	GGGAGGCGAAGACCTACACGTGGGGAATTCAGCAATGAAATTCGATCATCTAGGTAAACG	4560
Oy	4561	CGTATCTGTGCTTTTCCAAAGTGGCCACTTCAAGGCTGGATCAAAATCAGAACGATG	4620
Db	4561	CGTATCTGTGCTTTTCCAAAGTGGCCACTTCAAGGCTGGATCAAAATCAGAACGATG	4620
Oy	4621	CTATCGATTCCAGAGAGGTGGACAGCAACCAATTCGTAAACGAACTCACTCATATT	4680
Db	4621	CTATCGATTCCAGAGAGGTGGACAGCAACCAATTCGTAAACGAACTCACTCATATT	4680
Oy	4661	TATATTTGATATTCCTTCACTCATATTGGATTCCTTTTCACTCAATCTGTTCATTTGTG	4740
Db	4661	TATATTTGATATTCCTTCACTCATATTGGATTCCTTTTCACTCAATCTGTTCATTTGTG	4740
Oy	4741	TTATCATTTGATATTTTATATAGCAAAAAGAAAAGAGGATGATTCATTAGAAATGTTCA	4800
Db	4741	TTATCATTTGATATTTTATATAGCAAAAAGAAAAGAGGATGATTCATTAGAAATGTTCA	4800
Oy	4801	TGACAGAAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT	4860
Db	4801	TGACAGAAAGATCAGAAAAAGTACTATAATGCTATGAAAAAGATGGGCTCTAAAAAACCAT	4860
Oy	4861	TAAAAACCATTCCAAGACCAAGGGTGGGACCAACAGCAATATGTCTTTGAAATAGTAACCG	4920
Db	4861	TAAAAACCATTCCAAGACCAAGGGTGGGACCAACAGCAATATGTCTTTGAAATAGTAACCG	4920
Oy	4921	ATTAAGAAATTCGATATATATCATATATGTTATTCATTGGCTGACATGTTCCACATGACCC	4980
Db	4921	ATTAAGAAATTCGATATATATCATATATGTTATTCATTGGCTGACATGTTCCACATGACCC	4980
Oy	4961	TCGATCGTTACGATGCGTCGGACACGATATAACGGCGCTCTAGACTATCTCAATGCGATAT	5040
Db	4961	TCGATCGTTACGATGCGTCGGACACGATATAACGGCGCTCTAGACTATCTCAATGCGATAT	5040
Oy	5041	TCGTATGTTATTTTCAAGTTCCGAATGCTATTAATAATATTTGGCTTTACGATATCACTAAT	5100
Db	5041	TCGTATGTTATTTTCAAGTTCCGAATGCTATTAATAATATTTGGCTTTACGATATCACTAAT	5100
Oy	5101	TTATTTAGCCATGGAATTTATTTATGATGATGATGTCATTTTATTCATCTTAGGCTCTTG	5160
Db	5101	TTATTTAGCCATGGAATTTATTTATGATGATGATGTCATTTTATTCATCTTAGGCTCTTG	5160
Oy	5161	TACTTAGCGATATTTATCGAAGAACTTCGTGTCGCCGACCTTCGTCGAGTGTGCGTG	5220
Db	5161	TACTTAGCGATATTTATCGAAGAACTTCGTGTCGCCGACCTTCGTCGAGTGTGCGTG	5220
Oy	5221	TGGCGAAAGTGGGCGGTGTCCTTCGACTGGTGAAGGAGCCAAAGGGCATTTGGACACTGC	5280
Db	5221	TGGCGAAAGTGGGCGGTGTCCTTCGACTGGTGAAGGAGCCAAAGGGCATTTGGACACTGC	5280
Oy	5281	TCTTTCGGTGGGCAATGTCGTGCGCGGCCCTGTTCAACATCTGCTGCTGTTTCCGG	5340
Db	5281	TCTTTCGGTGGGCAATGTCGTGCGCGGCCCTGTTCAACATCTGCTGCTGTTTCCGG	5340
Oy	5341	TCATGTTCACTTTTGCAATTTTCCGCAATGTCGTTCAATGCACTGCAAGAGAGAAGACG	5400
Db	5341	TCATGTTCACTTTTGCAATTTTCCGCAATGTCGTTCAATGCACTGCAAGAGAGAAGACG	5400
Oy	5401	GCATTTAAGCAGCTGTAACAATCTTAAGAATTGGCCAGAGCATGATCTGTCTTTTACA	5460
Db	5401	GCATTTAAGCAGCTGTAACAATCTTAAGAATTGGCCAGAGCATGATCTGTCTTTTACA	5460
Oy	5461	TGTGACGTCACGCGGTGGATGTTGATCTGACGCGCATTTATCAATAGAGAAACATGCG	5520
Db	5461	TGTGACGTCACGCGGTGGATGTTGATCTGACGCGCATTTATCAATAGAGAAACATGCG	5520
Oy	5521	ATTCACCCGACAGCGCAAAAGGCTATCCGGGCAATTTGGTTACGACACGTTGGATATA	5580
Db	5521	ATTCACCCGACAGCGCAAAAGGCTATCCGGGCAATTTGGTTACGACACGTTGGATATA	5580
Oy	5581	CGTTTCTCTCTACACCTAGTTTAAAGCTTTTGTATGATTTATATATGTAATGTAATGCTG	5640

Db	5581	CGTTTCTCCTCTCACTACCTTAGTTAATGAAGCTTTTGGATAGTATTAATATATGACATTGCTG	5640
Qy	5641	TCATTTCCTGAGAACTTAATAGTCAGGCCACCCGAGACGTTGCAGAGAGGGTCTTAACCGACGACG	5700
Db	5641	TCATTTCCTGAGAACTTAATAGTCAGGCCACCCGAGACGTTGCAGAGAGGGTCTTAACCGACGACG	5700
Qy	5701	ACTACGACATGTACTATGATAGATCTGGGACGAATTCGATCCGAGAGGACCCAGTACACTATAC	5760
Db	5701	ACTACGACATGTACTATGATAGATCTGGGACGAATTCGATCCGAGAGGACCCAGTACACTATAC	5760
Qy	5761	GCTATGATCAGCTGTCCGAATTCCTGGAAGCTGACTGGAGCCCCCGCTGCAGATCCACAAC	5820
Db	5761	GCTATGATCAGCTGTCCGAATTCCTGGAAGCTGACTGGAGCCCCCGCTGCAGATCCACAAC	5820
Qy	5821	CGAACCAATGTAAGAATGCAATGATGAGCATACCACATGTGTCGGGGTCACTCATGTACT	5880
Db	5821	CGAACCAATGTAAGAATGCAATGATGAGCATACCACATGTGTCGGGGTCACTCATGTACT	5880
Qy	5881	GCGTCGACATCCTCGACCGCCCTTAAGAAAGACTTCTTTGCGCGGAGGGCAATCCGATAG	5940
Db	5881	GCGTCGACATCCTCGACCGCCCTTAAGAAAGACTTCTTTGCGCGGAGGGCAATCCGATAG	5940
Qy	5941	AGAGACCGGGTGAAGATTGGTGAAGTAAAGGGCCCGCCCGGATACGAGAGGGGCTACAGACCGC	6000
Db	5941	AGAGACCGGGTGAAGATTGGTGAAGTAAAGGGCCCGCCCGGATACGAGAGGGGCTACAGACCGC	6000
Qy	6001	TCTCATCAACCTGTGGCGTGCAGCGCTGAGAGAGTACTGCGCCCGGCTAATCCAGCACGCTT	6060
Db	6001	TCTCATCAACCTGTGGCGTGCAGCGCTGAGAGAGTACTGCGCCCGGCTAATCCAGCACGCTT	6060
Qy	6061	GGCGAAGACACAAGGCCGGCGCGCGAGAGAGTGGGTCTCTTGAAGCCGATACGATCATG	6120
Db	6061	GGCGAAGACACAAGGCCGGCGCGCGAGAGAGTGGGTCTCTTGAAGCCGATACGATCATG	6120
Qy	6121	GCGATGCGGGTGAATCCGATGCGCGGGAGACCCGGCCGCCGATGAACAAACGAGCGGATG	6180
Db	6121	GCGATGCGGGTGAATCCGATGCGCGGGAGACCCGGCCGCCGATGAACAAACGAGCGGATG	6180
Qy	6181	CGCCCGCTGGTGGAGATGGTATGTTAACGGTACTGCAAGAAAGAACTGCGATGCGGATG	6240
Db	6181	CGCCCGCTGGTGGAGATGGTATGTTAACGGTACTGCAAGAAAGAACTGCGATGCGGATG	6240
Qy	6241	AGAGTAATGTTAAATGTCGCGGGTGAAGATGCAGCGCGCGCGGACAGACGACGACGACG	6300
Db	6241	AGAGTAATGTTAAATGTCGCGGGTGAAGATGCAGCGCGCGCGGACAGACGACGACGACGACG	6300
Qy	6301	CGGCGGCGCGCGGACAGACGACGCGCGGAATGCCGAGACGGGGTATGCGCCGGCGACAG	6360
Db	6301	CGGCGGCGCGCGGACAGACGACGCGCGGAATGCCGAGACGGGGTATGCGCCGGCGACAG	6360
Qy	6361	CGGCGGTTCTCGTGAAGAGCGACGGGTTGTATCGAAGAAACGGGCAACAAAGTGTGTCATCC	6420
Db	6361	CGGCGGTTCTCGTGAAGAGCGACGGGTTGTATCGAAGAAACGGGCAACAAAGTGTGTCATCC	6420
Qy	6421	ACTCGGATCGCCGAGCATCACGTGCGCGGACGCGCGGATGTCTGAGCAGAGCTTCGCCCC	6480
Db	6421	ACTCGGATCGCCGAGCATCACGTGCGCGGACGCGCGGATGTCTGAGCAGAGCTTCGCCCC	6480
Qy	6481	CCCTCCAAATGACAGCGGAGTATTAAGCTTAA	6513
Db	6481	CCCTCCAAATGACAGCGGAGTATTAAGCTTAA	6513

RESULT 3  
ABL15853  
ID ABL15853 standard; cDNA; 6527 BP.

AC ABL15853;

DT 26-MAR-2002 (first entry)

DE *Drosophila melanogaster* expressed polynucleotide SEQ ID NO 42041.

“

KW Drosophila; developmental biology; cell signalling; insecticide;  
 KM pharmaceutical; gene; ss.  
 XX  
 OS Drosophila melanogaster.  
 XX  
 PN W0200171042-A2.  
 XX  
 PD 27-SEP-2001.  
 XX  
 PP 23-MAR-2001; 2001WO-US009231.  
 XX  
 PR 23-MAR-2000; 2000US-0191637P.  
 PR 11-JUL-2000; 2000US-00614150.  
 XX  
 PA (PEKE ) PE CORP NY.  
 XX  
 PI Venter JC, Adams M, Li PWD, Myers EW;  
 XX  
 DR WPI; 2001-656860/75.  
 DR P-PSDB; ABB71750.  
 XX  
 PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 PT genes from Drosophila and for elucidating cell signalling and cell-cell  
 PI interactions.  
 XX  
 PS Claim 1; SEQ ID NO 42041; 21bp + Sequence listing; English.

The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from *Protophila*. The invention is useful in developmental biology and in elucidating cell signaling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (AB1161716-AB130511), expressed DNA sequences (AB01840-AB116175) and the encoded proteins (ABBS73737-ABBS74022). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from [ftp.wipo.int/pub/published\\_pct\\_sequences](http://www.wipo.int/pub/published_pct_sequences)

Query Match	Similarity	95.3%	Score 6209.6	DB 4	Length 6527
Best Local	Similarity	97.9%	Pred. No. 0		
Matches	6355	Conservative	0	Mismatches	34
				Indels	105
				Gaps	2
QY	1	TC TAGACGTTGGCCCGCATGACATGACAGAAAGATTCCGACTCCATATCTGAGAAAGAAC	60		
Db	109	TCTCATCTGGCCCGCATGACAAATGACAGAAAGATTCCGACTCGATATCTGAGAAAGAAC	168		
QY	61	GCAGTTGTTCGCGCCCTTACCCCGCATCATTTGTGTCAATCAACAACGATTTGCGC	120		
Db	169	GCAGTTGTTCGCGCCCTTACCCCGCATCATTTGTGTCAATCAACAACGATTTGCGC	228		
QY	121	CTGAACATGAAAAAGCAGAGAGCTGGAAGAAAGAAAGCCGAGGAGAGTGCCTGCAT	180		
Db	229	CTGAACATGAAAAAGCAGAGAGCTGGAAGAAAGAAAGCCGAGGAGAGTGTATCT	288		
QY	181	ATGTGTGCAAGAAAAAACAAGAAATCCGATATGATGACAGGACGAGATGAAGTTC	240		
Db	289	ATTGTGTGCAAGAAAAAACAAGAAATCCGATATGATGACAGGAGATGAAGTTC	348		
QY	241	CACAACCGGATCTCACTTGAACAAGGTGTGCCAAATCCTGTTCGATTGACGGGACGT	300		
Db	349	CACAACCGGATCTCACTTGAACAAGGTGTGCCAAATCCTGTTCGATTGACGGGACGT	408		
QY	301	TCCCGCCGGAATTGGCTTCACTCTCTTCGAGAGATATGCAATCCCATCAACAATGTAC	360		
Db	409	TCCCGCCGGAATTGGCTTCACTCTCTTCGAGAGATATGCAATCCCATCAACAATGTAC	468		
QY	361	TGACATTCGTAGTTGTGAACAAGAAAGATATTTTTCGCTTTCTGCATCAAAAGCAA	420		
Db	469	TGACATTCGTAGTTGTGAACAAGAAAGATATTTTTCGCTTTCTGCATCAAAAGCAA	528		
QY	421	TGTGATGCTCGATTCATTCAATCCGATACGTGTGTGGCATTTAATCTTAGTGTCATC	480		

Db 529 TGTGATCTGATCATTTCAATCCGATACGTCGTGTGGCCATTACATTAGTCATC 588  
Qy 481 CATTATTTTCCCTATTCAATCAACACAAATTCGTCAATCGATCCTGATGATATGC 540  
Db 589 CATTATTTTCCCTATTCAATCAACACAAATTCGTCAATCGATCCTGATGATATGC 648  
Qy 541 CGACAAAGCCCAAGGTTGATGCTGATGATGATATTTCAACCGGATCTACATTTGAT 600  
Db 649 CGACAAAGCCCAAGGTTGATGCTGATGATGATATTTCAACCGGATCTACATTTGAT 708  
Qy 601 CAGCTGTAAAGATGATGCAAGAGGTTTCAATTTATGCGGTTTACGATCTTAGATG 660  
Db 709 CAGCTGTAAAGATGATGCAAGAGGTTTCAATTTATGCGGTTTACGATCTTAGATG 768  
Qy 661 CATGGAATTTGCTGATCTTGTATGATGATGATGATGATGATGATGATGATGAT 720  
Db 769 CATGGAATTTGCTGATCTTGTATGATGATGATGATGATGATGATGATGATGAT 828  
Qy 721 TAGGTAATCTAGACAGCCCTGCGAAGTTTATGAGTCTGAGAGCCTTAAACCGTAGCA 780  
Db 829 TAGGTAATCTAGACAGCCCTGCGAAGTTTATGAGTCTGAGAGCCTTAAACCGTAGCA 888  
Qy 781 TTGTGCGAGGCTTGAAGCAATGTCGAGCGCGTATGGAATCGGTGAAGATCTGCGG 840  
Db 889 TTGTGCGAGGCTTGAAGCAATGTCGAGCGCGTATGGAATCGGTGAAGATCTGCGG 948  
Qy 841 ATGTGATTAATCTGACCAATGTTCTCTGTGCTGATGATGATGATGATGATGATGAT 900  
Db 949 ATGTGATTAATCTGACCAATGTTCTCTGTGCTGATGATGATGATGATGATGATGAT 1008  
Qy 901 ATATGAGGCTGCTCAAGCAAGATGATCAAGAAATTCCTGTCGATGATGATGATGAT 960  
Db 1009 ATATGAGGCTGCTCAAGCAAGATGATCAAGAAATTCCTGTCGATGATGATGATGAT 1068  
Qy 961 ATTCGACCGAGAGAACTGGGACTATCACAATGCAATGCTTCAATGATGATGATGAT 1020  
Db 1069 ATTCGACCGAGAGAACTGGGACTATCACAATGCAATGCTTCAATGATGATGATGAT 1128  
Qy 1021 ACAGAGGAGATCATTTCCGTTATGCGGCAATATATCCGTCGCGGAGCAATGCGAGC 1080  
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Db 4843 ACGTAAACGGGCTCTAGACTATCTCAATGCGATATTCGATTAATTTCCGAA 4902  
Qy 5064 TGTCTATTAATAATTTGCGCTTACGATATCAATTTTATTTAGCCATGAAATTTAT 5123  
Db 4903 TGTCTATTAATAATTTGCGCTTACGATATCAATTTTATTTAGCCATGAAATTTAT 4962  
Qy 5124 GATGTAGTATGTTGATTTATTCATCTTAAAGTCTTGTACTTAAAGATTTATCGAAG 5183  
Db 4963 GATGTAGTATGTTGATTTATTCATCTTAAAGTCTTGTACTTAAAGATTTATCGAAG 5022  
Qy 5184 TACTTGTGTCCCGCACTCTGCTCCGATGCGTGTGGGAAAGTGGGCGTGTCTT 5243  
Db 5023 TACTTGTGTCCCGCACTCTGCTCCGATGCGTGTGGGAAAGTGGGCGTGTCTT 5082  
Qy 5244 CGACTGTGTAAGGAGCCAAAGGCAATTCGACACTGCTTTTCGCTTGGCCATGTGCTG 5303  
Db 5083 CGACTGTGTAAGGAGCCAAAGGCAATTCGACACTGCTTTTCGCTTGGCCATGTGCTG 5142  
Qy 5304 CCGGCTCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5363  
Db 5143 CCGGCTCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5202  
Qy 5364 GCGATGTGCTTCAATGACGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5423  
Db 5203 GCGATGTGCTTCAATGACGTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5262  
Qy 5424 AAGACCTTTTGGCCAGACATGATCTGCTTTCAAGATGCACTGACGCTGGGAT 5483  
Db 5263 AAGACCTTTTGGCCAGACATGATCTGCTTTCAAGATGCACTGACGCTGGGAT 5322  
Qy 5484 GGTGTACTGAGCGCATTTATCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5543  
Db 5323 GGTGTACTGAGCGCATTTATCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5382  
Qy 5544 TATCCGGGCAATTTGCTGCTCAAGCAGCTTGGAAATTAACCTTTCTCTCATACCTAG 5603  
Db 5383 TATCCGGGCAATTTGCTGCTCAAGCAGCTTGGAAATTAACCTTTCTCTCATACCTAG 5442  
Qy 5604 ATAACTTTTGTATGATTAATTAATGATATGATGATGATGATGATGATGATGATGATG 5663  
Db 5443 ATAACTTTTGTATGATTAATTAATGATATGATGATGATGATGATGATGATGATGATG 5502  
Qy 5664 GCCACCGAGAGCTGTGAAGAGGCTTAACCGACGACGACGACGACGACGACGACGACG 5723  
Db 5503 GCCACCGAGAGCTGTGAAGAGGCTTAACCGACGACGACGACGACGACGACGACGACG 5562  
Qy 5724 TGGCAGCAATTCGATCCGAGGAGGACCCAGTACATACGCTATGATCAGCTGTCGAATTC 5783  
Db 5563 TGGCAGCAATTCGATCCGAGGAGGACCCAGTACATACGCTATGATCAGCTGTCGAATTC 5622  
Qy 5784 CTGACGCTACTGAGACCCCGCTGCTGCAATTCACAAACCAACCAACCAACCAACCAAC 5843  
Db 5623 CTGACGCTACTGAGACCCCGCTGCTGCAATTCACAAACCAACCAACCAACCAACCAAC 5682  
Qy 5844 ATGACATCAACCACTGTGCGGCTGACCTCATGCTGCTGACATCTCTGACGCGCTT 5903  
Db 5683 ATGACATCAACCACTGTGCGGCTGACCTCATGCTGCTGACATCTCTGACGCGCTT 5742  
Qy 5904 ACGAAAGACTTCTTTGGCGGAAAGGCAATCCGATAGAGGAGACGGGTGAGATTTGGT 5963  
Db 5743 ACGAAAGACTTCTTTGGCGGAAAGGCAATCCGATAGAGGAGACGGGTGAGATTTGGT 5802  
Qy 5964 ATAGCCGCCCGCCGATTAAGAGGCTGAGAGGCTGATCAACAGCTGTGAGCTGAG 6023  
Db 5803 ATAGCCGCCCGCCGATTAAGAGGCTGAGAGGCTGATCAACAGCTGTGAGCTGAG 5862  
Qy 6024 CGTGAAGATGACTGCGCCGCTATTCAGACAGCTTGGGAAAGCAAGAGGCGCGGCG 6083  
Db 5863 CGTGAAGATGACTGCGCCGCTATTCAGACAGCTTGGGAAAGCAAGAGGCGCGGCG 5922

QY 6084 GAGGAGGTGGTCTTTGAGCCGATACGATCATGCGGATGGCGGATGCC 6143  
 DB 5923 GAGGAGGTGGTCTTTGAGCCGATACGATCATGCGGATGGCGGATGCC 5982  
 QY 6144 GGGGACCCGCGCCCGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6203  
 DB 5983 GGGGACCCGCGCCCGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6042  
 QY 6204 GTTACGGTACTGCAAGAGAGCTCCGATGCGGATGAGATGTAATGTCCGGT 6263  
 DB 6043 GTTACGGTACTGCAAGAGAGCTCCGATGCGGATGAGATGTAATGTCCGGT 6102  
 QY 6264 GAGATGACGCGCGCGCGGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6323  
 DB 6103 GAGATGACGCGCGCGCGGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6162  
 QY 6324 GCGGAGGTGCGGAGCGGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6383  
 DB 6163 GCGGAGGTGCGGAGCGGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6222  
 QY 6384 GGGTTCGATGAGCAAGAGAGCTCCGATGCGGATGAGATGTAATGTCCGGT 6443  
 DB 6223 GGGTTCGATGAGCAAGAGAGCTCCGATGCGGATGAGATGTAATGTCCGGT 6282  
 QY 6444 TCGGACGCGCGGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6503  
 DB 6283 TCGGACGCGCGGATGAGCAACGAGCGGATGCGCCCGCTGTGTGAGATGTGT 6342  
 QY 6504 TAGCTTAG 6512  
 DB 6343 TAGCATGAG 6351

## RESULT 5

AAV40629 standard; cDNA; 6318 BP.

AAV40629;

27-OCT-1998 (first entry)

Musca domestica voltage-sensitive sodium channel gene.

voltage-sensitive sodium channel; insecticide; sensitivity; resistance;

Musca domestica.

Location/Qualifiers

1. 6318

/product= "voltage-sensitive sodium channel"

W09828446-A1.

02-JUL-1998.

18-DEC-1997; 97WO-US024256.

24-DEC-1996; 96US-00772512.

(CORR ) CORNELL RES FOUND INC.

Soderlund DM, Knipple DC, Ingles PJ;

WPI; 1998-377674/32.

P-PSDB; AAW57772.

New isolated voltage-sensitive sodium channel polypeptides - obtained from house flies, which are capable of conferring sensitivity or resistance to an insecticide in insects.

Claim 5; Page 42-45; 96pp; English.

XX The sequence is that encoding a voltage-sensitive sodium channel (VSSC) of *Musca domestica* (NADIM strain). Such a VSSC is capable of conferring sensitivity or resistance to an insecticide. It can be used to screen a cDNA library for other VSSC genes. Antibodies raised the VSSC can be used to detect VSSCs and these can be used in drug screening. Antisense CC nucleic acids and vectors containing the sequence may be used to reduce VSSC expression in an insect. The VSSCs can be used for conferring sensitivity or resistance to insecticides such as DDT and analogues and pyrethroids in insects such as house flies, fruit or vinegar flies, CC tobacco budworm, Colorado potato beetle, German cockroach or yellow fever mosquito

Sequence 6318 BP; 1713 A; 1341 C; 1597 G; 1667 T; 0 U; 0 Other;

Query Match 68.3%; Score 4447.8; DB 2; Length 6318;  
 Best Local Similarity 82.0%; Pred. No. 0;  
 Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;

QY 24 ATGACAGAGATTCGACTCGATATCTGAGAGAGAGCACTTTGTCCTTAC 83  
 DB 1 ATGACAGAGATTCGACTCGATATCTGAGAGAGAGCACTTTGTCCTTAC 60  
 QY 84 CGGATATCTGATGCAATGCAACAGCACTTCCGCTGAAACATGAAAGAGAG 143  
 DB 61 CGGATATCTGATGCAATGCAACAGCACTTCCGCTGAAACATGAAAGAGAG 117  
 QY 144 CTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203  
 DB 118 CTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148  
 QY 204 GAAATCGATATGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
 DB 149 AGATACAGATATGATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207  
 QY 264 CAGGATGCGCAATACCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
 DB 208 CAGGATGCGCAATACCTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAG 267  
 QY 324 CTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 383  
 DB 268 CTTCTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 327  
 QY 384 GGAAGAGATATTTTCTGATGATGATGATGATGATGATGATGATGATGAT 443  
 DB 328 GGAAGAGATATTTTCTGATGATGATGATGATGATGATGATGATGATGAT 387  
 QY 444 CCGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 503  
 DB 388 CCGATACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 447  
 QY 504 ACCAATATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 563  
 DB 448 ACCAATATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 507  
 QY 564 ACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 623  
 DB 508 ACTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 567  
 QY 624 GGTTCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 683  
 DB 568 GGTTCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627  
 QY 684 GTAATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 743  
 DB 628 GTAATAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687  
 QY 744 ACGTTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 803  
 DB 688 ACGTTAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 747  
 QY 804 GTGCGCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863





QY	3009	GTGCTCTGGCGAGAA	TGGA	TGAGAGCCAA	TTGTCGGA	CTGCAATGTA	CGTGGCGGAGTCTCG	3068				
Db	2941	GTGCTGTGCGGAGAG	TGGATGGA	GTCCATGTGGGA	CTGCATGTATGTGGGCGAGTCTGAGC	3000						
QY	3069	TGCATTTCCCTTCTT	CTTGGSCA	CCGTTTGCAT	TCGGCAATCTTGTGTACTTAA	CCCTTTC	3128					
Db	3001	TGTATACCTTCTTCT	TTCGCA	CGGTGCTGAT	TAGGCAATCTTGTGTTCTTATCTTTTC	3066						
QY	3129	TTAGCTTGTCTTTT	GTCCAA	TTTTGGCTCAT	CTAGCTTATCATGCGCGCGATGCGATAC	3188						
Db	3061	TTAGCTTGTCTTTT	GTCCAA	CTTGGCTCAT	CTAGCTTATCATGCGCGCGATGCGCAAT	3120						
QY	3189	GATACGAA	TAAATATP	CCGAGGCTTCA	TATGGAATGGCCGATTTAA	AAAGTTGGTTAAG	3248					
Db	3121	GATACCAAT	TAAATATP	CGAGAGCCCTTCA	TGCTGTATGCTTTTAA	AAACCTGGGTGAA	3180					
QY	3249	CGTATATAT	TGCTGATTTGTTT	CAAGTTATAC	GTAA	CAATATGACAAATCAATATAGTAT	3308					
Db	3181	CGTATATAT	TGCGCGATTTGTTT	TATGATTA	TTGGAA	TATATGCAATCAATATATAGTATC	3240					
QY	3309	CAACCAT	CAGGTGAGAGG	CAACCA	GATCAGTTGATTTT	GAGGAAAGACATGTATC	3368					
Db	3241	CAACCATC-----	-----	-----	-----	AGAACATGGCAT	3261					
QY	3369	AACCAAT	CTGAGAGCTGGG	CCACGACGAT	TCTCGCCGACGGCTCAT	TAAAGAGGAGTC	3428					
Db	3262	AATGAA	CTGAGAGTTGGGT	CATGACCA	MAATCATGGCCGATGGCTTGAT	CAAAAAGGTTATG	3321					
QY	3429	AAGAG	CGACGACCA	CTGAGAGTGGCCAT	TCGGGGATTCGGA	TGGAATTCAGATTCACGGC	3488					
Db	3322	AAGGCG	GAGACCCAGCTG	AGAGTGGCCAT	TGGCGATGGCA	TGAGATTCACATATATGGC	3391					
QY	3489	GACAT	GAAAGAA	CAACCA	CCGAGAAATCCAA	TATCTTAA	TTAACGACATGATTGGC	3548				
Db	3382	GATAT	GAAAAACA	CAAGCCGAGAA	ATCAAA	TTCA	TGAAACAACA	CGATATTTGSA	3441			
QY	3549	AAC	CTAATTA	CCACCA	GAACAT	ATGACTGAA	ACGACTTAA	CCATATGAGTTGTCC	3608			
Db	3442	AAC	CTAATTA	AAACCA	CAATATGAT	CTGAA	CA	TGACTTAA	CCATATGAGTTGTTC	3501		
QY	3609	TTAC	GAGACG	ACGAC	CACTGCGACAT	TTA	CTCAT	TGTATCCAT	TATGACCAATTC	3668		
Db	3502	ATAC	GAGACGATGAC	ACTG	CCACATTTA	CTCAT	TATGATGATAC	CA	TATGACCAATTC	3561		
QY	3669	AAG	ACGAGAC	CCCA	CAAGGCGAC	GGCCGACAG	ACGATGAGAGGCGGAGAA	CCGCGACCC	3728			
Db	3562	AAG	ACGAGAC	CCCA	CAAGGCGAC	GGCCGACAG	CA	TCGAGGGCGAGAGAA	CCGCGACCTC	3621		
QY	3729	AGCA	AGAGAT	TTAGT	CTCTGACG	AGGA	CTGACG	AGGAGGCGAA	TGCGAGAGGGC	3788		
Db	3622	AGCA	AGAGAG	CACTCG	GCCTGACG	AGGA	CTGACG	AGGAGGCGGAGAGGCGGAGTGA	GGGC	3681		
QY	3789	CGC	CTCGACGGT	GAAT	ATCATTA	CTATC	---	A	CA	CGACGAGATATCTGATGA	ATAT	3845
Db	3682	CAG	CTGATGATG	ATCATTA	CTATCAT	TATGCGAA	ACGACG	AGATAT	GACGACAT	3741		
QY	3846	CCA	CTGATTTG	CTGCCC	CGATTCG	TATGATA	AAATTT	CGATCTTA	TAGCCGATGACAT	3905		
Db	3742	CCG	CGACATCT	TTTCCCGAC	CTCG	TATCA	AGAA	AGTTCCGAC	CTTGGCGGCGACGAG	3801		
QY	3906	GACT	CGCCGTTCT	GCGACAGAT	GGGCGCA	TTTACG	ACTGAA	AACTTT	CAATTA	ATGGA	3965	
Db	3802	GACT	CGCCGTTCT	GCGACAGAT	GGGCGCA	TTTACG	ACTGAA	AACTTT	CAATTA	ATGGA	3861	
QY	3966	AAT	TAAATTT	TTTGA	AAACGCT	TTATCA	CTATGAT	TTTA	TATGATGAT	AGTTAG	CTTTGGCA	4025
Db	3862	AAT	TAAATTT	TTTGA	AAACGAG	TTATCA	CTATGAT	TTTA	TATGATGAT	AGTTAG	CTTTGGCC	3921
QY	4026	TTAG	AAGATG	TACATCT	CGCA	CAAA	AGCCAT	TCGACAGAT	TTTATAT	CTATATGAG	4085	
Db	3922	TTAG	AAGATG	ATCTCAT	TTTAC	CCGATC	GCATGAC	AGATAT	ATCTAT	CTACATGAG	3981	
QY	4086	AGAA	TATTTAC	GATTATAT	TCTCTT	GTGAA	TGTTA	TCAAG	TGATGGCGCT	CGGCTTC	4145	

Db	3962	AGGATATTACGGTGAATATCTTTTGGAGATGTTGATCAATAGGTGGCCCTTG6CTTT	4041
Qy	4146	AAAGGTACTTCACCAACGCGTGGTGGTGCATTTTCGATATGTCATGTAATCGCTT	4205
Db	4042	AAAGTTTACTTCACCAATGCGCTGGTGTGGCTGGATTTTCGATATGTCATGTAATCGCTT	41010
Qy	4206	ATCAACTTCGTGCTTCACTTTGTGAGCTGTGTGATTTCAAGCTTCAACATATGCGA	4267
Db	4102	ATTAATTTGGTGGCCGTTTGGTCCGGGCTTAATATATATAGCCGCTTTAGATCAATGCGC	4161
Qy	4266	ACGTTAAGACACTGAGACCACTAGCCGATGTCGATCCGCTATGCAAGGCGATAGGGTGGTC	4325
Db	4162	ACACTGCGCGCTTAAGGCGCATGCGTGTGTCTCTTAATGGAAGGATATAAAGTTGTCTC	4221
Qy	4326	GTTAATGGCGTGTGATCAAGCTATACCGTCCATCTTTCATGTGCTATGTTGTGTATATA	4385
Db	4222	GTGAATGGCGTGTGATCAAGCTATACCGTCCATCTTTCATGTGCTATGTTGTGTATATA	4281
Qy	4386	TTTTGGCTAATTTTTCGCAATATGAGGTGTACAGCTTTTGTCTGAAAAATTTTAAGTGC	4445
Db	4282	TTTTGGCTAATTTTTCGCAATATGAGGTGTACAGAGCTTTTGTCTGAAAAATTTTAAGTGT	4341
Qy	4446	GAGACATGATGTCACGACAGCTCAGCAGAGATCATACCAATTCGAATGCGAATGCGCGAG	4506
Db	4342	AAAGGTGTAATGACACTGTGCTGAGCCGTAATCATACCGAATCGTAATGCGCGCAAA	4401
Qy	4506	AGCGAAGACTACAGTGGGTGAATTCAGCAATGATTTTCATGATGTAGTAAAGCGTAT	4565
Db	4402	AGTGAATATCTACACTGTGGAAAAATTCGCGCATGAACTTCGATCATGTATGTATATTCGAT	4466
Qy	4566	CTGTGCTTTTCCAAAGTGGCCACTTCCAAAGGCTGATACAAATCATGAACGATGCTATTC	4625
Db	4462	CTGTGCTAATTTCAAGTGGCCACTTTCAAAGGCTGATACAGATTAATGAACGATGCTATTC	4521
Qy	4626	GATTCACGAGGGTGTGACACCAACCAATTTGTGAAACGAACATCTCATGTATTTATAT	4685
Db	4522	GATTCACGAGGGTGTGACACCAACCGATTCGAAACCAATATCTCATGTATTTATAT	4581
Qy	4686	TTTCGATTCCTCATCATATTTTGAATGATCCCTTTTTCACATCAATCTGTTCATTTGGTATATC	4745
Db	4582	TTTCGATTCCTCATCATATTTTGAATGATCAATTTTTCACATCAATCTGTTCATTTGGTATATC	4641
Qy	4746	ATTGATATTTTAAATGACAAAGAAAAAAGACAGTGTGATATTAGAATGTTCATGACA	4805
Db	4642	ATTGATATTTTAAATGACAAAGAAAAAGCTGTGTGATATTAGAATGTTCATGACA	4701
Qy	4806	GAAATTCGAAAAAGTACTATATATGCTATGAAAAAGTGGGCTCTAAAAAACCATTTAAA	4865
Db	4702	GAAATTCGAAAAAGTACTATATATGCTATGAAAAAGTGGGCTCTAAAAAACCATTTAAA	4761
Qy	4866	GCCATTCGAAACCAAGGTGGCGACCAAGACATATAGCTTTGAAATATGTAACCGATTAAG	4925
Db	4762	GCCATTCGAAACCAAGGTGGCGACCAAGACATATAGTATTCGAAATATGTTACAGATAAA	4821
Qy	4926	AAATTCGATATATCATTTATGTTATTCATTTGCTGTGAACATGTTCAACCATGACCCTCGAT	4985
Db	4822	AAATTCGATATATCATTTATGTTATTCATTTGCTGTGAACATGTTCAACCATGACCCTCGAT	4881
Qy	4986	CGTTACGATGCGTGGGACAGTATACGCGGTCTTACATATCTCAATGCGATATTTGCTA	5045
Db	4882	CGTTACGATGCGTGGGACAGTATACGCGGTCTTACATATCTCAATGCGATATTTGCTA	4941
Qy	5046	GTATATTTTCACTTCGAGATGCTATTTAAAAATATTCGTTTACAGATATCATATTTTAT	5105
Db	4942	GTATATTTTCACTTCGAGATGCTATTTAAAAATATTCGTTTACAGATATCATATTTTCAA	5001
Qy	5106	GAGCCATGGAATTTATTTGATGTATGATGTTGTCAATTTTATCCATTAAGTCTTGTAAT	5165
Db	5002	GAGCCATGGAATTTATTTGATGTATGATGTTGTCAATTTTATCCATTAAGTCTTGTAAT	5061
Qy	5166	AGCATATTTATCGAAGAGTACTTGTGTGCGCGACCTGTCTCGAGTGTGTGCTGTGGCG	5225

Db	5062	AGCGCATCATTTGAAAGATATTTTCGATTCGCCGACACTCTCCGTGTGAGATGGCC	5121
Oy	5226	AAAGTGGGCGGTGCTCCCTCGACTGTGTAAGGAGCCAAAGGCAATTCCGACACTGCTCTTC	5285
Db	5122	AAAGTGGGTGTGTCCGCTTGAGTTCAGAGGGTGCAGAGGGATATCCGAGCGTTGCTGTTC	5181
Oy	5286	GCGTTGGCCATGTTCGCTCCGGGCGCTGTCAATCGCTGCTGTCTCCGGGTATG	5345
Db	5182	GCGTTACCAATGTGCTGCTGCTTAATTAACAATTGTCTGTTCCTTTGGTGAATG	5241
Oy	5346	TTCACTTTTCCATTTTCGGCATGTCTGTTCTTCATGCACTGATGAGGAGAAAGCGGCAAT	5405
Db	5242	TTATCTTTGGTATCTTTGGCATGTCTCTTCATGCACTGCAAAAGAGAGCGGCATA	5301
Oy	5406	AACGACGCTTACACTTCAAGACTCTTTGGCAGAGCATGATCTCGTCTTTAGATGTG	5465
Db	5302	AATCTGTGTATATATTTTAAAGCACTTTGGCCAAAGTATGATGTCTGTTCAAGATGCT	5361
Oy	5466	ACGTGAGCGGTTTGGATGTGTACTGAGCGCATTTATCAATGAGAGAGCATGCGATCCA	5525
Db	5362	ACCTGAGCGGTTTGGATGTGTACTGAGCGCATTTATCAATGAGAGAGCATGCGATCCA	5421
Oy	5526	CCGACACGCAAGGCTATCCGGGCAATTGTGCTTCAAGACCGTTGGAAATTAAGTTT	5585
Db	5422	CCGACACACGCAAGGCTATCCGGGCAATTGTGCTTCAAGACCGTTGGAAATTAAGTTT	5481
Oy	5586	CTCCTTCATCTAGTATTAATAGCTTTTGTGATGTATTAATATGTATGATTTGCTGTCAAT	5645
Db	5482	CTCCTTCATCTAGTATTAATAGCTTTTGTGATGTATTAATATGTATGATTTGCTGTCAAT	5541
Oy	5646	CTCGAAGACTATAGTCAGGCGCACCGAGAGCGTGCAGAGAGGCTCTAACGACGACATAC	5705
Db	5542	CTCGAAGACTATAGTCAGGCGCACCGAGAGAGGCTCTAACGACGACATAC	5601
Oy	5706	GACATGTACTATGATATCTGGCAGCAATTCGATCCGAGGGGCAACCCAGTACATACGCTAT	5765
Db	5602	GATATGTACTATGATATCTGGCAGCAATTCGATCCGAGGGGCAACCCAGTACATACGCTAT	5661
Oy	5766	GATCAGCTGTCCGAATTTCTGAGAGTACTGAGAGCCCGCTCGAGATCCAAACCGAAC	5825
Db	5662	GACCAAGCTGTCCGAATTTCTGAGAGTACTGAGAGCCCGCTCGAGATCCAAACCGAAC	5721
Oy	5826	AAATTAACAAGTATATTCGATGAGCATACATCCATCTGTGCGGTGACCTCATGTCTGTCTC	5885
Db	5722	AAATTAACAAGTATATTCGATGAGCATACATCCATCTGTGCGGTGACCTCATGTCTGTCTC	5781
Oy	5886	GACATCTCTCGAGCGCTTACAGAAAGACTCTTTTGCAGGAGAGGGCAATTCGATAGAGAG	5945
Db	5782	GATATATTTGATAGCCCTCAGCAAGAGACTCTTTTGCAGGAGAGGGCAATTCGATAGAGAG	5841
Oy	5946	ACGGGTGAGATTTGTGAGATAGCCGCGCCCGCCGATACAGAGGGCTACAGAGCCCGTCTCA	6005
Db	5842	ACGGGTGAGATTTGTGAGATAGCCGCGCGCGACACCGAGCGGCTATGATCCGGTGTCTG	5901
Oy	6006	TCAAGCGCTGTGCGCTCAGCGTGAAGAGTATGCGCCCGGCTTAATTCAGACAGCTCTGCGCA	6065
Db	5902	TCAAGCGCTGTGCGCTCAGCGTGAAGAGTATGCGCCCGGCTTAATTCAGAGAGGCGTGTGCGG	5961
Oy	6066	AAAGCAACAAGCGCGCGCGAGGAGAGTGGGTCTTTGAGCCGGAATCGGATCATGGCGAT	6125
Db	5962	CGTTACCAAGATGGC-----CCAGCCCAAGAGAGTGTAT	5994
Oy	6126	GCGCGGTATCCGGATGCCGGGGACCCCGCGCCCGATGTAAGCAACGAGCGGAGTGTGCGCC	6185
Db	5995	GAGGCGGAGCGCGCGTGTGGCCCAAGATGTGTGTAAGCGCGTGAAGAGGAGGACG	6054
Oy	6186	GCTGTGTGAGATGTGTATTAACGCTACTGCAAGAGAGCTGCGGATGCCGATGAAGAT	6245
Db	6055	GCGCGCGCGCGCGGTATGATGTGTCTCAGGACACAGGAGGACAGCGGCGCGCGGAGCC	6114
Oy	6246	AATGTAATATGTCCGGGTGAGATGACGCGCGCGCGGACAGACAGACAGACAGCGCGCG	6305
Db	6115	ACATCAACCTT-----CAGATTCAGATGTCCGGGAGGACAGATGTGTCCAGC	6159

Accession	Gene	Protein	Function	Location/Qualifiers
Y01491	CGCGCGCGGCA	CGACGACGCGCGGAA	GTCCGAGCGGGTACGCCGGCCACACACCGCC	6306
Y01492	GTCCGCGCGCC	CTTATGTCGCGGCTGTGTTATGTCGCGCAGTAAATGCGCGCAACCGCC		6160
Y01493	GTTCCTCGTGA	GAGCGACCGGGTTCTGTACAGAAACCGGCCACAAAGTGTGTCATCCATCG		6366
Y01494	GTTACTGCTGCA	AAACCGATGCTTTTGTTCACAAAACGGTCAATAGGTTGTAAATACACTCG		6220
Y01495	CGATCGCCGAG	CATCAGTCCGCGACCGCGGATGCTTGA		6426
Y01496	AGATCGCCGAG	CATTAATCAGGACGCGCAGATGCTGA		6280
Y01497	AAV82498	standard; cDNA; 6318 BP.		
Y01498	AAV82498	standard; cDNA; 6318 BP.		
Y01499	AAV82498	standard; cDNA; 6318 BP.		
Y01500	AAV82498	standard; cDNA; 6318 BP.		
Y01501	AAV82498	standard; cDNA; 6318 BP.		
Y01502	AAV82498	standard; cDNA; 6318 BP.		
Y01503	AAV82498	standard; cDNA; 6318 BP.		
Y01504	AAV82498	standard; cDNA; 6318 BP.		
Y01505	AAV82498	standard; cDNA; 6318 BP.		
Y01506	AAV82498	standard; cDNA; 6318 BP.		
Y01507	AAV82498	standard; cDNA; 6318 BP.		
Y01508	AAV82498	standard; cDNA; 6318 BP.		
Y01509	AAV82498	standard; cDNA; 6318 BP.		
Y01510	AAV82498	standard; cDNA; 6318 BP.		
Y01511	AAV82498	standard; cDNA; 6318 BP.		
Y01512	AAV82498	standard; cDNA; 6318 BP.		
Y01513	AAV82498	standard; cDNA; 6318 BP.		
Y01514	AAV82498	standard; cDNA; 6318 BP.		
Y01515	AAV82498	standard; cDNA; 6318 BP.		
Y01516	AAV82498	standard; cDNA; 6318 BP.		
Y01517	AAV82498	standard; cDNA; 6318 BP.		
Y01518	AAV82498	standard; cDNA; 6318 BP.		
Y01519	AAV82498	standard; cDNA; 6318 BP.		
Y01520	AAV82498	standard; cDNA; 6318 BP.		
Y01521	AAV82498	standard; cDNA; 6318 BP.		
Y01522	AAV82498	standard; cDNA; 6318 BP.		
Y01523	AAV82498	standard; cDNA; 6318 BP.		
Y01524	AAV82498	standard; cDNA; 6318 BP.		
Y01525	AAV82498	standard; cDNA; 6318 BP.		
Y01526	AAV82498	standard; cDNA; 6318 BP.		
Y01527	AAV82498	standard; cDNA; 6318 BP.		
Y01528	AAV82498	standard; cDNA; 6318 BP.		
Y01529	AAV82498	standard; cDNA; 6318 BP.		
Y01530	AAV82498	standard; cDNA; 6318 BP.		
Y01531	AAV82498	standard; cDNA; 6318 BP.		
Y01532	AAV82498	standard; cDNA; 6318 BP.		
Y01533	AAV82498	standard; cDNA; 6318 BP.		
Y01534	AAV82498	standard; cDNA; 6318 BP.		
Y01535	AAV82498	standard; cDNA; 6318 BP.		
Y01536	AAV82498	standard; cDNA; 6318 BP.		
Y01537	AAV82498	standard; cDNA; 6318 BP.		
Y01538	AAV82498	standard; cDNA; 6318 BP.		
Y01539	AAV82498	standard; cDNA; 6318 BP.		
Y01540	AAV82498	standard; cDNA; 6318 BP.		
Y01541	AAV82498	standard; cDNA; 6318 BP.		
Y01542	AAV82498	standard; cDNA; 6318 BP.		
Y01543	AAV82498	standard; cDNA; 6318 BP.		
Y01544	AAV82498	standard; cDNA; 6318 BP.		
Y01545	AAV82498	standard; cDNA; 6318 BP.		
Y01546	AAV82498	standard; cDNA; 6318 BP.		
Y01547	AAV82498	standard; cDNA; 6318 BP.		
Y01548	AAV82498	standard; cDNA; 6318 BP.		
Y01549	AAV82498	standard; cDNA; 6318 BP.		
Y01550	AAV82498	standard; cDNA; 6318 BP.		
Y01551	AAV82498	standard; cDNA; 6318 BP.		
Y01552	AAV82498	standard; cDNA; 6318 BP.		
Y01553	AAV82498	standard; cDNA; 6318 BP.		
Y01554	AAV82498	standard; cDNA; 6318 BP.		
Y01555	AAV82498	standard; cDNA; 6318 BP.		
Y01556	AAV82498	standard; cDNA; 6318 BP.		
Y01557	AAV82498	standard; cDNA; 6318 BP.		

Query Match 68.3%; Score 4447.8; DB 2; Length 6318;  
 Best Local Similarity 82.0%; Pred. No. 0;  
 Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;

24 ATGACAGAAAGATTCGATCTGATATCTGAGAGAAACGATTTGTCCTGCTTAC 83  
 1 ATGACAGAAAGATTCGATCTGATATCTGAGAGAAACGATTTGTCCTGCTTAC 60  
 84 CGCGATCATTTGGTGCATATCGAACACGATTTGCCGCTGAACATGAAAGAGAG 143  
 61 CGCGATCATTTGGTGCATATCGAACACGATTTGCCGCTGAACATGAAAGAG 117  
 144 CTGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203  
 118 CTGGAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148  
 204 GAAATCCGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
 149 -AGATACGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207  
 264 CAGGATGCTGATATCTGATATCGAACACGATTTGCCGCTGAACATGAAAG 323  
 208 CAGGATGCTGATATCTGATATCGAACACGATTTGCCGCTGAACATGAAAG 267  
 324 CCTCTCGAGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 383  
 268 CCTCTCGAGATATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 327  
 384 GAAAGAAAGATTTTGGTGCATATCGAACACGATTTGCCGCTGAACATGAA 443  
 328 GAAAGAAAGATTTTGGTGCATATCGAACACGATTTGCCGCTGAACATGAA 387  
 444 CGGATACGCTGATATCTGATATCGAACACGATTTGCCGCTGAACATGAA 503  
 388 CGGATACGCTGATATCTGATATCGAACACGATTTGCCGCTGAACATGAA 447  
 504 ACCACAAATTTCTGATATCGAACACGATTTGCCGCTGAACATGAA 563  
 448 ACCACAAATTTCTGATATCGAACACGATTTGCCGCTGAACATGAA 507  
 564 ACTGAGGATATTTTGGTGCATATCGAACACGATTTGCCGCTGAACATGAA 623  
 508 ACAAGAGATATTTTGGTGCATATCGAACACGATTTGCCGCTGAACATGAA 567  
 624 GATTTCATTTTATGCTGATATCGAACACGATTTGCCGCTGAACATGAA 683  
 568 GATTTCATTTTATGCTGATATCGAACACGATTTGCCGCTGAACATGAA 627  
 684 GTAATAGCTTATGATATCGAACACGATTTGCCGCTGAACATGAA 743  
 628 GTAATAGCTTATGATATCGAACACGATTTGCCGCTGAACATGAA 687  
 744 ACGTTAGGATGCTGATATCGAACACGATTTGCCGCTGAACATGAA 803  
 688 ACGTTAGGATGCTGATATCGAACACGATTTGCCGCTGAACATGAA 747  
 804 GTGCGCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 863  
 748 GTGCGCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 807  
 864 TCCCTGCTGATATCGAACACGATTTGCCGCTGAACATGAA 923  
 808 TCCCTGCTGATATCGAACACGATTTGCCGCTGAACATGAA 867  
 924 TGCAATCAAGATTTCCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 983  
 868 TGCAATCAAGATTTCCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 927  
 984 TATCAATCAAGATTTCCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1043  
 928 TATCAATCAAGATTTCCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 987

1044 TGCGCAATATATCCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1103  
 988 TGCGCAATATATCCGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1047  
 1104 GATTCGATATCGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1163  
 1048 GATTCGATATCGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1107  
 1164 GCTTCGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1223  
 1108 GCTTCGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1167  
 1224 GCGGACCATGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1283  
 1168 GCGGACCATGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1227  
 1284 GTGATTTGATTTTGGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1343  
 1228 GTGATTTGATTTTGGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1287  
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 1288 GAGAGAGAGCTGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1347  
 1404 GCGGACCATGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1463  
 1348 GCGGACCATGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1407  
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 1408 GCGGACCATGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1467  
 1524 TATGATATTTTGGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1583  
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 1528 ATTGAGAGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1587  
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 1588 ACCACAGACCAACGATATCGAACACGATTTGCCGCTGAACATGAA 1644  
 1704 GATTTCATTTTATGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1763  
 1648 GATTTCATTTTATGCTGATATCGAACACGATTTGCCGCTGAACATGAA 1704  
 1764 GATTCGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1823  
 1708 GATTCGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1764  
 1824 CAGGATGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1883  
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 1828 GAGAGAGAGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1884  
 1944 TCGATATCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 2003  
 1888 TCGATATCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 1944  
 2004 ATGCGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 2063  
 1948 ATGCGCTGATATGATATCGAACACGATTTGCCGCTGAACATGAA 2004  
 2064 CGCATATCAATGATATGATATCGAACACGATTTGCCGCTGAACATGAA 2123  
 2008 CGCATATCAATGATATGATATCGAACACGATTTGCCGCTGAACATGAA 2064  
 2124 CTGAT-----CATCGGACATGAAATTTGCCGCTGAACATGAA 2168

2065 CCCGATGCCAATCAAGGAAACAAAGGATTAATGGAATGGGTGAGATTATACAGCGAA 2124  
2169 GCGGCAAGATTAAACATCATGACAAATCCCTTTATGAGCCCGCTCCAGACACAAACGCTG 2228  
2125 GCTGGCAAAATTAACACACGACAAATCTTTTATGAGCCCGCTCCAAATCTCAACAGTG 2184  
2229 GTTGATATGAAGATGTGATGTCTGTAATGACATCATGCAAGCCCGCTGGTCCGAC 2288  
2185 GTAGACATGAAGATGTATGTCTTAATATGATATGATGACAAACCGCTGGTCCGCAAT 2244  
2289 AGTCGGCAAGCATGCGCGTCTCCGTTACTATTTCCCAACAGAGACGATGACGAG 2348  
2245 AGTCGTGCTAGTAAACGAGT-----GAGACGATGACGAA 2280  
2349 GATGGGCGCAGTTCAAAAGCAAGCACTGAAAGTATCCTCAAGGCAATCGATGTGTT 2408  
2281 GATGTCGCCAATTCAGAGACATCGCCCTCGAATACATCTTAAAGGCAATCGAAATCTTT 2340  
2409 TGTGTGGGACCTGTGCTGGGTTTGTGAAATTTCAAGAGTGGGTATCGCTCATCGTC 2468  
2341 TGTGTAGGACCTGTGTGGGTGTGTTAAATTTCAAGAAATGGGTGTCTTTATTTGTG 2400  
2469 TTGATCCCTCGTCGAGCTCTTCATGAGGTGATGTTGGTCAACAGATGTCATG 2528  
2401 TTGATCATCTCGAGGCTCTTCATTAACCTGTATGTGATGATACATGATGTTATG 2460  
2529 GCAATGATCAACGATATGAACAAAGAGATGAACGCGTCTCAAGATGSCAACTAT 2588  
2461 GCATGATATCATCAACGATGAATCCGGAATAGAAAGGTGCTGAAATGTTAACTAT 2520  
2589 TTCTTCAACCCGACCTTTGTCATGAGGCCAATGAAAGTAAATGGCAATGAGCCCAAG 2548  
2521 TTCTTCAACGACCTTTTGAATGAAGCCAGATGAAGTGAAGTGAAGCCGCAAG 2580  
2649 TACTATTTCCAGAGGCGTGAACATCTTGCACTTATTCGAGCCCTATGCTATTG 2708  
2581 TACTACTTCAGAGAGGCTGGAACATTTGCAATTTCAATTTGTGCGCTGTCTGCTG 2640  
2709 GAACTGGAGCTCGAGGGTGTCCAGAGTCTGTCCGATTTGCGTCTTTCGATTTGCTGCT 2768  
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2769 GTATTTCAAATGCGCAAGTCTTGGCCCACTTAATTTACTCAATTTGATTTAGGAGCGC 2828  
2701 GTATTTCAAATTTGCAAAATATCAATGCCCCAATCAATTTACTCATTTGATTAATGAGCGC 2760  
2829 ACCATGGGCGCTTTGGGTAATCTGACATTTGATCTTTGCAATTTATCATCTTTCATCTTGGC 2888  
2761 ACAATGGGTGATGGGTATCTGACATTTGATCTTTGCAATTTATCATCTTTCATCTTGGC 2820  
2889 GTGATGGGAATGCAACTGTTCGAAAGAAATTAATCATGATCAAGAGACCGCTTCCGAT 2948  
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2949 GCGCACTCGCGCGCTGGAATTTCAACGACTTATGACAGCTTCAAGATGATGTTCCG 3008  
2881 CATAATTAATCCGCGCTGAACTTCAACGACTTCAAGACAGCTTCAAGATGATGTTCCG 2940  
3009 GTGCTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3068  
2941 GTGCTTCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000  
3069 TGCATTCCTTCTTCTTGGCCACCGGTGTCAATGCGCAATCTTGTGTGATCTTAACCTTTC 3128  
3001 TGTATACCTTCTTCTTGGCCACCGGTGTCAATGCGCAATCTTGTGTGATCTTAACCTTTC 3060  
3129 TTACCTTCTTCTTGTGCAATTTTGGCTCATCTGATCATGAGCGCACTGCGGATTAAC 3188  
3061 TTACCTTCTTCTTGTGCAATTTTGGCTCATCTGATCATGAGCGCACTGCGGATTAAC 3120  
3189 GATACGATTAATAATAGCCGAGCTTCAATGCAATTTGCGGATTAATAAGTTGGGTTAAG 3248

3121 GATACCAATTAATAATAGCAGAGCCCTTCAATGATGATGCTGTTTAAAGACTGGTGAA 3180  
3249 CGTAATATTGCTGATTTGTTTCAAGTTAATAGCTAACAAATTTGACAAATCAATTAATGAT 3308  
3181 CGTAATATTGCTGATTTGTTTCAAGTTAATAGCTAACAAATTTGACAAATCAATTAATGAT 3240  
3309 CAACCATCAAGTGAAGAGCAACACAGATCAAGTTGATTTGAGCGGAAGCATGATGAC 3368  
3241 CAACCAT-----AGACATGGCGAT 3261  
3369 AACGAATGAGCTGGGCGCACGACAGATCTCTGCGACCGCTCATCAAGAGGAGATC 3428  
3262 AATGAATGAGTGGGTATGACCAATCATGGCGATGCTGATCAAAAAGGATATG 3321  
3429 AAGAGACAGCCCACTGAGGTGGCTATCGGGATTCGATGGAATTCACGATACAGGCG 3488  
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3382 GATATGAAGAAACAAACAGCCGAAGAAATCAATTAATTAACGCAACGATGATGGA 3441  
3549 AACTCAATTAACCAACCAAGCAATTAAGTGAACAGACTTAACCATTAAGGATTTGCTC 3608  
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3502 ATACAGAGAGAGACACTGCGCAGCATTTAATGATGATGATGATGATGATGATGATGATG 3561  
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3562 AAGAGACAGAGCCCAAGGGGACCGCGAGACGATGAGAGGGGAGAGAGAGCGGACGCGC 3621  
3729 AGCAGAGAGATTTAGGTCTTCAACGAGAACTGAGACGAGAGAGGCGGAATGCGAGAGGCG 3788  
3622 AGCAGAGAGAGCTCGCGCTTCAACGAGAACTGAGAGAGAGGCGGAGGCGGAGGCGC 3681  
3789 CGGCTGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3845  
3682 CAGCTGAGAGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3741  
3846 CCAGCTGATTTGCTGCGCCGATTTGATCTTAAGAAATTTCCGATCTTTAGCCGCTGACAT 3905  
3742 CCGGCGAGCTGTTCCCGGCTGATCTAAGAAATTTCCGATCTTTAGCCGCGGACGAG 3801  
3906 GACTCGCGCTTCTGCGAGAGATGAGGCAATTTACGATGAGGCAATTTTCAATTAATGAA 3965  
3802 GACTCGCGCTTCTGCGAGAGATGAGGCAATTTACGATGAGGCAATTTTCAATTAATGAA 3861  
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3862 AATTAATTTTGAACAGCTGTTATCAATGATTTTATGAGTATGAGTATGAGTATGAGTATG 3921  
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3922 TTGAAGATGATCATTTACCGGATTCAGCTGATCAGAGATTAATCTGATCAATGAGAC 3981  
4086 AGAATTTTATGAGTATTTATCTTCTTGAAGATTTTATGAGTATGAGTATGAGTATGAGTATG 4145  
3982 AGAATTTTATGAGTATTTATCTTCTTGAAGATTTTATGAGTATGAGTATGAGTATGAGTATG 4041  
4146 AAGGTATCTTCAACCAACGCGGTGATGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTG 4205  
4042 AAGGTATCTTCAACCAATGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTGATTTGCTG 4101  
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4102 ATTAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4161  
4266 ACCTTAAGACATGAGACCACTAAGGCAATGCTCCGATGATGAGGAGCATGAGGCTGCTG 4325  
4162 ACATGCGCGCTTAAGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4221

QY 4326 GTTATGCGTGTGCAAGCTATACGTCATCTTCAATGCTATGCTGTGCTATTA 4385  
Db 4222 GTGAATGCGCTGTTCAGCTATACCGTCATCTTCAATGCTATGCTGTGCTGATA 4281  
QY 4386 TTTTGGCTAATTTTGGCATAATGGGTGTAACGCTTTTGTGCGAAAAATATTTTAAGTGC 4445  
Db 4282 TTTTGGCTAATTTTGGCATAATGGGTGTAACGCTTTTGTGCGAAAAATATTTTAAGTGC 4341  
QY 4446 GAGCATGATGAGCAAGAACTCAGCAAGATCATACCAATCGCAATGCTGCGAG 4505  
Db 4342 AAAGATGATATGACATGCTGTGAGCATGAATCATACCGAATCGTAATGCTGCAAA 4401  
QY 4506 AGCGGAATCTACACGTGGGTGAATTCAGCAATGAATTTGATCATGATGATGATACCGGTAT 4565  
Db 4402 AGTGAATCTACACCTGGGAAAAATTCGCAATGAATTCGATCATGATGATGATACCGGTAT 4461  
QY 4566 CTGTGCTTTTCCAGTGGCCCACTTCAAAAGGCTGATACAAATCATGATGATGATACCGGTAT 4625  
Db 4462 CTGTGCTTTTCCAGTGGCCCACTTCAAAAGGCTGATACAAATCATGATGATGATACCGGTAT 4521  
QY 4626 GATTACGAGAGGTGAGCAAGCAACCAATTCGTGAAGCAAGCATCTACATGATATATAT 4685  
Db 4522 GATTACGAGAGGTGAGCAAGCAAGCAACCAATTCGTGAAGCAAGCATCTACATGATATATAT 4581  
QY 4686 TTCCGATCTTCTCATATATTTGATGATCTTTTCAACATCATCTGTTCAATGATGATATC 4745  
Db 4582 TTCCGATCTTCTCATATATTTGATGATCTTTTCAACATCATCTGTTCAATGATGATATC 4641  
QY 4746 ATTGATATTTTATGAGCAAAAAGAAAAAGCAGGTGATCATGAAATGTTCAAGCA 4805  
Db 4642 ATTGATATTTTATGAGCAAAAAGAAAAAGCAGGTGATCATGAAATGTTCAAGCA 4701  
QY 4806 GAAAGTCAAAAAAGTACTATATATCTATGAAAAAGATGGGCTTAAAAAACATTAAAA 4865  
Db 4702 GAAAGTCAAAAAAGTACTATATATCTATGAAAAAGATGGGCTTAAAAAACATTAAAA 4761  
QY 4866 GCCATTTCCAAAGCCAGGTGGGAGCAAGCAAGATGCTTTGAATGATGATGATGATGATG 4925  
Db 4762 GCCATTTCCAAAGCCAGGTGGGAGCAAGCAAGATGCTTTGAATGATGATGATGATGATG 4821  
QY 4926 AAATTCGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4985  
Db 4822 AAATTCGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 4881  
QY 4986 CGTATGATGCTGCGAGACGATTAACCGGCTCTGAGCTATCTCAATGCGATATCTGTA 5045  
Db 4882 CGTATGATGCTGCGAGACGATTAACCGGCTCTGAGCTATCTCAATGCGATATCTGTA 4941  
QY 5046 GTTATTTTCACTTCCGATGCTATTAATAAATATTCGCTTACGATATCAATTTTATTT 5105  
Db 4942 GTTATTTTCACTTCCGATGCTATTAATAAATATTCGCTTACGATATCAATTTTATTT 5001  
QY 5106 GAGCATGGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5165  
Db 5002 GAGCATGGAATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5061  
QY 5166 AGCGATATATGAGAACTCTGCTGTCGCGACCTGCTCGAGTGGTGGTGGCG 5225  
Db 5062 AGCGATATATGAGAACTCTGCTGTCGCGACCTGCTCGAGTGGTGGTGGCG 5121  
QY 5226 AAAAGTGGGCGGTGCTTCTGACGTGTAAGGAGCGAAGGCAATTCGACATGCTCTTC 5285  
Db 5122 AAAAGTGGGCGGTGCTTCTGACGTGTAAGGAGCGAAGGCAATTCGACATGCTCTTC 5181  
QY 5286 GCGTTGGCATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTG 5345  
Db 5182 GCGTTGGCATGCTGCTGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTG 5241  
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Db 5242 TTTCATCTTTGCAATCTTTGGGAGTGTGTTCTTCAATGACGTAAGAGAGAGCGCGCAT 5301

QY 5406 AACGAGCTCTAACATTCGAAGACCTTTGGCCAGAGCATATCTGCTTTCAAGATGCTG 5465  
Db 5302 AATGCTGTGATTAATTTTAAAGCATTTGGCCAAAGTATGATGCTGCTTTCAAGATGCT 5361  
QY 5466 ACGTCAGCGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5525  
Db 5362 ACGTCAGCGGTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5421  
QY 5526 CCGGACGAGCAAAAGGCTATCCGGGCAATTTGCTTCAAGCAAGCCTGTTGAATACGTTT 5585  
Db 5422 CCGGACGAGCAAAAGGCTATCCGGGCAATTTGCTTCAAGCAAGCCTGTTGAATACGTTT 5481  
QY 5586 CTCTCTGATCTAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5645  
Db 5482 CTCTCTGATCTAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5541  
QY 5646 CTGGAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5705  
Db 5542 CTGGAATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5601  
QY 5706 GACATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5765  
Db 5602 GATATGATCTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5661  
QY 5766 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5825  
Db 5662 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5721  
QY 5826 AAGTACAAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5885  
Db 5722 AAGTACAAATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5781  
QY 5886 GACATCTGAGCGCTTCAAGAAAGCTTTTGGGCGGAAAGGCAATTCGATGATGATG 5945  
Db 5782 GATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5841  
QY 5946 ACGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
Db 5842 ACGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
QY 6006 TCAACGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6065  
Db 5902 TCAACGCTGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5961  
QY 6066 AAGCAAAAGCGCGGCGGAGGAGTGGGCTTTGAGCCGATACGATATGATGATG 6125  
Db 5962 CGTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5994  
QY 6126 GCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6185  
Db 5995 GAGGCGAGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6054  
QY 6186 GCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
Db 6055 GCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6114  
QY 6246 AATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6305  
Db 6115 AATGTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6159  
QY 6306 GCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6365  
Db 6160 GCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6219  
QY 6366 GTTCTGCTGAGAGAGCGGCTTCTGTAAGAAAGAGCGCAAGAGTGTGATGATGATG 6425  
Db 6220 GTTCTGCTGAGAGAGCGGCTTCTGTAAGAAAGAGCGCAAGAGTGTGATGATGATG 6279  
QY 6426 CGATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6464  
Db 6280 AGATGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6318

RESULT 7  
AAV40630 standard; cDNA; 6315 BP.  
AAV40630;  
27-OCT-1998 (first entry)  
Musca domestica voltage-sensitive sodium channel gene.  
Musca domestica voltage-sensitive sodium channel; insecticide sensitivity; resistance;  
Vasc1 gene; ss.  
Musca domestica.  
Location/Qualifiers  
Key 1.6315  
CDS /product= "voltage-sensitive sodium channel"  
MO9828446-A1.  
02-JUL-1998.  
18-DEC-1997; 97WO-US024256.  
24-DEC-1996; 96US-00772512.  
(CORR ) CORNELL RES FOUND INC.  
Soderlund DM, Knipple DC, Ingles PJ;  
WPI; 1998-377674/32.  
P-PSDB; AAM57773.  
New isolated voltage-sensitive sodium channel polypeptides - obtained  
from house flies, which are capable of conferring sensitivity or  
resistance to an insecticide in insects.  
Claim 8; Page 45-49; 96BP; English.  
The sequence is that encoding a voltage-sensitive sodium channel (VSSC)  
of Musca domestica (kdr strain). Such a VSSC is capable of conferring  
sensitivity or resistance to an insecticide. It can be used to screen a  
cDNA library for other VSSC genes. Antibodies raised the VSSC can be used  
to detect VSSCs and these can be used in drug screening. Antisense  
nucleic acids and vectors containing the sequence may be used to reduce  
VSSC expression in an insect. The VSSCs can be used for conferring  
sensitivity or resistance to insecticides such as DDT and analogues and  
pyrethroids in insects such as house flies, fruit or vinegar flies,  
tobacco budworm, Colorado potato beetle, German cockroach or yellow fever  
mosquito  
Sequence 6315 BP; 1711 A; 1344 C; 1595 G; 1665 T; 0 U; 0 Other;  
Query Match 68.1%; Score 4434.2; DB 2; Length 6315;  
Best Local Similarity 81.8%; Pred. No. 0;  
Matches 5284; Conservative 0; Mismatches 1013; Indels 162; Gaps 8;  
QY 24 ATGACAGAAAGTTCGACTCGATATCTGAGAGAAAGCAGATTGTTCCGCTTAAAC 83  
DB 1 ATGACAGAAAGTTCGACTCGATATCTGAGAGAAAGCAGATTGTTCCGCTTAAAC 60  
QY 84 CGCGAATCATTTGTCGAATCGAACACGATTGCGCTGAACATGAAAGAGAGAG 143  
DB 61 CGCGAATCATTTGTCGAATCGAACACGATTGCGCTGAACATGAAAGAGAG 117  
QY 144 CTGGAAGAAAGAGCGCGAGAGAGAGTCCGCGATATGTCGGAAGAAAAACAATA 203  
DB 118 CTGGAAGAAAGAGCGCGAGAGAGAGC----- 148  
QY 204 GAAATCCGATATGATGACGAGAGACGAGATGATGATCCCAACCGGATCTTAACTTGA 263

DB 149 -AGATACATATGATGACGAGAGCAAGATGAGAGTCCACAGCGGATCCACACTTGA 207  
QY 264 CAGGATGTCGAATACCTGTTGATTCAGAGGACAGCTTCCGCGGAATTTGGCTTCACT 323  
DB 208 CAGGATGTCGAATACCTGTTGATTCAGAGGACAGCTTCCGCGGAATTTGGCTTCACT 267  
QY 324 CCTTCGAGAGATTCGATCCCTACAGCAATGATGACATTCGTGTTGTAAGCAAA 383  
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QY 384 GGAAGAAATATTTTCGCTTTTCGATCAAAAAGCAATGTGATGCTGCATTCAT 443  
DB 328 GGAAGAAATATTTTCGCTTTTCGATCAAAAAGCAATGTGATGCTGCATTCAT 387  
QY 444 CCGATACGTCGTGAGCCATTACATTCTAGTCATTCATTTTCCCTATCATATC 503  
DB 388 CCGATACGTCGTGAGCCATTACATTCTAGTCATTCATTTTCCCTATCATATC 447  
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DB 448 ACCAACAATTCGTCAACGATCCGATGATTAAGCCGACAAAGCCGCTTGAATCC 507  
QY 564 ACTGAGTATATTCACCGGAATCTACATTTGAATCAGCTTTAAAGTATGACAGCA 623  
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Qy 4506 AGGAGAACTACAGGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAGG 4565  
Db 4402 AGGAGAACTACAGGAGGAGGATGAGGAGGATGAGGAGGATGAGGAGGATGAGG 4461  
Qy 4566 CTGCTGCTTCTTCAAGTGGCCACCTTCAAGGCTGATATCAATATGAGAGGATC 4625  
Db 4462 CTGCTGCTTCTTCAAGTGGCCACCTTCAAGGCTGATATCAATATGAGAGGATC 4521  
Qy 4626 GATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4685  
Db 4522 GATTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4581  
Qy 4686 TTGCTATTTCTTCAATATTTGATGATGATGATGATGATGATGATGATGATGAT 4745  
Db 4582 TTGCTATTTCTTCAATATTTGATGATGATGATGATGATGATGATGATGATGAT 4641  
Qy 4746 ATTGATATTTTATGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4805  
Db 4642 ATTGATATTTTATGAGCAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4701

QY 4806 GAAGATCAGAAAAAGTACTATTAATGCTATGAAAAAGTGGGCTCTTAAAAAACATTAAAA 4865  
 DB 4702 GAAGATCAGAAAAAGTACTATTAATGCTATGAAAAAGTGGGCTCTTAAAAAACATTAAAA 4761  
 QY 4866 GCCATTCAGAACCAAGGTGGCGACACAGCAAGCAATGCTTTGAAATAGTAAACGATAAG 4925  
 DB 4762 GCCATTCAGAACCAAGGTGGCGACACAGCAAGCAATGCTTTGAAATAGTAAACGATAAG 4821  
 QY 4926 AAATTCGATTAATCAATTAATGATTAATCAATGCTGTAACATGTTCAACATGACCTCGAT 4985  
 DB 4822 AAATTCGATTAATCAATTAATGATTAATCAATGCTGTAACATGTTCAACATGACCTCGAT 4881  
 QY 4986 CGTTAGCAGTCGCGACACGATTAACGCGCTCTTACATCTCAATGCGATATTCGTA 5045  
 DB 4882 CGGTACACACCTCCGAGGCGTACACATGCTCTTCAACAACTCAATGGAATATTCGTA 4941  
 QY 5046 GTTATTTTCAGTCCGAAATGCTATTAATAAATATGCTTTAGCATCACTATTTATTTAT 5105  
 DB 4942 GTTATTTTCAGTCCGAAATGCTATTAATAAATATGCTTTAGCATCACTATTTATTTCAA 5001  
 QY 5106 GAGCATGAAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5165  
 DB 5002 GAGCATGAAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
 QY 5166 AGCGATTTTCCAGAAAGTACTGCTGCTCCGACCTGCTCCGAGTGGCGTGGCGG 5225  
 DB 5062 AGCGACATCATTTGAAAGTATTTGATGATGATGATGATGATGATGATGATGATGATGAT 5121  
 QY 5226 AAATGGGCGGTGCTTTCAGACTGCTGTAAGAGGACCAAGGACCAATTCGACACTGCTTTC 5285  
 DB 5122 AAATGGGCGGTGCTTTCAGACTGCTGTAAGAGGACCAAGGACCAATTCGACACTGCTTTC 5181  
 QY 5286 GCGTTGGCCATGCTGCTGCGGCGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTG 5345  
 DB 5182 GCGTTACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5241  
 QY 5346 TTCAATCTTTCGATTTTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5405  
 DB 5242 TTCAATCTTTCGATTTTCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5301  
 QY 5406 AACGACGCTTACACTTCAAGACCTTTGGCGACAGCATGATCTGCTCTTTCAGATGCTG 5465  
 DB 5302 AATGCTGTATTAATTTTAAGACATTTGGCCAAAGTATGATGATGATGATGATGATGAT 5361  
 QY 5466 ACCTGACCGGTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5525  
 DB 5362 ACCTGACCGGTTGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5421  
 QY 5526 CCGGACGCGACCAAGGCTATCGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5585  
 DB 5422 CCGGACGCGACCAAGGCTATCGGGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5481  
 QY 5586 CTTCCTTCATACCTAGTATTAAGCTTTTGAATGATTAATATGATGATGATGATGATGAT 5645  
 DB 5482 CTTCCTTCATACCTAGTATTAAGCTTTTGAATGATTAATATGATGATGATGATGATGAT 5541  
 QY 5646 CTGAGAACTATAGTACGCGACCAAGGACGCTGCAAGAGGCTTAAACCGAGACGATAC 5705  
 DB 5542 CTGAGAACTATAGTACGCGACCAAGGACGCTGCAAGAGGCTTAAACCGAGACGATAC 5601  
 QY 5706 GACATGATCTATGATCTGAGCAATTCGATCCGAGGCGACCCAGTACATACGCTAT 5765  
 DB 5602 GATATGATCTATGATCTGAGCAATTCGATCCGAGGCGACCCAGTACATACGCTAT 5661  
 QY 5766 GATCAGCTGCTCGAATTCCTGAGCGTACCTGAGCCCGCTGCGATGACCAACCGAAC 5825  
 DB 5662 GATCAGCTGCTCGAATTCCTGAGCGTACCTGAGCCCGCTGCGATGACCAACCGAAC 5721  
 QY 5826 AAGTACAAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5885  
 DB 5722 AAGTACAAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5781  
 QY 5886 GACATCTCTGAGCGCCTTACGAAAGACTTTTGGCGGAGGAGGCAATCCGATGAGAGG 5945

DB 5782 GATATATTCGATGCTCTGACCAAGACTTTCTTTGGCGGAGGATATCCGATCGAGGAG 5841  
 QY 5946 ACGGTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
 DB 5842 ACGGTGAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
 QY 6006 TCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 6065  
 DB 5902 TCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5961  
 QY 6066 AAGCACAAGCGCGCGGAGGAGGATGCTTTGACCCGATACGATCATGCGCAT 6125  
 DB 5962 CGTTACAAAGATGCG----- 5976  
 QY 6126 GCGGTGATCCGATGCTCCGAGACCCGCGCCGATGAAACGACGAGCGCATGCGCC 6185  
 DB 5977 CCACCCGAGAGGATGATGAGGCGGAGCGCGCTGCTGCGGAAAGATGCTGAAGCGGT 6036  
 QY 6186 GCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
 DB 6037 GAGGTGAAAGCGGCGAGCGCGCGCGCGCGATGATGATGATGATGATGATGATGATGATG 6096  
 QY 6246 AATGTAATATGCTCCGAGTGAAGATGACGCGCGCGCGCGACGACGACGACGACGCGG 6305  
 DB 6097 GAGGCCATTCACCCACAGATCCAGATGCGCGGAGGACGATGATGATGATGATGATGAT 6156  
 QY 6306 GCGCGCGGACGACGACGCGCGGAAATCCCGAGCGGCTGACGCGCGCGGACGACGCGG 6365  
 DB 6157 GGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 6216  
 QY 6366 GTTCTGCTGAGAGCGAGCGGCTTCTGACGAAAGACGACCAAGGCTGATTCACCTG 6425  
 DB 6217 GTTCTGCTGAGAGCGAGCGGCTTCTGACGAAAGACGACCAAGGCTGATTCACCTG 6276  
 QY 6426 CGATCGCGGACATCACGTCGCGACGCGCGGATGCTGA 6464  
 DB 6277 AGATCGCGGACATCACGTCGCGACGCGCGGATGCTGA 6315

RESULT 9  
 AAV58423  
 ID AAV58423 standard; cDNA; 6586 BP.  
 AC AAV58423;  
 AC 01-DEC-1998 (first entry)  
 DT 01-DEC-1998 (first entry)  
 XX PN4 sodium channel clone variant.  
 DE PN4 sodium channel clone variant.  
 XX Tetrodotoxin-sensitive sodium channel; rat; PN4 sodium channel; stroke;  
 KW nervous system disorder; epilepsy; brain injury; diabetic neuropathy;  
 KW AIDS-associated neuropathy; therapy; ss.  
 XX Rattus sp.  
 OS Rattus sp.  
 XX Key Location/Qualifiers  
 FT misc\_feature 2051..2080  
 FT /tag= a  
 FT /note= "insert sequence"  
 XX MO9838302-A2.  
 XX 03-SEP-1998.  
 XX 20-FEB-1998; 98MO-EPD00997.  
 XX 26-FEB-1997; 97US-0039447P.  
 XX (HOFF) HOFFMANN LA ROCHE & CO AG F.  
 XX Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran J;



DR WPI; 1998-481204/41.

XX New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNA - for  
PT detecting inhibitors which alleviate pain, and treating nervous system  
PT disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.

XX Claim 18; Page; 87pp; English.

CC This sequence represents the isolated rat PNA sodium channel cDNA clone  
CC of the invention. This sequence was isolated from a peripheral nerve from  
CC a rat dorsal ganglia. The PNA sodium channel sequences are tetrodotoxin-  
CC sensitive sodium channels. The protein is used in assays for detecting  
CC inhibitors of tetrodotoxin-sensitive sodium channels, which alleviate  
CC pain. The probes can be used to detect and isolate the DNA or protein in  
CC tissues. The antibodies can also be used to isolate the protein. The  
CC protein is used as a therapeutic target for compounds to treat disorders  
CC of the nervous system, such as epilepsy, stroke and brain injury.  
CC diabetic neuropathy, and AIDS-associated neuropathy, etc. Note: This  
CC variant sequence was created by the indexer using the information given  
CC in the specification, and the sequence shown in AAV58419

XX Sequence 6586 BP; 1632 A; 1732 C; 1745 G; 1475 T; 0 U; 2 Other;

Query Match 15.7%; Score 1021.4; DB 2; Length 6586;  
Best Local Similarity 52.5%; Pred. No. 2.3e-245;  
Matches 3125; Conservative 0; Mismatches 2486; Indels 342; Gaps 27;

QY 186 CGCAAGAAAAAACAAGAAATCCGATATGATGACGAGACGAGATGAGATCCACAA 245  
DB 268 CTCAAGAAACCAACCAAGGCGATGACGACCGGAGAGACGATGAGACGAGAGCC 327  
QY 246 CCGATCTCTACCTGAAACAGGCTGTCATACCTGTCATGAGGAGGACCTTCCG 305  
DB 328 AAGCCAAACAGTACCTGAGGCTGAGAGAGATTTGCTTCATCTACCGGAGACATCCG 387  
QY 306 CCGAATTTGGCTCTCACTCTCTCGAGATATGATCCCTACATACGACATGATGACA 365  
DB 388 CAGGCTGCTGTCGCTGCTCTCGAGAGACCTTACCTTATTTAGACGAGAAAC 447  
QY 366 TTCTGATTTAGAGAAAGAAATTTTCTGCTTTCTGATCAAAAGCAATGAG 425  
DB 448 TTTGATGATTTAAACAGAGGAAATCTCTCAATTTAGGCAACCTCTCTGAC 507  
QY 426 ATGCTGATTCATTCATTCGATAGTGTGTCGATTTATCTAGTATGATCAATTA 485  
DB 508 ATTTAAGCCCTTTAACTGATTAAGAAATGATTAATTAATTTGATACCTCAGT 567  
QY 486 TTTTCCCTATTTCATCATCAACCAATTCCTGCACTGATCTGATGATTAATGCGACA 545  
DB 568 TTCAAGCATGATCATGATGACCACTCTGACCACTGTGTGATGACCTTTAGTAC 627  
QY 546 ACGCCACAGTTGATTCATCTGAGTG--ATATTTACCGAATCTACATTTGATCA 602  
DB 628 CTTCAAGATGATGTCAGAAATGATGATTAACATTTACATTTGATCA 687  
QY 603 GCTGTTAAGATGATGATGATGATTTTATTTATGCGGTTTACGATCTTGAATGCA 662  
DB 688 CTAGGAAATATCATGCAAGAGTTTCTGATTAAGCGCTTCACTTTCTGAGAACCG 747  
QY 663 TGGAAATTTGCTGATCTTCTGATTAATGATTTAGCTTATGATGATGATTAATTA 722  
DB 748 TGGAACTGTTAGATCTTCAATGATGATGATGATGATGATGATGATGATGATG 807  
QY 723 GGTATTTAGACAGCTTCTGAGAACTTTAGAGTGTGTCGAGCGCTTAAACCGTACCAT 782  
DB 808 GGCATATGCTCAGCGCTGAGAACTTCAAGGCTTCTCCGAGCTTGAATCTCTGTA 867  
QY 783 GTGCAAGCTTGAAGACATGCTGCGCGCTGATCGAATGCTGTAAGATTTGGCGAT 842  
DB 868 ATTCAAGGCTGAGAAACATGCTGCGCGCTTAAATTCAGTCTGTAAGAAAGTGTGAGAC 927  
QY 843 GTGATTTATCTGACCATGCTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 902

DB 928 GTGATGATCTGACAGTGTCTGCTGATGTTTTCGCTGATTTAGGCTGACGCTTTC 987  
QY 903 ATGGCGTGTCTACCGAGATGCAAT-----CAAGAGTTCCCGCTGACGCTTCC 953  
DB 988 ATGGGAACTTTCGAAACAGATGCTGTGTGCGCCATTAACCTTCAACAGAGCTAACCTG 1047  
QY 954 TGGGGCAATCTGACCGAGAGAACTGGGACTATCAATTCGATATGCTCAATTTGTAT 1013  
DB 1048 GAGAACCGACACAGAGCTTTGATCTGAGAGATATATCAACATTAACAACTTTTAC 1107  
QY 1014 TCCGAGACAGAGGATCTCATTTTCTGATGCGCAATATATCCGCTGCGGAGATGCG 1073  
DB 1108 ATGTTTCTGAGATCTGAAACCTTGTCTGCGGAAACAGTTGATGCTGCGCAATGCG 1167  
QY 1074 GACGACATTAACGTTGCTGTCAGAGGTTTGTGCTGCAATTCGATTAATGCTACACGAC 1133  
DB 1168 CCAGAGGAGATTCAGATGATGAAAG---CAGGAGAAACCCCACTACGCTTACACGAC 1224  
QY 1134 TTGATGTTGTTGAGATGAGGCTTCTGTCGCTTCCGCTGATGATGACAGAGCTTTCG 1193  
DB 1225 TTGACACCTTACGCTGAGCTTCTTGTGATTTATTCGCTTATGACCAAGACTATTTGG 1284  
QY 1194 GAGATCTGTAACAGCTGATGTTGCGCGCGCGGACCATGACATGACATGCTTCTTATA 1253  
DB 1285 GAGAACTTATACAGCTGATGACCTTACGACCGCTGAGAAACGATACATGATCTTCTTGTG 1344  
QY 1254 GTCATATCTTCTAGTTCATTTCTTGTGAATTTGATTTGATTTGCTGCTGCTGCTG 1313  
DB 1345 TTGATCATCTTCTGATGCTTCTTCTGATGATTTGATGATTTGATGATTTGATGATG 1404  
QY 1314 TCGATGACGATTCGAAAGAGAGGCGGAGAGAGAGGCTGCGGAGAGAGAGAGAGAT 1373  
DB 1405 GCTTATGAGAA--CAAGAACAGGCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1457  
QY 1374 CGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1433  
DB 1458 CGAGTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1512  
QY 1434 CAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1493  
DB 1513 GCTGCAATGAGGACCTCAGCGGCACTGCTCTGAGAGAGAGAGAGAGAGAGAGAG 1569  
QY 1494 GCAAGAGTCCGAGATTTCTTGCATGAGATATGATGATTTGTTGGGCGAGAGAGAG 1553  
DB 1570 GAGATGAGGATGAGCTTCTCAGAGAGCTTCTGAGAGCTTCTGAGAGCTTCTGAGAG 1629  
QY 1554 AACGATGACAAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1613  
DB 1630 GCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1673  
QY 1614 GTGAGCTTTATTAACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1673  
DB 1674 GCTCTGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1720  
QY 1674 AAAGTGAACAGATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCTTATCT 1733  
DB 1721 CAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1780  
QY 1734 GGTAGTTCTCAAGATACAGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1793  
DB 1781 GGAAGTTTTCATATGATATGATGATGATGATGATGATGATGATGATGATGATGATG 1840  
QY 1794 GATGTAAGCAATTTGATTTGATCAATATGATGATGATGATGATGATGATGATGATGAT 1853  
DB 1841 GACATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1899  
QY 1854 GACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1913  
DB 1900 GAGCTCTGAGAGAG-----AGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1947  
QY 1914 TACTATGAGCAATTTAGGCTCCGACACTCATGATGATGATGATGATGATGATGATGAT 1973  
DB 1948 AGCGAGGCGGCGGAGATGCTGCTCTTATCTCCGATCCGCGCGCGGAGAGAGAGAG 2007

QY 1974 TATACCTCACATGCGCATCTACTGCGCGCATGCGCGTCATGCGCGCTGACCAATAGCC 2033  
DB 2008 TACAGTGGCTACAGCGGCTACAGCTCAAGTCAAGCCGCTCGTGGTGAATAATAGAGC 2067  
QY 2034 AAGAGAGCAAAATGCGCAACCGCAACACGCAATCAATCAATGCGCGCCACCAATGGC 2093  
DB 2068 AGCTAGGGAAGAGCGCATCTTCCCAAGCTGCGGCGCAGCGTGAAGCGCAACACAGCGTG 2127  
QY 2094 GGCACCACTGTCTGACACCAATCAACAGCTGATCATGCGGAGCTACGAAATGGCGTG 2153  
DB 2128 GACTGCAACGCGGAGTGTACTCATCTGCGCGCTGCTACACATCGGCGGCTCTGCTC 2187  
QY 2154 GAGTGCACGACGCAAGCTGGCAAGATTAAATCATCATCAATCTTTATGAGCCGCTC 2213  
DB 2188 GAGGCAACGACTGAGTGAATTAAGAGAAAGCCCTGGATCTCTTTAGTTTCTATG 2247  
QY 2214 CAGACACAAACGCTGTTGATATGAAAAGATGTAGTGTCTGAAATGACATCATGAAAG 2273  
DB 2248 GACCAACTCGCTCTACGAGCGGAAGGA-----CAGATCAACAGCATTAATGAG 2297  
QY 2274 GCGCGTGTGCGGCAAGTGGGCGAAGGATGCGGCTGTCTCCGTTTACTATTTCCCAAG 2333  
DB 2298 CGTGTCAAAACGCTAGTGAAGAGCTGAAGATCTCAGAGAA----- 2344  
QY 2334 GAGGACATGACGAGATGGCGCGACGTTCAAGACAAAGCACTGAAATGATCTCAAA 2393  
DB 2345 -----AGTCCCAACGCTGTGTATTAAGTTTGCACACCTTCTCTCA-- 2386  
QY 2394 GGCATCATGTGTTTGTGTGTGGGACGTGTGCGGCTTGTGAATTTGAGAGTGG 2453  
DB 2387 -----TCGGAAGTCAACCCCTACATGGAATAAATCGAAGAAATC 2427  
QY 2454 GTATGCTCATCTGCTTGTGATCCCTGCTGCGAGCTCTTCAATCAAGCTGTGATGTGTC 2513  
DB 2428 GTGAATTAATGCTATGAGACCTTTTGTAGACTTGAACATCAATCATGATGATGTCG 2487  
QY 2514 AACACGATGTTCAATGCAATGATCAACGATATGAACAAGAGATGAACGCTGCTC 2573  
DB 2488 AATACGCTATTATTAATGCAATGAGACCATCCATGACACCAAGTTGAAACAGTCTTG 2547  
QY 2574 AAGAGTGCACATATTTCTTCAACGCGCACTTTGCGATCGAGGCCACCATGAAGCTAATG 2633  
DB 2548 GCCGTAAGAAATCTGTGTCTTCAACGGAATCTTCAAGCGGAAATGTTTCTGAAGTCA 2607  
QY 2634 GCCATGACCCCAAGTACTATTTCCAGAGGCGTGAACATCTTGAATCTTATATGTCG 2693  
DB 2608 GCCATGACCCCTTACTATTAATTTCCAGAGGCTGAACATTTTGAAGATTAATGTC 2667  
QY 2694 GCCCTATGCTATTTGAAACTGGGACTCGAGGCTTCAGGAGTCTGCTGATATGCTTC 2753  
DB 2668 TCCCTCAATTAATGAGAGTGAAGTCTCGAGATGAGAGGAGGCTCTCAAGTGTGCGTCT 2727  
QY 2754 TTTGATGCTGCTGTATTAATCAACTGGCCAAAGTCTTGGCCCACTTAATTAATCTAAT 2813  
DB 2728 TTTCCAGTGTCTCGAGTCTTCAAGTGTGCAAGTCTTGGCCCACTTAATCAATGCTGATC 2787  
QY 2814 TCGATTAATGAGCAGCAATGCGCGCTTGGGTAATCTGAATTTGTACTTTGATTAATC 2873  
DB 2788 AAGATCATCGGGAACCTCGTGGGTGCGCTGGGCAACCTGAACCTGTGTGCGCATATC 2847  
QY 2874 ATCTTCACTTTTGGCGTGAATGGAATGCAACTGTTGCAAGAAATTAATCATGA--TCAC 2930  
DB 2848 GTCTTCACTTTGCGCGTGTGGGATGAGCTGTGTGGAAGATTAAGAGAGTGTGCTC 2907  
QY 2931 AAGGACCGCTTTCGCGATGCGACCTGCGCGCTGGAACCTTCAACGACTTTATGACAGC 2990  
DB 2908 TGTAAATCAACAGGAGTGAAGTCCGCGCTGGCAATGACGACTTCTTCCATCC 2967  
QY 2991 TTTCAATATGTGTTCGCGGTGCTCTGCGAGAAATGATGATGATGAGGAGCTGCAAG 3050  
DB 2968 TTTCTCATGTCTTTCGAGTGTGTGTGGAGTGAAGACATGTGGGACTGCAATG 3027

QY 3051 TAGCTG---GGGATGTCTGCTGATCTCCCTTCTTTGGGCAACCGTGTGATCGCAAT 3107  
DB 3028 GAGTGTGCGCGGCGAGGCGCATGTGCTCATGTGCTTCAATGATGTATGTGATGCGCAAC 3087  
QY 3108 CTTGTGTACTTAACCTTTTCTTACCTTGTGCTTTTGTCCAAATTTTGGCTCATTAAGCTTA 3167  
DB 3088 CTGTGTGTCTGAATCTTATCTTCTGCGCTTGTGCTTGTGAGCTCTTCAAGCGGACAACTCG 3147  
QY 3168 TTAGCGCGCATGCTCGGATTAAGATTCGAATTAATAGCCGAGGCTTCAATGAAATTTGGC 3227  
DB 3148 GCGGCAACAGACGAGCGGGAATGAACA----- 3179  
QY 3228 CGATTTAAAGTTGGTTAAGGTAATATGTGATGTTTCAAGTTAATAGTAACAA 3287  
DB 3180 ----- 3179  
QY 3288 TTGACAAATCAATTAATGATCAACCATCAAGTGAAGAGCAACCAAGATCAATTGAT 3347  
DB 3180 -----CCTGCAATCTCAAGTGTATC 3198  
QY 3348 TGAAGCAAGACATGTGTACAACGAATGAGCTGGGCAAGAGAGATCTGCGCGAC 3407  
DB 3199 CGATCAAGAGCGCGTGTGCTGACCAAAATGAAGTGCAGCGCTTCAATGAGGCTCAC 3258  
QY 3408 GGCCTCATCAAGAGGAGATCAAGGACAGACGCACTGAGGTGCGCATGCGGATCGG 3467  
DB 3259 TTCAACAGCGGAGCGGATGAATGAATGAACCTCTGACGACTGTATGAAGAAAGGCC 3318  
QY 3468 ATGAAATTCAGATACACGCGCATGAAGAAACACAGCCGAAGAAATCCAAATATCTA 3527  
DB 3319 ACTGATCGCCCAACCAACGCGCGTGTATTCACCGGAACGCGCATTCAGAAAGAAC 3378  
QY 3528 AATTAAGCAACGATGATGGAATCAATTAACCAAGACAAATGAATGAAACAGAG 3587  
DB 3379 GGAAGAAACCAACCGCATGCGCAGAGGTGGAAGATGATCATGACGAGAC 3438  
QY 3588 CTAAACCATTAAGATTTGCTTCAAGACGACGACGACGACGACGACGACGACGACGAC 3647  
DB 3439 CAC-----TGTCTTCAATTAACAC-----CCAACTCAACGCTCGGGT 3479  
QY 3648 AGCCATTAAGATGACCATTTCAAGACGAGGCAAGAGGCGCGGCGAGCATGAG 3707  
DB 3480 GCCATTTGCTGTGGGAGTCT-----TGACTTGAAGCTTCAACACAGAGATGTTAGC 3534  
QY 3708 GCGGAGGAGAGCGCGACCGCCAGCAAGAGATTAAGTCTGACGAGAACTGACGAG 3767  
DB 3535 AGCGAATCAACCTTGAAGGCAAGAAATTA-----ACTGACATACCACTCTCA 3588  
QY 3768 GAGGCGAATGCGAGAGGCGCGCTGACGATGATCATTTATGACACACAGAG 3827  
DB 3589 GAAGGAAGTACATGACATCAAGCTGAGGTGAAGAAAGTCCCGTGAAGCAACTGAG 3648  
QY 3828 GATTAATCGATGAATATTCAGCTGATGTGCGCCGATCTGATTAAGAAATTTCCG 3887  
DB 3649 GAATACTTGG-----ATCCGAGCGCTGCTTTACAGAGGTTGCGTCCAGCGGTTAAG 3702  
QY 3888 ATCTTACCGGTGACATGACTGCGCTTGTGCAAGAGTGGGCAATTTACACTGA 3947  
DB 3703 TGTGCGAGAGCAACATCGAGAGACTAGGCAAGTGTGTGAGATCTTGCAGAAACC 3762  
QY 3948 ACTTTCAATTAATGAAATAATTTTGAAGACAGCTTATCACTATGATTTAATG 4007  
DB 3763 TGCTTCTCATTTGTGAGCAAAATGTTGAGCTTCAATCATCTTCAATGATTTCTC 3822  
QY 4008 AGTAGCTTAGCTTGGCATTAAGAGATGATCATCTGCAAGAACCAATCTGACAGAT 4067  
DB 3823 AGCAGTGGCGCTGCGCTTTGAGAGCATCTACATTAAGAGAGAGAACCATCCGAC 3882  
QY 4068 ATTTTAATCTAATATGACAGAAATTTAAGGTTAATTTCTTTGGAATGTTAATGAG 4127  
DB 3883 ATCTGAGATATGAGCAAGAGTCTTCACTTCAATCTTCAAGATGTTGCTCAAG 3942  
QY 4128 TGTGTGGGCTGCGCTTCAAGTGTACTTCAACCAAGCGGTGTGTGCTGATTTGCTG 4187

Db 3943 TGGACGCTACGGCTTGTCAAGTCTTTCACCAATGCTGTGTGATGATCTTCTC 4002  
 Qy 4188 ATTGTCATGATGCTTATGCTTATCACTTGTGCTTCACTTGTGAGCTGTGATTCAA 4247  
 Db 4003 ATTGCTGTCTCTTGTAGTCAAGCTTATAGCTAATGCCCTGGGCTACTCGGAATAGT 4062  
 Qy 4248 GCTTCAAGACTATGCGAAGCTTAAGACACTGAGACCACTACGTGCCATGCTCCGTATG 4307  
 Db 4063 GCCATTAAGTCCCTTAAGACCTTAAGACCTTGAAGACCTTAAAGACCTTATCAAGATT 4122  
 Qy 4308 CAGGAGCATGAGGAGTGTGCTTATATCGCTGATCAAGCTATACGCTCATCTTCAATGTG 4367  
 Db 4123 GAAGGATGAGGAGTGTGCTTATATCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4182  
 Qy 4368 CTATGCTGTGTCTATATATTTTGGCTAATTTTGGCATATGAGGTGAACAGCTTTTGTCT 4427  
 Db 4183 CTGCTGTGTGTCTATCTTCTGTGCTGATTTTCAAGCATATGAGGATTAACCTGTTTGC 4242  
 Qy 4428 GGAATATTTTAAAGTGC---GAGACATGATGAGCAAGAGCTTACGCCAGATCTATA 4484  
 Db 4243 GGGAAATACCACTGCTTTTAAATGAGCTTCTGAATCCGGTTCGAATGATATGTC 4302  
 Qy 4485 CCAATCGCAATGCTGTGCGAG-----AGGAGAACTACACGTGGTG 4526  
 Db 4303 AACATTAAGAGGAGCTGTGAGAGGAGCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAG 4362  
 Qy 4527 AATTGAGCAATGAATTTGATCATGTAGTAAAGGATCTGTGCTTTTCCAGTGCC 4586  
 Db 4363 AATGTCAAGATCACTTGTGACATGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4422  
 Qy 4587 ACCTTCAAGGCTGTGATCAATATGAAAGATGTATGATTCACGAGAGTGAAGCAAG 4646  
 Db 4423 ACCTTCAAGGCTGTGATGACATATGATGATGATGATGATGATGATGATGATGATGATGAT 4482  
 Qy 4647 CAACCAATTCGTGAAGCAATCTCAATGATTTATTTTGTGATTTTGTGATTTTGTGATTTT 4706  
 Db 4483 CAGCTGACTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4542  
 Qy 4707 GGATCTTTTTCACACTGATCTGTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 4766  
 Db 4543 GGTCTCTTCTTCACTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 4602  
 Qy 4767 AAGAAAAAGAGGATGATCTATGAAATGTTTATGATGATGATGATGATGATGATGATGATGATGAT 4826  
 Db 4603 AAGAAAA--GTTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4659  
 Qy 4827 AATGCTATGAAAGATGAGGCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4886  
 Db 4660 AATGCTATGAAAGATGAGGCTTAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4719  
 Qy 4887 CGACCAAGCAATGATCTTGAATATGAAATGATGAAATGATGAAATGATGAAATGATGAAATGAT 4946  
 Db 4720 AAATATCAAGGAGGATGATCTTGAATATGAAATGATGAAATGATGAAATGATGAAATGATGAAAT 4779  
 Qy 4947 TTATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5006  
 Db 4780 ATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4839  
 Qy 5007 TATAAGCGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5066  
 Db 4840 ATGAGAGCAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4899  
 Qy 5067 CTATTAATAATATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5126  
 Db 4900 GTGCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4959  
 Qy 5127 GTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5186  
 Db 4960 TTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5019  
 Qy 5187 TTGCTGTGCGGAGCCCTGCTCCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5246

Db 5020 TTGCTTCCCAACCTTATCCAGTTATCCGATTTGGCCGGTATGGGCGCATCTGGCT 5079  
 Qy 5247 CTGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5306  
 Db 5080 CTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5139  
 Qy 5307 GCCCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5366  
 Db 5140 GCCCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5199  
 Qy 5367 ATGTGCTTCTCATGCAAGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5426  
 Db 5200 ATGTGCAACTTCCGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5259  
 Qy 5427 ACCTTGGCCAGAGCATGATCTGCTCTTTCATATGTCAGTCAAGCCGCTTGGATGCT 5486  
 Db 5260 ACATTTGGCAACACATGATCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5319  
 Qy 5487 GTACTGAGCGCATTAACAA-----TGAGGAAGCATGCAATCCAGCCGAGGAGC 5537  
 Db 5320 CTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5379  
 Qy 5538 AAAGCTATCCGAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5597  
 Db 5380 AGTGGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5439  
 Qy 5598 CTAGTTAAGCTTTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5657  
 Db 5440 ATCATATCTCTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5499  
 Qy 5658 AGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5717  
 Db 5500 AGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5559  
 Qy 5718 GAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5777  
 Db 5560 GAGATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5619  
 Qy 5778 GAATTCCTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5837  
 Db 5620 GACTTTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5679  
 Qy 5838 ATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5897  
 Db 5680 ATGCTCATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5739  
 Qy 5898 GCCCTTACGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5957  
 Db 5740 GCCCTTACGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5799  
 Qy 5958 GGTGAG-----ATAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6011  
 Db 5800 GAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5859  
 Qy 6012 CTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6071  
 Db 5860 CTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5919  
 Qy 6072 AAGGCGGCGGCG 6084  
 Db 5920 TTGGCTAAGGCGG 5932  
 RESULT 10  
 AAVS8421  
 ID AAVS8421 standard; cDNA; 6007 BP.  
 XX AAVS8421;  
 XX AC  
 XX 01-DEC-1998 (first entry)  
 XX DT  
 XX Tetrodotoxin-sensitive sodium channel PNa4 coding sequence.

KM Tetradotoxin-sensitive sodium channel; rat; PN4 sodium channel; stroke;  
 nervous system disorder; epilepsy; brain injury; diabetic neuropathy;  
 AIDS-associated neuropathy; therapy; ss.

XX Rattus sp.

XX Key Location/Qualifiers  
 XX CDS 22..598  
 XX /\*tag= a

XX MO9838302-A2.

XX 03-SEP-1998.

XX 20-FEB-1998; 98WO-EP000997.

XX 26-FEB-1997; 97US-0039447P.

XX (HOPF ) HOFFMANN LA ROCHE & CO AG F.

XX Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran L;

XX WPI; 1998-481204/41.

XX P-PDB; AAM69362.

XX New rat tetradotoxin-sensitive sodium channel alpha subunit and DNA - for  
 PT detecting inhibitors which alleviate pain, and treating nervous system  
 PT disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.

XX Claim 19; Page 33-36; 87pp; English.

XX This sequence represents the isolated rat PN4 sodium channel cDNA clone  
 CC of the invention. This sequence was isolated from a peripheral nerve from  
 CC a rat dorsal ganglia. The PN4 sodium channel sequences are tetradotoxin-  
 CC sensitive sodium channels. The protein is used in assays for detecting  
 CC inhibitors of tetradotoxin-sensitive sodium channels, which alleviate  
 CC pain. The probes can be used to detect and isolate the DNA or protein in  
 CC tissues. The antibodies can also be used to isolate the protein. The  
 CC protein is used as a therapeutic target for compounds to treat disorders  
 CC of the nervous system, such as epilepsy, stroke and brain injury,  
 CC diabetic neuropathy, and AIDS-associated neuropathy, etc

XX Sequence 6007 BF; 1490 A; 1559 C; 1609 G; 1349 T; 0 U; 0 Other;

XX Query Match 15.7%; Score 1019.4; DB 2; Length 6007;

XX Best Local Similarity 52.8%; Pred. No. 7e-245;

XX Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;

XX 186 CGCAAGAAAAAAGAAATCCGATATGATGACGAGACGAGATGAAGTCCAA 245

XX 121 CTCAGAAACCAACCAAGGCGGATGCGACGACCGGAGAGCATGAACAGCAAGCCC 180

XX 246 CCGGATCTTACACTTGAACAGGGTGTGCAATACCTGTTGCAATGCAAGGCTTCCG 305

XX 181 AAGCAAAACAGTGAACCTGAGGCTGGGAAAGTTGCTTCACTACGAGGACATCCG 240

XX 306 CCGGATTTGGCTCCTCCTCTGAGGATATGATTCCTTCTACAGCATATGATCA 365

XX 241 CAAGGCTGTGGTGGCTTCCCTGAGGACCTTGAACCTTACCTTATTTGACGCAAAAAC 300

XX 366 TTGCTAGTTGTAGCAAGAAAGATATTTTGTGCTTTTGTGATCAAAAGCAATGG 425

XX 301 TTGTAGATTAAGAGAGGAAACCTCTTCAATTTAGTGCACACCTGCTTGTAC 360

XX 426 ATGCTGATTCATTCATTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 485

XX 361 ATTTAAGCCCTTTAACTGATTAAGAAATAGCTATTAATTTTATATCACTCACTT 420

XX 486 TTTTCCCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT 545

XX 421 TTGAGCATGATCATGATGACCAATCTGACCAACTGTGTGTATATACCTTTAGTAC 480

XX 546 AGCCCAAGGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 602

DB 481 CTCCAGATAGTCCAAAGATGTGAGATGACATTTCAAGGATTTACATTTGATCA 540

DB 603 GCTGTTAAAGTATGAGCAAGAGTTTCAATTTATGCCCCGTTTACGATCTTATGATGCA 662

DB 541 CTAGTAAATATCATGCAAGAGGTTTCTGATAGAGGCTTCACTTCTTCTGAGACCCG 600

DB 663 TGGATTTGGCTGAGATTTGGTATAGCTTATAGCTTATGATGACCATGGATATAGATTTA 722

DB 601 TGGAACTGGTTAGACTTCACTGATCATGATGATGATGATGATGATGATGATGATGAT 660

DB 723 GGTAAATAGCAAGCCCTGGAACGTTTAAAGGTGCTGCAAGGCTTAAACCGTACCAATT 782

DB 661 GGCATATGTCAGCCCTGAGAACATTTCAAGGTTCTCCAGCTTTGAAACATATCTCTGTA 720

DB 783 GTCCAGAGCTTAAAGACATGCTGCGCCCGCTCATGCAATGAGTAAAGATGCGCAT 842

DB 721 ATTCCAGGCTTGAACATGCTGAGGCTTAAATCAATGCTGTAAGAGCTTGTGAGAC 780

DB 843 GTGATTTATCCAGCATGTTCTCCCTGTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCT 902

DB 781 GTGATGATCTTCAAGATGTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 840

DB 903 ATGGGCTGCTCAACGAGAGTGAT-----CAAGATTTCCGCTGACGCTTCC 953

DB 841 ATGGGGAACCTTCAAAACAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900

DB 954 TGGGGCATCTTCAACGAGACGAGGCTGAGCTTCAATTCGCAATGAGCTTCAATTTGAT 1013

DB 901 GAGAACGCAACAGAGGCTTGAATGAGGAGATATATCAATTAACAAACCTTTTAC 960

DB 1014 TCCGAGACGAGGAGCATCTCATTTCCGTTATGCGCAATATATCCGCTGCGGCGCATTC 1073

DB 961 ATGCTTCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020

DB 1074 GACGACGATTAAGTGTGCTGCAAGGCTTGTGCTGCAATTCGCAATTCGCAATTCGCA 1133

DB 1021 CCAGAGGATTTCCAGATGATGAAG---CAGAGAGAACCCCAACGCTTACACACAC 1077

DB 1134 TTGATTTGTTGAGGAGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1193

DB 1078 TTGACACCTTCACTGCTGCTGCTTCTTGGATATTCGCTTATGACCAAGCATATTGG 1137

DB 1194 GAGATCTGTACCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1253

DB 1138 GAGAACCTTATACAGCTGACCTTACGAGCGCTGAGAAACGATATGATCTTCTTGTG 1197

DB 1254 GTCATATCTTCTTATGATCTTATCTTATGATTTGATTTGCTGCTGCTGCTGCTGCT 1313

DB 1198 TTGATCATCTTGTGCTGCTTCTTATCTGATGATGATGATGATGATGATGATGATGAT 1257

DB 1314 TCGTATGACGATTTGCAAGAGAGGCGCAAGAGAGGCTGCGCAAGAGAGGCGATTA 1373

DB 1258 GCTTTATGAGAA---CAGAACAGGCAACATGAGAGGCAAGAGCAAAAGAGGC--- 1310

DB 1374 CGTGAACGAGAGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1433

DB 1311 CGAGTTCAAGGCAATGTGAGCACTCAAG---AAGAGAGAGAGAGAGGACAGGCT 1365

DB 1434 CAGGCTCAGGACAGAGGATGCGGCTGCGCGCAAGAGGCTCACTGATCCGGAATG 1493

DB 1366 GCTGCAATGCGACCTTACGCGGCACTGTTCGGAAG---CGCATTAAGAGAGAGG 1422

DB 1494 GCCAAGTCCGACGATTTCTTCACTAGCTATGATGATTTTGTGCGGCGGAGAGGCG 1553

DB 1423 GAGATGAGGATGAGCTTCCAGAGAGCTTCTGAACTGCTAACTCAATTCAGTTCCAGAG 1482

DB 1554 AAGCATACAAACAAAGAGAGATGATTCATTCGAGGCTCGAGGTGAGTGTGAGTGTG 1613

DB 1483 GCGAAGAGCGCGGAA-----CGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1526

DB 1614 GTGAGGCTTATTAACAAAGACAGCACTTACACAGCACACCAAGCTTACAAAGTTGCT 1673

1527 GCTCTGTAAGGCGAGAGAAAGGGAGCCGGAGAGAGGTTTAA-----GT 1573  
1674 AAAGTAGACAGACATCTTCTTACCTGTTACCGTTTAAATACGACGGGATCA 1733  
1574 CAGAGTCGAAAGACGATAGAGAGAGAGCCCTCCGCTGCAACAACAGATAGGGA 1633  
1734 CGTAGTCTCAAGATACAGATACGAGAACGAGCGTGGCCGTTGGTATACCGGTAGC 1793  
1634 GGAAGTTTTCATCATGATCATGATGCTGCTCAGCATTCAGAGCTGCCCTTCTCTCC 1693  
1794 GATCGTAAGCCATTGGTATTTGTCAATATCAGATGCGCCAGACAGCACTTGGCCCTTTC 1853  
1694 GACATTAACAGAAAGACAGATCTTCAGCTTCGGGGACCG-GTGGTTCGGGACCC 1752  
1854 GACGACTGATGCTCCGCTCAACCCGATGCTCCGAGAGAAAGAGGAGATAGTCCGCTG 1913  
1753 GGCCTGAGAAATG-----AGTTGCGAGAGATGAACAGAGACCGTGAAGAG 1800  
1914 TACTATGCAATCTTAGGCTCCCGACATCATGTATACCTGSCATCAGTCCGAAATATCG 1973  
1801 AGCGAGGCGCGGCTGATCTGCTTCTTCAATCCGATCCGCGCCGCGAGCGCCGACGAC 1860  
1974 TATACCTCAATGCGCATCTACTCGGCGGATGCGCCGTCATGCGCGTGAAGCAATGAC 2033  
1861 TACAGTGGCTACAGCGGCTACAGCGAGCGAGCGCTGCGCGCATCTTCCCGACCTG 1920  
2034 AAGGAGACAAATTCGCGACCGGCAACAGCAATCATCATGAGGCGCCACCATGCG 2093  
1921 CGGCGACGCGTGAAGCGGACAGCA-----CGGTGACCTGCAACGCG 1962  
2094 GGACACACCTGTCTGGAACCAATCAAGCTCGATCGGAGTACGAAATGGGCTG 2153  
1963 G-----TAGTCTACTCATTCGGGCGCCGCTCAACATGCG 1997  
2154 GAGTGACGAGAGAGCTGCGAAGATTAACATCAATGCAATCTTTATGAGCCGCTC 2213  
1998 GCGGCTCTGCTGAGTGAATA-----GATTAAGGAGCTACGAGACGCGCA 2046  
2214 CAGACCAAAAGGTTGATGATGAAAG---ATGTGATGCTCTGATGATGATCATCGAA 2270  
2047 ACGACTGAGTGAATTAAGAAAGAGAGCCCTGATCTCTTTAATGTTATGAGACAA 2106  
2271 CAGGCGGCTGGTGGCAAGTCGCGGAGCGATGCGGCTGCTCGTTTATCATTTTCCA 2330  
2107 CTGCGCTCTCAAGAGAGAGAGACAGAAATCAACAGCAATATGAGCTGTGTCACAAACG 2166  
2331 ACAGAGAGAGATGACAGAGATGGGCGGAGCTTCAAGACAAAGGCACTGGAATGCTTC 2390  
2167 CTAGTGAAGAGCTGGAGAG-----GTCTAGAGAAAGTCCACCGTGTGTA 2216  
2391 AAAGGATCATGATGTTTGT-GTGTGGAGCTGTGCTGGTTGGTGAATTTACAGA 2449  
2217 TAAAGTTCGCAACTTTCCTCATCTGGAGTGTCAACCTTACGATTAATACTGAAGA 2276  
2450 GTGGATATCGCATGCTGCTGATCCCTGTGAGAGCTTTCATCAGCTGATGATGT 2509  
2277 GATGTGAATTAATGCTATGAGACCTTTTGTATTAAGCTTACCATCATCTGATGT 2336  
2510 GGTCAACAGATGTTTCATGAGATGATACACAGATATGAACAAGAGATGAACGGCT 2569  
2337 TCTGAATACGCTATTAATGAGATGAGACCATTCCTATGACACAGAGTTGGAACAGT 2396  
2570 GCTCAAGATGAGATATTTCTTCAACGCGACCTTTGCCATCGAGGCCACCATGAGCT 2629  
2397 CTGGCCGTAGAAATCTGATGTTCAACGAGATCTTCAACGCGGAAATGTTTCTGAAGCT 2456  
2630 AATGGCCATGAGCCCAAGTACTATTTTCAGAGGGGCTGAACATCTTCACTTAT 2689  
2457 CATAGCCATGAGCCCTTACTTATTTTCCAGAGAGGCTGGAACATTTTGAACGATTTAT 2516  
2690 CGTGGCCCTTATCGCTATTTGAACCTGGAACCTGAGGGTGTCAAGGCTGTGCTGATTCG 2749  
2517 TGTCTCCTCAAGTTTAAATGAGCTGAGTGTGCAAGATGTGAAGGGGCTCTAGTGTCTCG 2576

2750 TTCCTTGGATTGCTGCTGATTAATCAAACTGGCCCAAGTCTTGGCCACATTAATTTACT 2809  
2577 GTCTTTCGACTGCTCCAGTCTTCAAGTGTGAGCCCAAGTCTGGCCACCTGAACATCT 2636  
2810 CATTTGATTAATGAGACCAACATAGGCGCTTGGGTATCTGACATTTGATTTGAT 2869  
2637 GATCAAGATCATGGGAATCTCGTGGTGGCCCTGGGCACTGACCTGGTGTGGCAT 2696  
2870 TATCATCTTCACTTTTGGGTGATGAGATGCAACTGTTGGAAAGAAATATCATGA-- 2926  
2697 CATGCTTTTCACTTTCGCGGTGGGATGAGATGACATGTTTGAAGATTAAGAGAGTG 2756  
2927 TCACAGAGACCGCTTTCGAGATGCGACCTGCGCCGCTGGAATTCACCGACTTATGCA 2986  
2757 GGTCTGTAAGATCAACAGAGTGCAGACTCCGCGTGGCAATGAACGACTTCTTCA 2816  
2987 CAGCTTCAATGATCGTGTTCGGGTGCTCTGCGAGAAATGATGAGTCCATGTGGGACTG 3046  
2817 CTCCTTCTCATCTGCTTTCGAGTGTGTGTGGGAGTGGATCGAGACATGTGGACTG 2876  
3047 CATGTACGTG--GGGATGTCTGTGATTCCTTCTTGGCCACCGTTGTATCGG 3103  
2877 CATGAGGTGGCGCGGACGAGCATGTGCTTATGTCTTATGATGTTATGTCATTTG 2936  
3104 CAATCTGTGTACTTAACCTTTTCTAGCTTGTCTTTGTCCAAATTTGGCTCATCTAG 3163  
2937 CAACCTGTGTGTGATTAATCTTATCTGCGCTTCTTGTGAGCTCTTCAACGCGACAA 2996  
3164 CTATACGCGCGGACCTGCGGATTAAGATACAAATTAATAAGCCAGGCTTCAATCGANT 3223  
2997 CTTGGCGGCGACAGACAGACGAGGAAATGAACA----- 3032  
3224 TGCCCGATTAAAGTTGGTTAAGCTATATGTTGATTTTCAAGTTAATACGTA 3283  
3033 ----- 3032  
3284 CAATTAAGCAATTAATTAAGTATCAACCATGAGTGAAGAGACCAACGATCAGTTG 3343  
3033 -----CTGCAATCTCAGT 3047  
3344 GATTGAGCGAAGAGATGATGACAAAGACTGAGCTGGGCGACGAGATCTTGC 3403  
3048 GATCCGATTAAGAGGCGGTGCTGAGCAAGTGAAGTGAACGCTTCAATGACGCG 3107  
3404 CGAGCGCTCATCAAGAGGAGATCAAGAGACAGACGCACTGAGGTGCTATCGGGA 3463  
3108 TCATCTTCAAGAGGCGGAGGAGATGAAGTGAACCTCGACGAGCTGTATGAAGAA 3167  
3464 TCGGATGATTCAGATACCGGCGACATGAAGAAACAAAGCCGAAAGAAATCCAATA 3523  
3168 GGGCAATGCAATTCGCAACCAACAGGCGGTGATATCACCGGAACGGGCACTTCCAGAA 3227  
3524 TCTAATTAAGCAACGATGATGTCACACTCAATTAACCAAGACAAATATAGCTGAACA 3583  
3228 GAAAGGAGAGAGACACACAGCGGATCGGAGAGGTGAGAGATCATCATGAGCA 3287  
3584 CGAGCTAAACCATAGAGTGTCTTACAGAGAGACGACACTCGACATTAATCTCATTA 3643  
3288 GAGCACCA-----TGTCTTATTAACA-----CAAACTGACCGTCC 3328  
3644 TGTGAGCATTAAGATGACCATTTCAAGAGAGACCAAGGCAAGCGCGAGAGAT 3703  
3329 GGGTGCATATGCTGTGGGCGAGTC-----TGACTTGAAGAACTCAACAGAGAGATG 3383  
3704 GGAAGGCGAGAGAGAGCGGACGCGCAAGAGAGATTTAGTCTCAAGAGAACTGGA 3763  
3384 TAGAGAGATCAACACCTTGAAGGACAAAGATTA-----ATGAGACGATACAGGTC 3437  
3764 CGAGAGGCGAATGCAAGAGAGGCGCTCGACGCTGATATCTTAATGACACAGCA 3823  
3438 CTCAGAAAGAAATCAATCAATCAAGCTGAGGTGAAGAGTCCCGTGGAGCAAC 3497

OY	3824	CGAGGATATCTCGATGCAATATCCAGCTGATTTTCGCCGCCGATTCGGTACATATAAGAAAT	3883
Db	3498	TGAGGAATACTTGG-----ATCCGAGCGCTCTTTTACAGAGGGTTGGCTCCAGCGGTT	3551
OY	3884	TCCGATCTTTCAGCGGTGACATGACTGCACGGTTCTGGCAAGATGGGGCAATTTACACT	3943
Db	3552	CAAGTGTCCAGGTCAACATCGAGGAAGGACTAAGCAAGTCGTGGTGAACTTTGGCGAA	3611
OY	3944	GAAAACTTTCAATTAATTGAAAATAATTTTGAACAAGCTGTTATCACTATGATTTT	4003
Db	3612	AACTGCTCTCTCAATGTGAGCGCAATTTGGTTGAACCTTCATCTTCATGAAATTC	3671
OY	4004	AATGATAGCTTACTCTTTGGCATTAAGAAGATGATCTGCCAAGAAGCCCATCTGCA	4063
Db	3672	GCTCAGCAGTGGGCCCGCTGGCTTTGAGACATCTACATTTGAGAGAGGAAGCAATCCG	3731
OY	4064	GGATATTTTATATCATATGACAGAAATATTTACGGTTATATCTTTCTTGGAAATGTTAAT	4123
Db	3732	CACCATCTCGAGATGACGGGCAAGAGCTTCCATCCATCATCTTCATCTCGAAGATGTTGCT	3791
OY	4124	CAATGTGTGGCGCTCGGCTTCAAAAGTACTTACCAAGCGCGGTGGTGGCTGCATTT	4183
Db	3792	CAAGGGACACCTCAGCGCTTCGTCAAATTTTACCAATGCCGTGGTGGTGTGAAT	3851
OY	4184	CGTATTTGTCAATGATGCTTATCAACTTCGTGCTTCACTTGTGAGCTGGTGAT	4243
Db	3852	CCTCATTTGGCTGTCTCTTTTAACTCAGCTTAATGCTAATGCCCTGGGCTAATCCGAATC	3911
OY	4244	TCAAGCCTTCAAGACTAATGGAAGGTTAAGGACCTGAGACCACTACGTGCATGTCCG	4303
Db	3912	AGGTGCCAATAAGTCCCTTAAGACCCCTTAAGACTTTGAGACCTTAAGAGCTTATACG	3971
OY	4304	TATCAGAGGCAATGAGGGTCTGTTAATGCGCTGGTCAAGACTAATCCGTCCATCTTCA	4363
Db	3972	ATTGGAAGGATGAGGGGTGGTGGTGAATGCTTGGTGGCGCCATCCCTTCATCATGA	4031
OY	4364	TGTGCTATTTGGTGTCTAATATTTTGGCTAATTTTGCATATATGAGGTGACGCTTT	4423
Db	4032	TGTGTGTGTGGTGTCTCATCTTCTGCTAATTTTCAAGCAATGGAGTTAACTGTT	4091
OY	4424	TGCTGGAATAATTTTAAATGTC---GAGACATGATATGGCAGAGCTCAGCCAGAT	4480
Db	4092	TGCGGGGAATATCACATCTGCTTAAATGAGACTTGAAATCCGGTTCGAAATCGATAT	4151
OY	4481	CATACCAATTCGCAATGCCCTGGAG-----AGCGAATCTACAGTG	4522
Db	4152	TGTCACAATATAAACGGACTGTGAGAGCTCATGAGGGCAACAGCACGAGATCCGATG	4211
OY	4523	GGTGAATTCAGCAATGAATTTGCATCATGTAGTAAACCGATCTGTCCTTTTCAAGT	4582
Db	4212	GAAAGATGTCAGATCAACTTTGACAAATGTGAGACAGAGTACCTGGCCCTTTCAAGT	4271
OY	4583	GGCCACCTTCAAAAGCTGGATACAAATCATGAAATGATCGATCTATCGATTACAGAGGTGA	4642
Db	4272	GGCAACTTCAAAAGCTGGATGAGATCATGTATATCCGCTGAAATTCGAAAGCCAGA	4331
OY	4643	CAGGAAACCAATTCGTGAAGAAGAAATCATCACTGATATTTATTTTTCGATCTTCATCAT	4702
Db	4332	CGAGCAGCTTGACATGAGGGCAATCTACATGTACATCTTCTGTCTCATCTTCATCAT	4391
OY	4703	ATTGGATCTTTTTCACACTCAATCTGTCATTTGTTGTGTTATCATTTGATTAATTTATGA	4762
Db	4392	CTTCGGCTCTCTTCTTCAACCTCAACCTGTTTCACTGGTGTCACTCATCGCAACTTCACCA	4451
OY	4763	GCAAAAGAAAAAGCAGGTGATCATTTGAATTTGTCATGACAGAAATCGAAGAAAGTA	4822
Db	4452	GCAAGAAAGAAA--GTTTGGAGTTCAGGACATCTTCATGACAGAGGAACGAAAGATTA	4508
OY	4823	CTATATGCTATGAAAAAGATGGGCTTAAAAAACCATTTAAAGCCATTCAGAACCAAG	4882
Db	4509	CTACATGTGCATGAAGAAAGCTGGGCTCAAGAAAGCCAGAGCCATCTCCCGACCTTT	4568
OY	4883	GTGGCGACCAAGACATATGCTCTTTGAATATGATTAACGATTAAGAAATTCGATATATGAT	4944

Db	4569	GAA	CAAAATCC	CAAGGAGATGCTTTATATTCG	CACTCAACAGCCTTGA	CAATTGTGAT	4628		
QY	4943	TAT	GTAATTCAT	TGATGATCTG	CAACATGTTCC	ACCATGACCCTCGATCGTTACGATGCGTCGGA	5002		
Db	4629	CAT	GATGCTCAT	CTGCTTCAACATGATG	CAATGATG	GAGACAGACACTCAGAGCAA	4688		
QY	5003	CAC	GTAATAC	CGCGGCTT	AGACTATCTCAATGCG	GAAATTTGTAGTTATTTTCAGTTCCGA	5062		
Db	4689	GC	AATGAGAGAA	CAATCTTTACTG	ATATATCGGCTTGTGATCTTTCAC	CTTCGCA	4748		
QY	5063	AAT	GCTATTA	AAAAATATGCTT	TACGATCACTATATTTATG	AGCCATGAAATTTAT	5122		
Db	4749	GTT	GTTGCTCA	AAATATGTTT	GCTTGAACACTATTTTCA	CCATTTGCGTGAACAATCTT	4808		
QY	5123	TGA	TGATGAT	GATTGTCAATTTTAT	CCATCTTAGGCTTTGA	CTTACGATATTTATCGA	5182		
Db	4809	TGA	CTTTGTGTG	TGATCTCTCCATTTG	GGAATGTTTCTG	CGATATCAATGAGAA	4868		
QY	5183	GTA	CTTGCTG	TCGCGGCA	CCCTGCTCCGAGTGGTGGCGGTG	GGCGGAGTGGGCGGTGCT	5242		
Db	4869	GTA	CTTGTCT	CCCCCA	CCCTATTCGAGTTATTCGAT	TGGCCGATATGGGGCAATCTT	4928		
QY	5243	TCG	ACTGTGA	AGGAGCC	CAAGGCAATTTG	GAACACTGCTCTTGCGGTTG	CCATGTGCT	5302	
Db	4929	GCG	CTGATCA	AGGGCC	CAAAAGGAATCC	CAACCTCTCTTGCTTAA	TGATGTGCT	4988	
QY	5303	GCG	CGCCCTG	TTCAACATTCG	CCGCTGCTGCTGCTGCTGAT	GTCAATCTTTGCACTTT	5362		
Db	4989	GCC	CGCCCTG	TTCAACATTCG	CCCTGCTGCTGCTGCTGAT	GTCAATCTTTGCACTTT	5048		
QY	5363	CGG	CATGCTG	CTTCTTCA	CGTGAAGAGAA	GAGCGGCATTA	CGACGTTCAACTT	5422	
Db	5049	TGG	CATGTC	CACTTCCATAC	CGTGAAGACAGAGGCGG	GATTTGACCA	CAATGTTCAACTT	5108	
QY	5423	CAA	GACCTTT	TGGCCAGAC	GTGATCCGCTCTTCA	ATGTCGACGTCA	GCGGCTTGGA	5482	
Db	5109	CGA	ACATTTG	GCAACAGCAT	GATCTTGTTGTTCCAA	GTATCAACAGTCTG	CTGGCTGGGA	5168	
QY	5483	TGT	GTA	CTGGA	CCCATTTATCAA-----TG	AGAAACATGCATCC	ACCCGACG	5533	
Db	5169	TGG	CTGCTG	TGTCGATC	CTTGAAACCGG	CCCCCTGAC	TGCGACTTGA	CAAAAGAGACCC	5228
QY	5534	CGA	CAAAAG	CTATCCGG	GCAATTTGTGTTAG	CGACCGTTGG	AATACGTTTCTCCTC	5593	
Db	5229	AGG	GATG	GGCTTCA	AAAGGGA	CTGTGGAA	CCCTCGGTGG	CAATCTTCTTTGTGAG	5288
QY	5594	AAT	ACAGTT	TAAGCTTTT	TGATAGTATTAAT	ATGATGCACTT	GTCTGATCTTGAGAA	5653	
Db	5289	CTA	CTATCA	TATCATCT	CTCTTCCGATTT	GTGTGA	CAATGTACATTCG	CAATCTTGAGAA	5348
QY	5654	CTA	TATG	CAGGCC	ACCGAGAC	GTGTGAAGAGG	GTTAACGACGAC	CACTACGATGTA	5713
Db	5349	CTT	CAGCTG	GCAC	CCGAGGAG	CGCGCA	CCCTCTGTG	ATGAGATGACTTTCGACATTT	5408
QY	5714	CTA	TGATG	ATCTGG	AGCAATTCGATCCG	AGAGGACCCAGT	ACATACGCTAT	TGATCACT	5773
Db	5409	CTA	TGATG	ATCTGG	AGAAATTTGA	CCGACAGCC	CAAGTTCA	TCATCGATCTGTAACT	5468
QY	5774	GTC	CGAAT	TCTG	AGCTG	GAGCCCCCGCTG	CAGATCCACAA	CCGAAACAACTAACAA	5833
Db	5469	GGA	CAACT	TTTGCC	CGACGCTTG	AGGACCCGCTCG	AGATACCA	AGCCCAACACCATGAA	5522
QY	5834	GAT	CTAT	TCGATG	AGCATAC	CAACCATCTG	TCGCGGTG	CACTCATATGATCTGCTGCA	5893
Db	5529	GCT	ATAC	CGCATG	AGACTCG	CCATGTGTGA	CGGAGATG	CACTCACTCTTGGA	5588
QY	5884	CGA	CGCCCT	TACGAA	GAATCTTTT	TCGCGGAAGG	GCATCCGAT	ATAGAGAGACGCGGTGA	5953
Db	5589	TTT	GCCCTT	ACCAAG	CGAGTCTGT	GAGACAGTGG	AGATTTGA	CATCTGCGGACAGA	5648
QY	5954	GAT	TGTGTAG-----	ATAG	CGGCCCCCGG	ATACGAGG	CTTACG	AGCCGCTTCAATC	6007



DB 5649 GATGAGAGGCGGTTCGTGCAATCCATTCCTTCAAGATGCTTACGAGCCTATCAGAC 5708  
QY 6008 AACGCTGTGGGTCTAGCTGAGAGTACTGCGCCCGCTAATCCAGACGCTTGGCGAAA 6067  
DB 5709 CACTCTGGGGGCGAAGAGAGAGGTGTCTGCACTGTGTCTGAGCGCTGCTTACAGGAG 5768  
QY 6068 GCACAAAGCGCGCGCGCG 6084  
DB 5769 ACACCTTGGCTAGGCGCGG 5785

RESULT 11  
ABT42021  
ID ABT42021 standard; DNA; 6586 BP.  
XX  
AC ABT42021;  
XX  
DT 26-JUN-2003 (first entry)  
XX  
DE Toxicity modelling related rat gene SEQ ID No 1723.  
XX  
KW Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
KW database; drug screening; toxicity assay; rat; ds.  
XX  
OS Rattus norvegicus.  
XX  
PN M0200235000-A2.  
XX  
PD 28-NOV-2002.  
XX  
PE 22-MAY-2002; 2002MO-US016173.  
XX  
PR 22-MAY-2001; 2001US-0292335P.  
PR 13-JUN-2001; 2001US-0297523P.  
PR 19-JUN-2001; 2001US-0298925P.  
PR 10-JUL-2001; 2001US-0303807P.  
PR 10-JUL-2001; 2001US-0303808P.  
PR 10-JUL-2001; 2001US-0303810P.  
PR 28-AUG-2001; 2001US-0315047P.  
PR 27-SEP-2001; 2001US-0324928P.  
PR 22-OCT-2001; 2001US-0330462P.  
PR 01-NOV-2001; 2001US-0330867P.  
PR 21-NOV-2001; 2001US-0331805P.  
PR 06-DEC-2001; 2001US-0336144P.  
PR 19-DEC-2001; 2001US-0340873P.  
PR 21-FEB-2002; 2002US-0357842P.  
PR 21-FEB-2002; 2002US-0357843P.  
PR 15-MAR-2002; 2002US-0357844P.  
PR 08-APR-2002; 2002US-0370144P.  
PR 08-APR-2002; 2002US-0370206P.  
PR 08-APR-2002; 2002US-0370247P.  
PR 17-APR-2002; 2002US-0372794P.  
PR 21-APR-2002; 2002US-0371679P.  
XX  
PA (GENE-) GENE LOGIC INC.  
XX  
PI Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;  
XX  
DR WPI; 2003-148464/14.  
XX  
PT Predicting at least one toxic effect of a compound, useful for toxicity  
PT modeling, comprises preparing a gene expression profile of a tissue or  
PT cell sample exposed to the compound, and comparing the gene expression  
PT profile to a database.  
XX  
PS Example 4; Page; 446pp; English.  
XX  
CC The invention relates to a novel method of predicting at least one toxic  
CC effect of a compound. The method comprises a gene expression profile of a  
CC tissue or cell sample exposed to the compound, and comparing the gene  
CC expression profile to a database comprising at least part of the data or  
CC information given in the specification. The methods are useful for

CC predicting at least one toxic effect of a compound, predicting the  
CC progression of a toxic effect of a compound, predicting the renal  
CC toxicity of a compound, or identifying toxicity markers in tissues or  
CC cells exposed to known renal toxin. The genes are useful as toxicity  
CC markers in drug screening and toxicity assays, in monitoring disease or  
CC physiological states, or disease progression. This polynucleotide  
CC represents a rat DNA sequence relating to the toxic effect database  
CC described in the specification. NOTE: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from the World Intellectual Property  
CC Organization  
SQ  
Sequence 6586 BP; 1632 A; 1732 C; 1745 G; 1475 T; 0 U; 2 Other;  
XX  
XX  
Query Match 15.7%; Score 1019.4; DB 10; Length 6586;  
Best Local Similarity 52.8%; Pred. No. 7.3e-245;  
Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;  
QY 186 CGCAAGAAAAAACAAGAAATCCGATATGATGACGAGAGAGAGATGCCA 245  
DB 268 CTCAAGAAACCAACCAAGCGGATGCGACCCGAGAGAGATGAAGACAGACAGCC 327  
QY 246 CCGATCCTACACTTGAACAGGGTGTGCCAATACCTGTTGATTGACAGGAGCTTCCG 305  
DB 328 AAGCCAAACAGTGAACCTGAGGCTGGAGAGTTTGCCTTTCATCTACGGGACATCCG 387  
QY 306 CCGAATTGGCTTCACCTCTCTCGAGATATGATCCCTTACAGCAATGTACTGACA 365  
DB 388 CAAGGCTGTGGGTGCTCCCTGAGGACTTGAACCTTACTATTGACCAAGAAACC 447  
QY 366 TTGCTAGTTGTAACGAAAGAAAGATTTTGGCTTTTGTGATCAAAAGCAATGCG 425  
DB 448 TTGTGATTAACAGAGGAAACCTCTTCAATTTAGTTCACACCTGCTTAC 507  
QY 426 ATGCTCATCATTCATTAATCCGATATGCTGTGSCCATTTTACCTTATGATCATCA 485  
DB 508 ATTTTAAGCCCTTTTAACCTGATTAAGAAATAGCTATTAATTTGATACCTGCTT 567  
QY 486 TTTTCCCTATTCATCATCACCACAAATCTGCTCACTGATCTGATGATATGCCACA 545  
DB 568 TTCAGCATGATCATCATGATGACCATCTGACCACTGTGTGTCATGACCTTTAGTAC 627  
QY 546 AAGCCACAGGTGATGTCACAGAGTG---ATATTCACCGGAATCTACATTGAAATCA 602  
DB 628 CTCACAGATGTCACAGAAATGTAAGTACATTCACAGGATTTACATTTGAAATCA 687  
QY 603 GCTGTAAGATGATGACAGAGTTTCAATTTATGCCGTTTACGTATCTTACAGATGCA 662  
DB 688 CTAGTGAATATCATTCGAGAGGTTTCTGCAATACAGGCTTCTTCCGAGACCG 747  
QY 663 TGAATTGGCTGACCTTGTATGTAATAGCTTTAGCTTATGTGACATGGATATGATTA 722  
DB 748 TGAATCTGTTAGACTTCAGTGTGATCATGATATGATGACAGAGTTTGTGACCTG 807  
QY 723 GGTAAATCTAGAGCCCTGCAACCTTTAGGTTGTGAGGCTTAAACCGTAGCAATT 782  
DB 808 GGCATGCTTCAAGGCTGAGAAACATTCAGGTTTCCGAGTTTGAAGAAATATCTCTGTA 867  
QY 783 GTGCCAGGCTTGAAGACATGTCGGGCGCTCATGCAATGGTGAAGAAATCTCGCAT 842  
DB 868 ATTCAGGCTTGAAGACATGTCGGGCGCTTATTCAGTCCGTAAGAGCTTCCGAC 927  
QY 843 GTGATTAATCTGACCATGTTCTCCCTGTGCTGTGCTGATGAGGCTTACAGATCTAT 902  
DB 928 GTGATGATCTGACAGTGTCTGCTGAGTGTTCGCCCGATGAGCTGCACTCTTC 987  
QY 903 ATGGCGCTGCTACCCGAGAGTGCAT-----CAAGAGTTCCCGCTGAGAGGTTCC 953  
DB 988 ATGGGAACCTTGCAGAAACAGTGTGTGTGTGCGCCATTAACAGAGAGTACCTG 1047  
QY 954 TGGGGCATCTGACCGAGCAAGTGAAGTGAATCATCATGACATGATCTCAATTTGTAT 1013  
DB 1048 GAGAACGCAACAGAGCTTTGACTGGAGGAATATATCAACATATAAACAATTTTAC 1107

1014 TCCGAGAGCAGAGGACATCTATTCGTTATGCGCAATATATCCGATCGCGGCGCATTC 1073  
Db 1108 ATGGTCTCGGACATGCTAGAACCTTGTCTGTGCGGAAACAGTTCTGATCTGGGCAATGC 1167  
Qy 1074 GACGACGATTACGTGTGCTGACAGGGGTTGTGCGAATCCGAATTATGCTTACACAC 1133  
Db 1168 CCAAGAGGATTCAGATGATGAAG--CAGGAAGAACCCCACTACAGTTACACACAC 1224  
Qy 1134 TTGGATTCTCGGATGAGGCTTCTGTGCGCTTCCGCTGATGACACAGACTTCTG 1193  
Db 1225 TTGGACCTTCAGCTGCGCTTCTGTGCAATATTCGCTTATGACCAAGACTTGG 1284  
Qy 1194 GAGGATCTACAGCTGTGTGCGCGCGCCGACATGACATGCTGTTCTTTAT 1253  
Db 1285 GAGAACCTTATACAGCTGACCTTACAGCGCTGGGAAACGTATGATCTTCTTGT 1344  
Qy 1254 GTCATCATCTTCTAGGTTCTATCTTATCTTGTGATTTGATTTTGGCCATTTGCGATG 1313  
Db 1345 TTGGTCACTTCGTGGGTTCTTCTATCTGTGAACTTGATCTTGGCTGTGCGCATG 1404  
Qy 1314 TCCGATACGAATTGCAAGAGAGCCGAAAGAAAGAGAGCTGCCGAAAGAGAGCAT 1373  
Db 1405 GCTTATAGAA--CAGAACAGGCAACCTGAGAGGCAAGCAAAAGAGC---- 1457  
Qy 1374 CGTGAAGCGAAGAGCTGCGCGCCGAAAGCGCCAGCTGAGAGAGCGCCCATGCG 1433  
Db 1458 CGATTCAAGGCAATGCTGGAGCAATCAAG--AAGCAGCAGGAGGAGGACAGGCT 1512  
Qy 1434 CAGGCTCAGGACAGAGGATGCGGCTGCGCGCAAGAGGCTGACCTGCACTCGGAAATG 1493  
Db 1513 GCTGCAATGCGCACTCAGCGGCGACTGTCTCGAACA--CGCATTTGAAGAAAGG 1569  
Qy 1494 GCCAAGAGTCCGAGGTATCTTGCATCAGCTATGAGCTATTTGTGCGCGAGAAAGG 1553  
Db 1570 GAATGAGGAGTAAAGCTCTCGAGAGAGCTTCTGAACTGTCTAACTCAATGCCAAGAGC 1629  
Qy 1554 AACGATGCAACAAAGAGAGATGCTTCTGAGAGCTGAGAGTGTGAGTGTGAGTGTG 1613  
Db 1630 GCGAAGGAGCGCGGAA-----CCGACGAAAGAGAGGAGGAGAAAG 1673  
Qy 1614 GTGAGCTTATCAAAAGCAACAGCACTTACAGACAGACACCAAGCTAACAAAGTTCTGT 1673  
Db 1674 GCTCTGAGAGCGAGAGAGAGGAGCCGAGAAAGTGTAA-----GT 1720  
Qy 1674 AAGGTGAGCAGACATCTTATCTTACCTGTTCACCGTTTAACTATCGAGGGATCA 1733  
Db 1721 CAGAGTGGAGAGCGGTATGAGAGAGAGGCTTCCGCTGCCAGACAAACAGATAGGGA 1780  
Qy 1734 GGTAGTTCTCAAGATACAGATACGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1793  
Db 1781 GGAAGTTTTCATCATGATGATGCTGCTCAGCATTCAGGCTCGCCCTTCTCTCC 1840  
Qy 1794 GATGTAGGCAATGATGTTGCAACATATCAGATGCGCAGACAGCACTTGCCTATGCC 1853  
Db 1841 GACATTAACGAAAGCAGCATTTCACTTCCGAGAGCCG-GTGCTTCCGAGAGCCG 1899  
Qy 1854 GACGATCGAATGCGGTCAACCCGATGTCCAGAGAGATGAGGAGAGAGAGAGAGAG 1913  
Db 1900 GGGCTGGAAGT-----AGTTCCAGAGATGAACAGAGACCGTGAAGAG 1947  
Qy 1914 TACTATGCAATCTAGGCTCCGAGACATCATGTTACTGTCATCACTGCGCAATTCG 1973  
Db 1948 ACGGAGGCGCGGAGCTGCTGCTTTCATCCCGATCCGCGCCGAGAGCGCGAGAGC 2007  
Qy 1974 TATACCTCATGAGGATCTACTCGCGGAGATGCGCTCATGAGGCTGAGCAATAGCC 2033  
Db 2008 TACAGTGGTAAAGCGGCTACAGCAGTGAAGCGGCTGTGCGGATCTTCCCGAGCTG 2067  
Qy 2034 AAGGAGCAAAATGCGCAACCGCAACAGCAATCAATCATGTTGGGCGCAACCATGGC 2093  
Db 2068 CGGCGCAGGCTGAGACGCAACAGCA-----CGTGAAGCTGCAACGCG 2109

2094 GGCACCACTGTCTGACACCAATCAAGCTGATCATCGGCACTAGAAATTTGGCTG 2153  
Db 2110 G-----TAGTCTACTATCGGGCCCGGCTCACACATCG 2144  
Qy 2154 GAGTCAAGCAGAGAGCTGCAAGTTAAACATCATGACATCTTTTATGAGCCGCTC 2213  
Db 2145 GCGGCTCTGCTGAGGTGAATA-----GATAGGACGCTACGAGAGCGCA 2193  
Qy 2214 CAGACAAAGGTGTGTTGATGAAAG--ATGTGATGTCTCGAATGACATCATGGA 2270  
Db 2194 ACGATGAGTGAATTAAGAAAGAGCCCTGATCTTTTATGTTCTATGACCA 2253  
Qy 2271 CAGGCGGTGTCGCGACAGTCCGCAAGCATCGCGGTGTCTCGTTTACTATTTCCA 2330  
Db 2254 CTGCGCTCTTACGACAGAGAGCAAGATCAACAGCATTAAGAGTGTGCAAAACG 2313  
Qy 2331 ACAGAGAGCATGACAGAGATGGCCGAGTTCAAAAGCAAGCACTGAAATGCTC 2390  
Db 2314 CTAGTGAAGAGCTGAAAG-----GTCTCAGAAAGTCCACCGTGTGTA 2363  
Qy 2391 AAGGCAATGATGTGTTGT-GTGTGGAATGTTGTGCGGTGTTGTTGAATTTCA 2449  
Db 2364 TAAGTTTGCACACATTTCTCATCTGGAAGTGAACCTTACTGATTAACAGGA 2423  
Qy 2450 GTGGGATGCTCATGCTCTTGCATCCTTGTGAGCTTTCATCAGCTGTGATGT 2509  
Db 2424 GATCGTAATTAATGCTATGACCTTTTGTATTAATTAAGCATCACATCTGATGCT 2483  
Qy 2510 GGTCAACAGATGTTCAATGCAATGATCAACAGATTAAGAAAGAGATGGAACGGT 2569  
Db 2484 TCGAATACGTAATTAATGCAATGAGCAGCATCCATGACACACAGTTGGAACAGT 2543  
Qy 2570 GCTCAAGATGCACTATTTCTCACCGCCACTTTGCGATCGAGCCACCATGAGT 2629  
Db 2544 CTGGCGGTAAGATCTGTGTTCAAGGAGATCTTCAAGGAGAAATGTTCTGAAGT 2603  
Qy 2630 AATGACCATGAGCCCACTACTATTTCAAGAGGCTGGAACATCTTGCATTAAT 2689  
Db 2604 CATAGCATGACCCCTACTATTAATTTCAAGAGGCTGGAACATTTTGAAGATTA 2663  
Qy 2690 CGTGGCTTATGCTATTTGGAATCTGGAGTCAAGGAGTCCAGGAGTGTCCGTATTGG 2749  
Db 2664 TGTCTCCCTCAATTATGAGAGTGAAGTCTGAGAGTGAAGAGGAGCTTCAGTCTGG 2723  
Qy 2750 TTCTTTCATGCTGCTGATTAATCAACTGCGCAAGTCTTGGCCCACTTAATTA 2809  
Db 2724 GTCTTTCAGAGCTCTCGAGTCTTCAAGTGTGCAAGTCTGGCCACCTGAAACATGT 2783  
Qy 2810 CATTCGATTATGAGCAGACCATGAGGCTTGGTAACTGACATTTGTACTTTGCAT 2869  
Db 2784 GATCAAGATCATGGAACCTCGGTGGTCCCTGGGCACTGACCTGTGTGCGCAT 2843  
Qy 2870 TATCATTTCAATTTGCGGTATGGAATGCAAGTTCGGAAGAAATTAATCATGA-- 2926  
Db 2844 CATGCTTCATTTGCGGTGAGAGTGAAGTCTTGTGAAGAGTTTACAGAGAG 2903  
Qy 2927 TCAAGAGACCGCTTTCGAGATGCGACCTGCGCGCTGGAATTCAACGACTTAATGA 2986  
Db 2904 GCTGTGAATGACACAGAGAGTGAAGTCCGCGCTGACATGAAGACTTCTTCA 2963  
Qy 2987 CAGCTTCATGATGTGTTCCGGGTCTCTGCGAGATGATGATGATGATGATGATGATG 3046  
Db 2964 CTCTTCTCATGATGTCTTCCAGTGTGTTGAGAGTGAAGTGAACATGAGGAGCTG 3023  
Qy 3047 CATGTAAGT--GGGAGTCTGAGATTCCTTCTTCTTGGCAACGTTGTGATCG 3103  
Db 3024 CATGAGAGCGCGGACAGGCAATGTGCTCATGTTCTTCAATGATGATGATGATG 3083  
Qy 3104 CAATCTTGTGATTAACCTTTTCTTGAAGCTTGTGTTTGTCAATTTGCTCATCTAG 3163  
Db 3084 CAACCTGTGTGATTAATCTATCTGAGCTTGTGATGCTTCAAGCCAGAGCA 3143  
Qy 3164 CTATATGAGCCGACATGCGATTAAGATTAAGATTAAGTGAAGGCTTCAATGAT 3223

Db 3144 CTGCGGCGCCACAGACGACGAGCGGGAAATGACAA----- 3179  
Qy 3224 TGCGCCGATTTAAAGTTGGTTAAAGCGTAATATGCTGATGTTTCAAGTAATATACGTA 3283  
Db 3180 ----- 3179  
Qy 3284 CAATATGCAAAATCAATTAAGTATCAACCATCAGGTGAGAGACCAACAGATCAATTG 3343  
Db 3180 -----CTGCAAGATCTCAGT 3194  
Qy 3344 GATTTGGAGCGAAGAGCATGTGTGACAAACAACTGAGCTGGGCGACGACGAGATCTCGC 3403  
Db 3195 GATCGGATTCAGAGAGGGGGGTGGCTTGACCAAAATGAAAGTGCACGCTTCATCATCAGGC 3254  
Qy 3404 CGACGGCTCATCAAGAGGGGATCAGAGACGCACTGGAGGTGGCCATCGGGA 3463  
Db 3255 TCACCTTCAAGCAGCGGGAGCGGATGAAGTGAACCCCTCGACGAGCTGTATGAGAGAA 3314  
Qy 3464 TCGGATGGAATTCAGATACACGGGACATGAGAGAAACAAAGCCGAGAAATTCAAATA 3523  
Db 3315 GGCCTATGCAATCGCAACACACGCGGCGTGAATATCAACGGAAAGCGCACTTCAGAA 3374  
Qy 3524 TCTAAATTAACCAACGATGATTTGGCACTCAATTAACCAACCAAGCAATTAAGCTGGAACA 3583  
Db 3375 GAAGGGGACCGAAGCCACACGCGCATCGCAGCAGCTGGAGAGTATCATGACGA 3434  
Qy 3584 CGAGCTAAACCATAGAGGTTGTCTTACAGACGACGACACTGCGACATTAATCTATA 3643  
Db 3435 GAGACACA-----TGCTCTTATTAACAC-----CCAACCTGACCGTCC 3475  
Qy 3644 TGTGACCATTAAGATGACCATTCAGAGACGAGAGCCAAAGGCGACGCGGACGAT 3703  
Db 3476 GGGTGCCCATGTGCTGTGGGCAATC-----TGACTTGAAGACCTCAACACAGAGATGT 3530  
Qy 3704 GAGGGGCGAGAGAGACGCGACGCGCAAGAGAGATTAGTCTCGACGAGAACTGGA 3763  
Db 3531 TAGACGCAATACAGACCTGAAAGGACGAAAGTAA-----ACTGACGATCCAGCTC 3584  
Qy 3764 CGAGAGGGCGAATGCGAGAGGGCGCTGACGCGTATCATTAATTCATGACAGCA 3823  
Db 3585 CTCAGAAAGGAATGACATGACATCAACCTGAGGTGAGAAAGTTCCCGTGAGACACC 3644  
Qy 3824 CGAGATTAATTCATGATGAATATCGAGCTGATTTGCTGCCCCCATTCGTATTAAGAAAT 3883  
Db 3645 TGAGGAATACTTG-----ATCGGAGCGCTGCTTTACAGAGGGTGCATCCAGCGGT 3698  
Qy 3884 TCCGATCTAGCCGCTGACGATGACTGCGCGTTCGCAAGATGGGCAATTTACGACT 3943  
Db 3699 CAATGCTGCGAAGTCAACATCGAGAGAGACTAGGCAAGTGTGTGATCTTGCGGA 3758  
Qy 3944 GAAAACTTTCAATTAATTAAGAAATTAATTTGAAACAGCTGTTACTATGATTTT 4003  
Db 3759 AACTGCTCTCTCAATGTGAGACAAATGGTTGAGACCTTCAATCATCTTCATGATTC 3818  
Qy 4004 AATGATGACTTAAGCTTTGAGATTAAGAGATGATGCGCAAAAGAACCATATGCA 4063  
Db 3819 GCTAGAGAGGGCGCGCCCTTGAGAGACATCTACATGAGACAGAGAAAGACATCG 3878  
Qy 4064 GGAATTTTAACTAATATGACAGAAATTTTACGGTTATTTCTTTGAAATGTTAT 4123  
Db 3879 CACATCTGAGAGATGAGGACAGAGTCTTCACTACATCTTCACTCGAGAGATGCT 3938  
Qy 4124 CAATGCTTGGCGCTCGGCTTCAAAAGTATCTTCAACAAAGCGTGTGTTGGCTGATTT 4183  
Db 3939 CAATGAGACAGCTTACGGCTTGTCAAGTCTTCAACCAATGCTGTGTGTTGAGTCT 3998  
Qy 4184 CGTATTTGATGATGATGCTTATCAACTTGTGTTCACTTGTGAGAGCTGTGTGAT 4243  
Db 3999 CCTATTTGTGCTGTCTTTAGTACGCTTATAGCTAATGCTCCGTGGGCTAATCGGAAT 4058  
Qy 4244 TCAAGCTTCAAGACTATGCAAGCTTAAAGACATGAGACCACTACGTCGATGTCGG 4303

Db 4059 AGTGGCAATTAAGTCCCTTAGGACCCCTAAGACTTTGAGACCCCTTAAGACCTTATCAG 4118  
Qy 4304 TATGAGGGCATGAGAGTGTGTGTTAATGCGCTGTGACAACTATACGTCATCTTCA 4363  
Db 4119 ATTTGAAGGATGAGGGGTGTGTGAATGCTGTGTGGGCCCATCCCTCATCATGAA 4178  
Qy 4364 TGTGCTATTTGCTGCTAAATTTTGGCTAAATTTTCCCTAATTTGGGTGACGCTTT 4423  
Db 4179 TGTGCTGTGTGTCTCATCTTCTGTGATTTTTCAGATCAATGGAAGTTAACCTGTT 4238  
Qy 4424 TGTGGAATAATTTTAAAGTCC---GAGACATGAATGCGAGAGCTCAGCCAGAT 4480  
Db 4239 TGCGGGGAATTAACACTACTCTTTAATGACATTTGAAATCGGTTTGAAATGAT 4298  
Qy 4481 CATACCAATGCAATGCTGCGAG-----AGCGAACTACAGCTG 4522  
Db 4299 TGTCAACAAATTAAGACGCTGTGAGAGCTGAGAGGCAACAGACGAGATCCGATG 4358  
Qy 4523 GGTGAATTCAGCATTTGATTTGATGATGATGATGATGATGATGATGATGATGATGAT 4582  
Db 4359 GAAATGTCAGATCACTTTGACAAATGTCGAGCAGAGGATACCTGCGCTTTCAGAT 4418  
Qy 4583 GGCACCTTCAAGGCTGATACAAATCATGATGAAGTCTATGATTCAGAGAGTGA 4642  
Db 4419 GCAACCTTCAAGGCTGATGACATCATGATGATGATGATGATGATGATGATGATGAT 4478  
Qy 4643 CAAGCAACCAATTCGTGAACGAACATCTACATGATTAATTTGATTTCTTCATCAT 4702  
Db 4479 CGACAGCTGATCAACGAGGCAACATCATGATTAATCACTTCGTCATCTTCATCAT 4538  
Qy 4703 ATTGATTCCTTTTCACTCATATGTTGATGATGATGATGATGATGATGATGATGAT 4762  
Db 4539 CTGCGCTCTTCTTCACTCATCTTCACTGATGATGATGATGATGATGATGATGATGAT 4598  
Qy 4763 GCAAAAGAAAAAGCAGGTGATCATTAAGATTTATGACAGAGTCAAGAAAAATGA 4822  
Db 4599 GCAAGAAAAA-----GTTGAGGTGACAGACATCTTATGACAGAGAAAGAAATGA 4655  
Qy 4823 CTATATGCTATGAAAAAGATGAGCTTAAAAAACAATTAAGACCATTCAGAACAG 4882  
Db 4656 CTACATGCTCAATGAAAAAGCTGAGCTCAAGAAACCAAGAGGCCATCCCGCACCTT 4715  
Qy 4883 GTGGCGACCAACACATATGCTTTGAAATGTAACGATAGAAATTCGATTAATCAT 4942  
Db 4716 GAACAAATCCAAAGGATGTCTTTGATTTGATCTCAACAGACCTTTGACATTTGAT 4775  
Qy 4943 TATGTTATTCATTTGCTGAACATGTTACCATGATGATGATGATGATGATGATGATGAT 5002  
Db 4776 CATGATGCTATCTGCTTAAACATGATGATGATGATGATGATGATGATGATGATGAT 4835  
Qy 5003 CACGATTAACGCGGTCTTAAGCTATCTAATGCAATGCGATTTGATTTTCACTTCCGA 5062  
Db 4836 GCAATGAGAAACATTTCTTAATGATTAATCTGCTTTGTCATCTTCACTGCGGA 4895  
Qy 5063 ATGCTATTAATAATTTGCTTTAAGATTAATCTAATTAATTTGAGCAATGAAATTAAT 5122  
Db 4896 GTGTGCTCAAAATGTTGCTTGAACACTATTAATTTCAATGAGCTGAAATCTT 4955  
Qy 5123 TGATGATGATTTGCTCAATTTTATTCATCTTAAGCTTTGATTTGAGCAATTTATCGAA 5182  
Db 4956 TGACTTTGTGTGTATCTCTTCAATTTGAGAAATTTCTGCTGATATTCATTTGAA 5015  
Qy 5183 GTAATTTGTGTGCGGACCTGCTCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5242  
Db 5016 GTACTTGTGTGCTCCCAACCTTATTCAGATTAATCGATTTGCGGTATTTGGGCACTT 5075  
Qy 5243 TCGAGGTGAAGGAGCCAAAGGCAATTCGAGCACTGCTCTGCGTGTGCGATGATGCT 5302  
Db 5076 GCGCTATCAAGGCGCCAAAGGATCGGACCTGCTCTTGGCTTTAATGATGTGCT 5135  
Qy 5303 GCGGCGCTGTTCAACATCTGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5362  
Db 5136 GCGGCGCTGTTCAACATGCGGCTCTGCTCTTCTGTCATGTCATCTTCTTCATTTT 5195

QY 5363 CGGATGTCGTTCTTCATGACGCTGAAGAGAGAGGCGATTACGACGTCACACTT 5422  
 DB 5196 TGGCATGTCGCAATTCGATCGATGAGACGAGGCGCGATTGACGATGTCACACTT 5255  
 QY 5423 CAAGACCTTTGCGCAGAGCATGATCTGCTCTTTCAAGATGTCAGCGTTCAGCGTTGGGA 5482  
 DB 5256 CGAGCATTTGGCAAGCATGATCTGTTGTTCCAGATCAACAAGCTGCTGGCGGGA 5315  
 QY 5483 TGGTGAATGAGACCCATTATCA-----TGAGAAAGCATGGATCCACCGACAG 5533  
 DB 5316 TGGCTGCTGCTGCTGCAATCTGAGACCGCCCTGAGCTGAGCAAGAGACCC 5375  
 QY 5534 CGAAGAGGCTATCCGGCAATGTTGGTTCAGCGACCGTTGAAATACGTTCTCTCTC 5593  
 DB 5376 AGGAGGCTTCAAGAGGGAATGTTGGAAACCCCTGGTGGGATCTTCTTTGTGAG 5435  
 QY 5594 ATACCTAGTTAAAGCTTTTGTAGTTAATGTAATGTAATGTCATGCTGCTCTTCAGAA 5653  
 DB 5436 CTACATCATCATCTCTCTCTGATGTTGTTGAACATGTAATGCAATGCAATCTCTGAGAA 5495  
 QY 5554 CTATATGACAGGCAAGAGACGTCGAAAGGGCTTAACGAGAGAGATACGATGTA 5713  
 DB 5496 CTTCAGGCTGCGCAAGAGAGAGCGCCGACCTCTGAGTGAAGATGATCTTCGAGACTT 5555  
 QY 5714 CTATGAGATCTGCGAGCAATTCGATCCGAGGGGACCCAGTACATACGCTATGATGACT 5773  
 DB 5556 CTATGAGATCTGCGAGCAATTCGATCCGAGGGGACCCAGTACATACGCTATGATGACT 5615  
 QY 5774 GTCCGAATTCCTGAGACTGATGAGCGCCCGCTGCAATCCAAACCGAAAGTAACA 5833  
 DB 5616 GGCAGACTTTGCGCAGCGCCCTGAGACCGCTCGAGTACCCAAAGCCAAACCATGCA 5675  
 QY 5834 GATCATATGATGAGCAATCCATCTGTCGCGGTGACCTATGATGCTGCTGCAATCT 5893  
 DB 5676 GCTATGCGCATGAGACTGCTGCGCATGTCGAGGAGATGCAATGCACTGTTGAGCATCT 5735  
 QY 5894 CGAGCGCTTTCAGAAAGCTTCTTTCGCGGAGAGGCAATCCGATGAGAGAGCGGTGA 5953  
 DB 5736 TTTGCGCTTTCAGAAAGCTTCTGCGGAGAGAGGAGAGTTGAGCATCTCTGCGGAGCA 5795  
 QY 5954 GATTGTGAG-----ATAGGCGCGCGCGGATACGAGGAGGCTACGAGCGCTCTATC 6007  
 DB 5796 GATGAGAGAGCGGTTCTGTCGATCAATCTTCCAAAGTGTCTTACGAGCTTATCAGAAC 5855  
 QY 6008 AACCTGTGCGGTGAGCGTGAAGTACTGCGCCCGGCTAATCCAGACGCTTGGCGAAA 6067  
 DB 5856 CACTCTGCGGCGCAAGCAGAGAGAGTGTCTGCAAGTGTCTCTGAGCGGCTTACAGGCG 5915  
 QY 6068 GCACAGAGCGCGCGCG 6084  
 DB 5916 ACACCTTGGCTAGGCGGG 5932  
 RESULT 12  
 ADS16302  
 ID ADS16302 standard; DNA; 6586 BP.  
 AC ADS16302;  
 DT 02-DEC-2004 (first entry)  
 DE Rat voltage-gated type 8 alpha protein (Scn8a) sodium channel DNA.  
 KW Voltage-dependent ion channel; drug candidate; epileps; arrhythmia;  
 KW aberrant electrical activity; muscle contraction; epilepsy; arrhythmia;  
 KW anticonvulsant; antiarrhythmic; rat; type 8 alpha protein; ds.  
 OS Rattus norvegicus.  
 XX  
 XX US200417561-A1.  
 XX  
 PD 09-SEP-2004.

PF 01-MAR-2003; 2003US-00377139.  
 PR 01-MAR-2003; 2003US-00377139.  
 PA (MACK/) MACKINNON R.  
 PA (MACK/) MACKINNON A L.  
 PA (JIAN/) JIANG Y.  
 PA (RUTA/) RUTA V.  
 PI Mackinnon R, Mackinnon AL, Jiang Y, Ruta V;  
 DR WPI: 2004-642122/62.  
 DR REFSQ; NM\_019266.  
 PT Screening drug candidates that target voltage dependent ion channel  
 PT protein, involves contacting screening protein with chemical compound,  
 PT which is drug candidate and determining whether chemical compound binds  
 PT to screening protein.  
 PS Disclosure; SEQ ID NO 14; 61pp; English.  
 CC The invention relates to the composition of matter suitable for use in  
 CC identifying chemical compounds that bind to voltage-dependent ion channel  
 CC proteins. The composition comprises a screening protein that consists of  
 CC an ion channel voltage sensor domain of the ion channel protein  
 CC immobilised on a solid support. The invention is useful for identifying  
 CC chemical compounds (drug candidate) that bind to voltage-dependent ion  
 CC channel proteins. The drug candidate of the invention is utilised for  
 CC treating a condition mediated by aberrant electrical activity that  
 CC initiates uptake or release of neurotransmitters and contraction of  
 CC muscles. The drug candidate of the invention is also utilised for  
 CC treating epilepsy and arrhythmia. The present sequence is a voltage-gated  
 CC sodium channel DNA.  
 SQ Sequence 6586 BP; 1632 A; 1732 C; 1745 G; 1475 T; 0 U; 2 Other;  
 Query Match 15.7%; Score 1019.4; DB 13; Length 6586;  
 Best Local Similarity 52.8%; Pred. No. 7.3e-245;  
 Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;  
 QY 186 CGGAGAAAAAACAAGAAATTCGATGATGACGAGAGAGAGTAAGTCCACAA 245  
 DB 268 CTCAGAAAACACCAAGCGAGTGGACACCGGAGAGAGATGAACAAGCAAGCCC 327  
 QY 246 CCGATCTCACTTAAGACGGGTGTGCCAATACCTGTTCGATTGAGGGGAGCTTCCG 305  
 DB 328 AACCAAAAGTGAAGCTGAGGCTGGAGAGTTGCTTATCAACGGGACATCCG 387  
 QY 306 CCGAATTTGGCTTCACTCTCTCGAGATATGATCCCTTACAGCAATGACTGACA 365  
 DB 388 CAAAGGCTGTGCGGTTCCCTGAGAGACTTTGACCTTATATTTGACGCAAAAACC 447  
 QY 366 TTGTAAGTTAAGCAAGAGAAAGATTTTGGCTTTTCGATCAAAAGCATGTGG 425  
 DB 448 TTTGTAATTAACAAGAGGAAACCTCTTGAATTAAGTCCACACCTGCTGTAC 507  
 QY 426 ATGCTGATCCATTCATCCGATACGTGTCGTCGCAATTAATTCATGATCAATTA 485  
 DB 508 ATTTTAAGCCCTTTTAACGATTAAGAAATGATTAATTAATTTGATACACTAGTT 567  
 QY 486 TTTTCCCTATTCATATCAACCAATTTCTGCACTGATCCTGATGATAAGCGGACA 545  
 DB 568 TTCAGCATGATCATCATGTCACACATCTGACCAACGTGTGTTCATGAGACTTAACTAC 627  
 QY 546 ACGCCACGGTTAGTCCAGTGGTGTG--ATATTCACCGGAATTCACATTTGAATCA 602  
 DB 628 CTTCAGAAATGTCGAAGATGAGATACATTCACAGGATTTACATTTGAATCA 687  
 QY 603 GCTGTAAAGTATGAGCAGAGGTTTCATTTTATGCCCGTTTACGATCTTAAGATGA 662  
 DB 688 CTATGAAATCATGCAAGAGGTTTCTGATAGAGCGCTTACACCTTCTGCGAGACCCG 747







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Qy 5003 CACGTATACCGGCTCTAGACTATCTCATGATGATATTCGATTTTTCAGTCCGA 5062
Db 4836 GCAATGAGAAACATTTCTTACTGATTAATCTGCTTTTGTACTCTTTCACCTGCGA 4895
Qy 5063 ATGTCTATTAATAATATTCGCTTAAAGATATCACTATTTTATGAGCAATGGAATTTAT 5122
Db 4896 GTGTGTCTCAAAATGTTGCTTGAGACACTACTATTTTACATTTGGCTGGAACATCTT 4955
Qy 5123 TGATGTACTAGTGTCTATTTATTCATCTTGTAGCTTTGTACTTACGATTTATGAGAA 5182
Db 4956 TGACTTTGTGTGTGCTCTCTCTCATTTGTGGAATGTTCTGCGCTGATTCATTAAGAA 5015
Qy 5183 GTACTTGTGTGCGGACCTGCTCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5242
Db 5016 GTACTTGTGTGCGGACCTGCTCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5075
Qy 5243 TCGACTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5302
Db 5076 GCGTCTGATCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5135
Qy 5303 GCGGCGCTGTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5362
Db 5136 GCGGCGCTGTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5195
Qy 5363 GCGGATGTGCTTTCATGCAAGTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5422
Db 5196 TGGCATGTCAACTTCGATACGTGAAGACAGAGGCGCGCATGACGATGATTCATTTA 5255
Qy 5423 CAGACCTTTGGCCAGACATGATCTGCTCTTTTCAGATGTCAGAGTCAGCGGTTGGGA 5482
Db 5256 CAGACATTTGGCCAGACATGATCTGCTCTTTTCAGATGTCAGAGTCAGCGGTTGGGA 5315
Qy 5483 TGGTGTACTGACCGCATTTCA-----TGAGAGAGTCGATTCACCCGACAG 5533
Db 5316 TGGCTGTGTGTGCAATCTGAAACCGCCCTGACTGACGCTTGACAAAGACACCC 5375
Qy 5534 CGACAAAGGCTATCGGCAATGTTGTTTCAAGCAGCGTGGGAATTAAGTTTCTCTC 5593
Db 5376 AGGAGTGTGCTTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5435
Qy 5594 ATACCTAGTTTAAAGCTTTTGTATGATTTATTAATGATATGCTGTCTATTTTCGAGA 5653
Db 5436 CTACATCATCATCTCTCTGATGTGTGTGAATGATCATCGCATCATCTCTGAGAA 5495
Qy 5654 CTATATGTCAGGCGACCGAGACGTGCAAGAGGCTTAAACGACGACGATCAACATGTA 5713
Db 5496 CTTCAGCGTGTGCGACCGAGAGAGGCGCGACCTCTGAGTGAAGATGACTTCGAGACTTT 5555
Qy 5714 CTATGAGTCTGGAGCAATTCGATTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5773
Db 5556 CTATGAGTCTGGAGCAATTCGATTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5615
Qy 5774 GTCCGAATTCCTGAGACGTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5833
Db 5616 GCGAGACTTTTCCGAGCGCTGAGAGACCGCTCCGATACCAAGCCCAACATGGA 5675
Qy 5834 GATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5893
Db 5676 GCTCATGCGCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5735
Qy 5894 CGAGCGCTTACGAAGACTTCTTTCGCGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5953
Db 5736 TTTTGCCTTCAAGAGGAGTCTGAGAGACAGTGGGAGTTTGAATCTTTCGCGAGCA 5795
Qy 5954 GATTGTGAG-----ATAGCGCGCGCGCGCGAGATACGAGGAGGATACGAGCGCTTCATC 6007
Db 5796 GATGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5855
Qy 6008 AACGCTGTGAGCTGAGCTGAGAGTACTGAGCGCGCTTATTCAGACGCGCTGGCGAAA 6067
Db 5856 CACTCTGTGGGCGAAGCAGAGAGGTGTCTGCAGTGTCTCTGAGCGTGTCTTACAGGG 5915
Qy 6068 GCACAAAGGCGCGCGCG 6084

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Db 5916 ACACCTTGGCTAGCGCGG 5932

RESULT 13
AAV58420
AAV58420 standard; cDNA; 5977 BP.
AAV58420;
01-DEC-1998 (first entry)
Tetrodotoxin-sensitive sodium channel PN4 coding sequence.
Tetrodotoxin-sensitive sodium channel; rat; PN4 sodium channel; stroke;
nervous system disorder; epilepsy; brain injury; diabetic neuropathy;
AIDS-associated neuropathy; therapy; ss.
Rattus sp.
Key Location/Qualifiers
CDS 22..5958
FT /tag= a
PN MO9838302-A2.
PD 03-SEP-1998.
PF 20-FEB-1998; 98MO-EP000997.
PR 26-FEB-1997; 97US-0039447P.
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
PI Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran L;
DR WPI; 1998-481204/41.
DX P-PSDB; AAM69361.
XX
XX New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNA - for
XX PT detecting inhibitors which alleviate pain, and treating nervous system
XX disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.
XX
XX Claim 2; Page 30-32; 87bp; English.
XX
XX This sequence represents the isolated rat PN4 sodium channel cDNA clone
XX of the invention. This sequence was isolated from a peripheral nerve from
XX a rat dorsal ganglia. The PN4 sodium channel sequences are tetrodotoxin-
XX sensitive sodium channels. The protein is used in assays for detecting
XX inhibitors of tetrodotoxin-sensitive sodium channels, which alleviate
XX pain. The probes can be used to detect and isolate the DNA or protein in
XX tissues. The antibodies can also be used to isolate the protein. The
XX protein is used as a therapeutic target for compounds to treat disorders
XX of the nervous system, such as epilepsy, stroke and brain injury,
XX diabetic neuropathy, and AIDS-associated neuropathy, etc
XX
SQ Sequence 5977 BP; 1478 A; 1554 C; 1600 G; 1345 T; 0 U; 0 Other;

Query Match 15.2%; Score 993; DB 2; Length 5977;
Best Local Similarity 52.4%; Pred. No. 3e-238;
Matches 3121; Conservative 0; Mismatches 2460; Indels 372; Gaps 28;

Qy 186 CGCAAGAAAAAAGAAAAAATCCGATGATGACGAGAGGAGTGCACAA 245
Db 121 CTCAGAAACACCAAGAGCGGATGCGACGCCGAGGAGGATGAAGACGACAGCC 180
Qy 246 CCGGATCTTACCTTGAAGAGGAGTGCCTTGTGATGTCGCGGAGCTCCG 305
Db 181 AAGCAAAACGTGACTGAGAGGCTGGAGAGGTTTGTCTTCACTACGAGGACATCCG 240
Qy 306 CCGGAATTTGGCTTCACTCTCTGAGAGATATCGATCCCTACTACAGCAATGTATGCA 365
Db 241 CAAGCGCTGTGGTGGCTTCCCTGAGAGACTTTGACCTTATCTTATGACGCAAAAAC 300

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QY 366 TTGAGTGTGTAAGCAAGAAAGAAATATTTTGGCTTTTCGATCAAAAGCAATGTG 425  
DB 301 TTGTGATTTAAAGAGAGAAACTCTCTTCAATTTAGTGCACACCTGGCTGTAC 360  
QY 426 ATGCTGATTCATCAATCCGATAGCTGCTGCGCAATTTACATTAGTGCATCATTA 485  
DB 361 ATTTTAAGCCCTTTTAACTGATTAAGAAAGATAGCTAATTAATTTTGAATACCTAGTT 420  
QY 486 TTTTCCCTTCAATCAACCAATTTCTGTCATCGATCTGATGATTAATGCCACA 545  
DB 421 TTGAGATGATCAATGTCACACTCTTCAACCACTGTGTCTTCACTGATTAATAC 480  
QY 546 ACCGCCACGGTTGATGCTCACTGAGGTG---ATAATCAACGAAATCTAACATTTGATCA 602  
DB 481 CTTCCAGAAATGTCAGAAAGATGTGAGTACACATTCACAGGAAATTAACATTTGATCA 540  
QY 603 GCTGTTAAATGATGCGACAGAGTTTCAATTTATGCCCGTTTACGATCTTAAGATGCA 662  
DB 541 CTAGTGAATAATCGACAGAGGTTTCTGATAGACGGCTTCACTTTTGCAGACCCG 600  
QY 663 TGGAAATGGCTGAGCTTGTAGTAATAGCTTTAGCTTATGACCAATGGGTATAGATTTA 722  
DB 601 TGGAACTGTTAACTTCACTTCACTGATCATGATGCAATGTGACAGAGTTTGTGACCTG 660  
QY 723 GGTAACTAGCAGCCCTGCGAAGCTTTAGGCTGTGAGCGCTTAAACCGTAGCCATT 782  
DB 661 GGCATGTCTCAGGCTGAGAAACATTCAGGGTTCTCCGAGCTTTGAATACTCTGTGA 720  
QY 783 GTGCCAGGCTTGAAGACCATGTGTGCGCGCTCATGCAATCGGTAAGAAATCTGCCGAT 842  
DB 721 ATTCAGAGCCGTAAGCAATGTGTGCGCCCTTAATCCAGTCCGTAAGAAAGCTGTCCGAC 780  
QY 843 GTGATTAATCTGACCATGTTCTCCCTGTGCGTGTTCGCGTGAATGGGCTTACAGATTAAT 902  
DB 781 GTGATGATCTGACAGAGTGTCTGCTGAGGTTTTCGCCCTGAATGGCTGACAGCTTTC 840  
QY 903 ATGGGCGTGTCTCAGCAAGAGTGCAT-----CAAGAACTTCCGCTGAGCGTTCC 953  
DB 841 ATGGGGAACCTTCCAAACCAAGTGTGTGTGTGCGCCCAATTAACCTTCAACGAGAGTACTG 900  
QY 954 TGGGGCAATCTGACCGACGAGAACTGGAACTATCAATCGCAATGCTCAATTTGGTAT 1013  
DB 901 GAGGAACGACCAAGGCTTTGACTGGAAGAAATTAATCAACATTAATAACAACTTTTAC 960  
QY 1014 TCCGAGACGAGGCACTCTATTTCCGTTATCGGCAATATATCCGCTGTGCGGGCAATGC 1073  
DB 961 ATGTTCTGTGCACTGATGAACCTTGTCTGCGGGAACAGTTCTGATGTGCGGCAATGC 1020  
QY 1074 GACGACGATTAAGTGTGCTGCGAGGGGTTGTGTCGGAATCCGAAATTAATGCTAACACAGC 1133  
DB 1021 CCAAGGGAATTCAGATGATGAAG---CAAGAAAGAAACCCCACTAGGTTTAAACACAGC 1077  
QY 1134 TTGATTCGTTCCGATGGGCTTTCTGTCCGCTTCCGGCTGATGACACAGACCTTCTGG 1193  
DB 1078 TTTAACACTTCACTGAGGCTTTCTTGTGCAATTAATTCGCTTAATGACCCAGAGACTATTTGG 1137  
QY 1194 GAGGATCTGTAACAGCTGTGTGTGCGCGCCGCGAACCATGGAACATGCTGTCTTTATA 1253  
DB 1138 GAGAACTTAATACAGCTGACCTTAAGAGCCGCTGGGAAACGTAATGATCTTCTTTGTGC 1197  
QY 1254 GTCAATCATCTTCTTAAGTTCAATTTCTTGTGAATTTGATTTTGGCATGTTGGCATG 1313  
DB 1198 TTGGTCATCTTCTGTGGGTTCTTTCTATCTGTGAACCTTGAATCTTGGCTGTGTGCGCATG 1257  
QY 1314 TCGATGACGAATTGCAAGAGGCGCGAAGAAAGAGGCTGCGCAAGAGAGGCGCATTA 1373  
DB 1258 GCTTAATGAGAA---CAGAACACAGCAACCTGAGAGGCGCAGAGCAAAAGAGGCG---- 1310  
QY 1374 CGTGAAGGGAAGAGGCTGCGCGCCGCAAGCGCGCAAGCTGAGAGAGCGGGCCCAATGCG 1433  
DB 1311 CGAGTTCAAGGCAATGTGAGCAACTCAAG-----AAGCAGACGAGAGAGGCGACAGGCT 1365

QY 1434 CAGGCTCAGCAGCAGCGGATGCGGCTGCGCCGCAAGAGGCTGCATCTCGGAATG 1493  
DB 1366 GCTGCAATGGCCACTCAGCGGCACTGTCTGGAAGA---CGCATTTGAAGAAAGAGG 1422  
QY 1494 GCCAAGATCCGACGTAATCTTGTGACATAGCAATGAGCTAATTTGTGGCGGCAAGAGGC 1553  
DB 1423 GAAGATGGGATGAGGCTCTCCAGGAGGCTCTTCTGAACGTCTAACTCAGTTCCAAAGAGC 1482  
QY 1554 AAGATGACACACAAAGAGAAAGATGTCTATTCCGAGCGTGCAGAGTGAAGTCCGAGTGC 1613  
DB 1483 GCGAAGAGCGCGGAA-----CCGACGGAAGAAAGAGAGCAAGAGGA 1526  
QY 1614 GTGAGGTTAATCAAGAACCAACAGACCTTACACAGCAACCAAGTACCAAAAGTGGT 1673  
DB 1527 GCTCTGGAAGCGAGAGAAAGGGAACCCGGAAGAGGTTTAA-----GT 1573  
QY 1674 AAAGTGAACACACATCTTTATCTTACCTGTGACCGTTTAACTAACATACAGAGGATCA 1733  
DB 1574 CAGAGTCGGAAGACGGTATGAGAGAAAGGCTTCCGGCTGCAGACAAACAGATAGGGA 1633  
QY 1734 CCGTATCTCAACAGTACAGATAGGAAACGACGTGCGCGCTTGTGATTAACCGGTAGC 1793  
DB 1634 GGAAGTTTTCATCAATGAATCAGTGTGCTGACGATTCAGAGCTGCGCTTCTCTCC 1693  
QY 1794 GATCGTAACCAATGGTATTTGTCAACATATCAGATGCCCCAGACACTTGCCTATGCG 1853  
DB 1694 GACATTAACGAAAGACAGATCTTACGTTCCGGGAGCCG-GTGCGTTCCGGGACCCG 1752  
QY 1854 GACGACTCGAATGCCGTACCCCGATGTCCGAAGAAATGGGCGCATCATGTGCCCGTG 1913  
DB 1753 GGCTCGAAGATG-----AGTTCCGACAGATGAACACAGCAACCGTGAAGAG 1800  
QY 1914 TACTATGGAACATCTAGGCTCCCGACACATCATGTAATCTCGCATCAGTCCGAAATATG 1973  
DB 1801 AGGAGAGGCGGCGTATCTGCTTTATCTTATCCGATCCGCGCCCGAGCGCGGACAGAC 1860  
QY 1974 TATACCTCAATGCGCATCTACTCTGCGGCAATGCGCGTCAATGAGCCATATGACC 2033  
DB 1861 TACAGTGGCTACAGCGGCTACAGCCAGTCAAGCGCTGCTGCGGATCTTCCACAGCTG 1920  
QY 2034 AAGAGACCAATTTGGCGAACCGCAACACAGCAATCAATCACTAGTGGCGCCACCAATGGC 2093  
DB 1921 CGCGCAGCGTGAAGGCGAA-----CAGCAGGTTG 1950  
QY 2094 GGCACACCTGTGAGACCAATCAACAGCTCATCTGCGCATACGAAATTTGCGCTG 2153  
DB 1951 GACTGCAACGCGTATGTAATCTATCATCTGCGGCCGCTCACATCTCGGGGCGCTCGCT 2010  
QY 2154 GAGTGAACGACGAACTGTGCAAGATTAACATCATGACATCTTTTATCGAGCCGTC 2213  
DB 2011 GAGGCAACGACTGAGGGAATTAAGAAAGGCCCTGGAATCTCTTTAATGTTTCTATG 2070  
QY 2214 CAGACCAAAAGGTGTTGATTAAGAAAGATGTGATGCTGTGAATGACATCTCAACAG 2273  
DB 2071 GACCAACTCGCTCTCAACGACGGAAGGA-----CAGATCAACAGCATTAATGAG 2120  
QY 2274 GCGCGTGTGGAACAGTGGGCAAGGATCGCGTGTCTCCGTTTACTATTTCCAAACA 2333  
DB 2121 CGTGTCAACAAACGCTATGAAAGCTGGAAGAGTCTCAAGAA----- 2167  
QY 2334 GAGGACGATGACGAGATGGGCGGACGTTCAAGAACAAAGCACTCGAAGTATCTCAAA 2393  
DB 2168 -----AGTCCCAACGCTGTGATTAAGTTTCCCAACACTTCTCA-- 2209  
QY 2394 GGCATCATGTGTTTGTGTGTGTGAGACTGTGCTGGTTTGTGTAATTTGAGAGTGG 2453  
DB 2210 -----TCTGGAGTGTACCCCTTACGTAATTAACCTGAAGAGATC 2250  
QY 2454 GATATGCTCATGCTTCAATCTTCTGATGAGACTCTTCACTCAACGCTGTGCTATTTGCTC 2513  
DB 2251 GTGAATCTTAATCTGATGAGACCTTTTGTGATGACTTACCATCACTGATCGTTCTG 2310  
QY 2514 AACAGATGTTTCAATGGAATGATCAACAGATTAAGAAAGAGATGGAACCGGTGCTC 2573

[illegible]

Db	3262	CACA-----TGTCTTATTAACAAC-----CMAACTGACCTTCGGGT	3302
Oy	3648	AGCCATAAGATTCACATTCAGGACGACGACCAAGGGCAGCGCCGACGATGGAG	3707
Db	3303	GCCATTGCTGTGGCGAGTCT-----GACTTCGAAACCTTCACACAGAGATGTTAGC	3357
Oy	3708	GGCGAGGAAGCCGACGACCGACGAGGAGATTAGTCTTCGACGAGAACTGACGAG	3767
Db	3358	AGCGAATCAGACCTCGAAGGACGAGAAAGATA-----ACTGACGATACCAAGCTCTCA	3411
Oy	3768	GAGGGCGAATCGAGGAGGGCCGCTGACGGGTATATCATTTATGACACAGAGAG	3827
Db	3412	GAGGAAGTACCATCGACATCAATCAAGCTGAGGTGAAGAAGTTCCCGTGAGCAACTGAG	3471
Oy	3828	GATATATCTCGATGAAATATCCAGCTGATTCGCGCCCGATTTGTACTATTAAGAAATTTCCG	3887
Db	3472	GAAATCTTGG-----ATCCGAGCGCCTGCTTTACAGAGGGTTCCGTCAGCGGTTCAAG	3525
Oy	3888	ATCTTAGCCGGTACGATGACTCGCCGCTTCGGCAAGAGTGGGCAATTTACGACTGAA	3947
Db	3526	TGTCGCCAGCTCAACATCGAAGAAAGACTAGGCAAGTGTGTGATCTTCGGAAAAAC	3585
Oy	3948	ACTTTCAATTAATTGAAAAATTAATTTTGAACAGCTGTATATCAATATTTATATG	4007
Db	3586	TGCTTCTCATATGAGGACCAAAATGGTTGTAGACCTTCATCATCTTCATATTTCTGTC	3645
Oy	4008	AGTACTTAGCTTTGGCAATTGAGAGATGACATCTGCCACAAAGACCATCTAGAGAT	4067
Db	3646	AGCAGTGGCGCCCTGGCTTTGAGACATCTACATTGACGAGAGAAAGACATCCGACC	3705
Oy	4068	ATTTTATATATATGACAGAAATTTTACGGTTATATTTCTTCTTGAATTTATATCAG	4127
Db	3706	ATCTCGAGTATGGGACCAAGGCTTTCACATCATCTTCACTCGAGAGATGTCTCAG	3765
Oy	4128	TGTTTGGCGCTCGGCTTCAAGGTACTTACCAACGGGTGTGTGGCTCGATTTGCTG	4187
Db	3766	TGGACAGCTTACGGGCTTCGTCACAAATTTCTTCACAATGCTGTGTGTTGGACTTCTCTC	3825
Oy	4188	ATTGTGATGATAGGCTTATCAACTTGGTGCTTCACTGTGTGAGCGGTGTGATTTCAA	4247
Db	3826	ATTGTGCTGTCTTTTAGTAGCTTATACCTAATGCTCCTGGGCTACTCGGAATAGGT	3885
Oy	4248	GCCTTCAAGACTATGCAACGTTAAGACACTGAGACCACTACGTGCATGTCCCGTATG	4307
Db	3886	GCCATTAAGTCCCTTAGGACCCCTAAGAGCTTTGAGACCCCTTAAGAGCTTATGACGATTT	3945
Oy	4308	CAGGGCATGAGGGTGTCTGTTAATGCGGTGTACAGACTATACGTCATTTCAATGTG	4367
Db	3946	GAAAGGATGAGGGGTGTGTGAATGCTGTGTGGCCCATCCCTCCATCATGAAATGTG	4005
Oy	4368	CTATTGGTGTCTAATATTTTGGCTAATTTTGGCCATATAGGGTGTACAGCTTTTGTCT	4427
Db	4006	CTGCTGGTGTCTCATCTTCTGTGCTAATTTTACGACATCAAGGAGTTAACTGTGTGCG	4065
Oy	4428	GAAAAATATTTTAAGTGC---GAGGACATGAAATGGCAGAACTCAGACGAGATGATA	4484
Db	4066	GGGAAATACCACTACTGCTTTAATGAGACTTTGAAATCCGGTTCGAAATGATATGTCTC	4125
Oy	4485	CCAAATGCAATGCTCGAG-----AGCGAATCTACCTGTGGGT	4526
Db	4126	AACATATAAACGAGCTGTGAGAGCTCATGAGGGCAACAGCAGGAGATCCGATGGAAG	4185
Oy	4527	AATTTCAGAAATGATTTTCGATCAGTGAATGATACGCGGATCTGTGCCCTTTTCAAATGGCC	4586
Db	4186	AATGTCAAGATCAACTTTGACAAATGTGAGACAGGGTACCTGGCCCTTTTCAAGTGGCA	4245
Oy	4587	ACCTTCAAAGGCTGATATCAAAATCATGATGAAGTCTATTCATTTCAAGAGGTGAGCAAG	4646
Db	4246	ACCTTCAAAGGCTGATGAGCATATATATGCGGCTTAAATTTCCGAAGCCAGACGAG	4305
Oy	4647	CAACCAATTTGTGAAGCAACATCTACATATTTATTTATTTTGGTATTTCTTCATCATATTT	4706
Db	4306	CAGCTTACTACGAGGGCAACATCTACATCTACATCTACTCTTCATCTTCATCTTCTC	4365

QY	4707	GGATCCCTTTTTCACACTGCATCTCGTTCATTGGGGTATCATATGATTAATTTTATATGACAA	4766
Db	4366	GGCTCCTTCTTTCACCCCTCAACCTGGTTCATCGGGTCACTATCGACAACTTCAACCGACGAG	4425
QY	4767	AAGAAAAAACAGAGTGATCATTTAAGAAATTTTCATGACAGAAATCAGAAAAATATCTAT	4826
Db	4426	AAGAAAAA-----GTTTGAAGGTCAAGACATCTTCATGACAGAGAAACAGAAAGATCTAC	4482
QY	4827	AATGCTATGAAAAAGATGGGCTCTTAAAAAACATTAAGCCATTCCAGACCAAGTGG	4886
Db	4483	AATGCCATGAAAAAGCTGGGGCTCCAGAAAGCCACAGAAAGCCATCCCCGACCTTGAAC	4542
QY	4887	CGACCAACAGCAATAGTCTTTGAAAATAGTAAACGATTAAGAAATTCGATATATCATATG	4946
Db	4434	AAAATCCAGAGGATTTGCTTTGATTTTGTCACTCAACAACCTTTGACATTTGATCATG	4602
QY	4947	TTATTCATTTGGCTGGAACATGTTCAACATGACCTCGATCGTTACATGATGCTGGACAG	5006
Db	4603	ATGCTCATCTGCTTAAACATGATGACATATGATGAGACAGACCTCAGAACAGACAG	4662
QY	5007	TATTAACGGGCTCAGACCTATCTGAATGCGCATTCGTAGTATTTTCAGTCCGAATG	5066
Db	4663	ATGGAAGACATCTTTTACTGGATTAATCTGTTCTTTGTCACTTTCTTCACTCGAGTGT	4722
QY	5067	CTATTTAAAAATATTCGCTTTTACGATATCACTATTTTATGACCATGAAATTTATTTGAT	5126
Db	4723	GTGCTCAAAATAGTTTGGCTTGAGACACTATATTTCACCATTTGGCTGAAACATCTTTGAC	4782
QY	5127	GTAATAGTGTTCATTTTATTCATCTTATGATCTTGTACCTTACCGATATTTATCGAAGATAC	5186
Db	4783	TTTGTGGTGTCACTCTCTCCATTTGTGGAAATGTTCTCGGCTGATATATTAAGAAATAC	4842
QY	5187	TTCTGATGCGACCCCTGCTCCGATGGTGTGCGTGGCGAAAGTGGGCGGTGCTCTTGA	5246
Db	4843	TTCTGCTCTCCCAACCTTATTCGAGTTATTCGATTTGGCCGGTATTTGGCCGATCTTGCT	4902
QY	5247	CTGTGAAGGAGGCCAAGGCAATTCGACACTGCTCTTCGCGTTGGCCATGTGCGTCCG	5306
Db	4903	CTGATCAAGGGCGGCCAAGAGGATTCGACACCTGCTCTTTGCTTAATGATGTGCTGCTCC	4962
QY	5307	GCCCGTTTCACATATGCTGCTGCTGTGTTCTCTGGATCATGTCATCTTTGACATTTTGGC	5366
Db	4963	GCCCTTTTCACATATGCTGCTGCTGCTCTCTCTCTCGTCAATGTCATCTTCCATTTTGGC	5022
QY	5367	ATGTGCTTCTTCAGCAGCTGAAGAGAAAGCGGCATTAACGACGTCTAACACTTCAAG	5426
Db	5023	ATGTCCAACTTCGCACTACGTGAAGACAGAGCGCGCATTTGACACATGTTCAACTTGAAG	5082
QY	5427	ACCTTTGGCGAGGATATCTGCTCTTTAGATGTGAGCGTACGCGGTTGGGATGTG	5486
Db	5083	ACATTTGGCACAGATGATCTGTTGTTTTCAGATCAACAATGCTGCTGGGCTGGGAATGGC	5142
QY	5487	GTACTGACGCGCATTTATCA-----TGAAGAGCATGCGATCAACCCGACAGCGAC	5537
Db	5143	CTGCTGCTGCGCAATCTGTGAACGCGCCCTGACTGCACTTGTGACAAAGACACCCAGGG	5202
QY	5538	AAAGGCTATCCGGGCAATTTGTGTCAAGGACCGCTTGAATAATGTTTCTCCTCTCATAC	5597
Db	5203	AGTGGCTTCMAAGGGGACGTGTGGAACCCCTCGTGGGGATCTTCTTCTTTGTGAGCTAC	5262
QY	5598	CTAGTTATTAAGCTTTTGTATGTATTAATATGATCATTTGCTGTCACTTCGAGAACTAT	5657
Db	5263	ATCATCATCTCTTCTCTGATTTGTGTGAACATGTCATATCGGCATCATCTCGAGAACTTC	5322
QY	5658	AGTCAGGCCACCGAGGACGTGCAAGAGGCTCTAACCGACAGCAGCTACGACATGTACTAT	5717
Db	5323	ACGCTGGCCACCGAGGAGAGCCCGACCTCTGAATGTGAGATGACCTTGAAGCTTCTAT	5382
QY	5718	GAGATCTGGCAGCAANTTGATCCGAGGGGCAACCGATACATACGCTATGATCAGCTGCC	5777
Db	5383	GAGATCTGGAGAAAGTTTACCAACGACCGCACCTCAAGTTTATGAGATCTGTAAAGCTGGCA	5442

QY	5778	GAATTTCCTGGACCGTACCTGGAGGCCCGCCCTCGACATCCACAACCGAACCAGTCCAGATC	5815
Db	5443	GACTTTGGCCACGGCCCTGGAGNACCCGCTCCGAGTACCAGGCCCAACCATCATGAGCTC	5502
QY	5838	ATTATCGATTGGACATACCCCATCTGTGCGCGGTGACCTCATGTATACCCGCTTCGACATCTCGAC	5897
Db	5503	ATGCCCATATGGACCTGGCCCATATGGTAGAGGAGAGATGCATCCATCTGTCGACATCTTTTC	5562
QY	5898	GCCCTTACGAAAGACTCTTTGCGCGGAGGAGCGCAATCCGATTAGAGAGACGGGTGAGATT	5957
Db	5563	GCTTTTCCAAAGCCAGATCTCTGGAGAGACATGGGGAGTTTGGACATCTGCGGCAAGCAATG	5622
QY	5958	GCTGAG-----AATGAGGCGCCCGCCCGGATATCGAGAGGGCTACAGAGCCCGTCTCATCAAG	6011
Db	5623	GAGAGCGCGTTTCGTGGCAATCCATCTTCCAAAGTGTCTTACGAGCCTATTCACAAACCACT	5682
QY	6012	CTGTGCGCTCAAGCGTGTAGAGAGTACTGCGCCCGGCTAAATCCAGCAAGCCTTGCGCAAAAGC	6071
Db	5683	CTGCGGGCCCAAGCAGAGAGAGATGTCTGCAAGTGTCTCTCGACGCGTGCTTACAGGGAGACAC	5742
QY	6072	AAGGCGCGCGGCGG	6084
Db	5743	TTGGCTAGCGCGG	5755

XX	AAV58419	standard; cDNA; 6556 BP.
XX	AAV58419;	
XX	01-DEC-1998	(first entry)
XX	PM4 sodium channel clone.	
XX	Tetrodotoxin-sensitive sodium channel; rat; PM4 sodium channel; stroke;	
XX	neurov system disorder; epilepsy; brain injury; diabetic neuropathy;	
XX	AIDS-associated neuropathy; therapy; ss.	
XX	Rattus sp.	
XX	W09838302-A2.	
XX	03-SEP-1998.	
XX	20-FEB-1998;	98WO-EP000097.
XX	26-FEB-1997;	97US-0039447P.
XX	(HOFF ) HOFFMANN LA ROCHE & CO AG F.	
XX	Delgado SG, Dietrich PS, Fish LM, Herman RC, Sangameswaran L;	
XX	WPI; 1998-481204/41.	
XX	New rat tetrodotoxin-sensitive sodium channel alpha subunit and DNA - for	
XX	detecting inhibitors which alleviate pain, and treating nervous system	
XX	disorders, e.g. epilepsy, stroke, diabetic and AIDS neuropathy.	
XX	Claim 1; Page 54-58; 87pp; English.	
XX	This sequence represents the isolated rat PM4 sodium channel cDNA clone	
XX	of the invention. This sequence was isolated from a peripheral nerve from	
XX	a rat dorsal ganglia. The PM4 sodium channel sequences are tetrodotoxin-	
XX	sensitive sodium channels. The protein is used in assays for detecting	
XX	inhibitors of tetrodotoxin-sensitive sodium channels, which alleviate	
XX	pain. The probes can be used to detect and isolate the DNA or protein in	
XX	tissues. The antibodies can also be used to isolate the protein. The	
XX	protein is used as a therapeutic target for compounds to treat disorders	
XX	of the nervous system, such as epilepsy, stroke and brain injury,	
XX	diabetic neuropathy, and AIDS-associated neuropathy, etc	
XX	Sequence 6556 BP; 1620 A; 1727 C; 1736 G; 1471 T; 0 U; 2 Other;	

Query Match 15.2%; Score 993; DB 2; Length 6556;  
 Best Local Similarity 52.4%; Pred. No. 3.2e-238;  
 Matches 3121; Conservative 0; Mismatches 2460; Indels 372; Gaps 28;

186 CGCAGAGAAAAACAAGAAATCCGATATGATGACGAGACGAGATGAAAGTCCACA 245  
 268 CTCAGAGAACCAACCAAGCCGATGCGACCCGAGGAGAGATGAGACGAGAGCC 327  
 246 CCGATCTTACATTGAAACAGGATGCGCAATACCTGTCATGACGAGGACGTTCCG 305  
 328 AAGCCAAACAGTACCTGAGGCTGGAAAGATTGCTTTCATCTACGAGGACATCCG 387  
 306 CCGAATGGGCTCCTCCTCTCGAGATATGATCCCTACTACAGCATCTAGCA 365  
 388 CAGAGCTGGTGGCGGTTCCCTGGAGACTTTCACCTTACTATTGACGAGAAAAAC 447  
 366 TTCGATGTTGTAAGCAAGAAAGATATTTTCGCTTTTCTGCAATCAAAAGCAATG 425  
 448 TTTGATGATTAACAGAGGAGAACTCTTTCAGATTAGTCCACACCTGCTTAC 507  
 426 ATGCTGCATTCATTCATCCGATACGTCGTGTCGCAATTAATCTAGTGCATTA 485  
 508 ATTTTAAGCCCTTTTAACCTGATTAAGAAATAGCTATTAATTTGATACATCAG 567  
 486 TTTTCCCATTCATCATCAACAAATTCCTGCACTGCACTGATGATATGCGACA 545  
 568 TTCAGCATGATCATATGTGACCACTCTGACCAATGTTGTTATATACCTTTAGTAC 627  
 546 ACGCCACGTTGATGACATGAGGTG---ATATTCACCGGATATACATTTGATCA 602  
 628 CTTCCAGATATGTCACAAATATGAGATACATTCACAGGATTTACACATTTGATCA 687  
 603 GCTTTAAAGTATGACGACGAGTTTCAATTTATGCCGTTTACGTAATCTTAGAGATCA 662  
 688 CTATGAAATCATGCAAGAGTTTTCATAGACGAGCTTCACTTCGAGAGACCG 747  
 663 TGGAAATGGCGGACTTGTATGTAATACCTTATGTTATGACATAGGATATGATTTA 722  
 748 TGGAACTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 807  
 723 GGTATCTAGACGCTCTGCAAGCTTTAGGGTGTGCGAGCGCTTAAACGATGACAT 782  
 808 GGCATATGTCAGCGCTGAGAACATTCAGGGTCTCCGAGCTTTGAAAATCTATCTGTA 867  
 783 GTGCGAGCTTGAAGACCATGTCGCGCGCTGATCGATCGATGAGAAATCTGCGCAT 842  
 868 ATTCAAGGCTGAGAGACATGTCGGGCGCTTAATCCAGTCGATGAGAGCTGTGAGC 927  
 843 GTGATTAATCTGACCATGTTCTCTGTCGATGTTGCGGTTGATGAGGCTTACATCTAT 902  
 928 GTGATGATCTGACAGTGTGCTGCTGATGATGATGATGATGATGATGATGATGATG 987  
 903 ATGGGCGTGTCAACCGAAGTGCAT-----CAGAAGTTCCGCTGAGCGGTTCC 953  
 988 ATGGGGAACCTTGCAGAACAGTGTGTGTGTGCGCCATTAACCTTCAAGAGAGCTACTG 1047  
 954 TGGGCAATCTGACCGACGAGAACTGAGATATCACAATCGCAATAGCTCAATTTGAT 1013  
 1048 GAGAAACGACACAAAGGCTTGAACCTGGAGAAATATATCAACAATAAAACATTTTAC 1107  
 1014 TCCGAGAGAGAGGACATCTATTTCCGTTATGCGGCAATATATCCGTCGCGGCAATGC 1073  
 1108 ATGATTCCTGACATGTAAGACCTTGTCTGTGCGGAAACAGTTCTGATGTGGGAAATGC 1167  
 1074 GACGACATTAACGTCGTCGTCAGAGGATTTGTCGATCCGAATCGAATTAATGCTACACGC 1133  
 1168 CCAAGGATTCAGATGATGAAG---CAGAGAGAAACCCCACTACGCTTACACACGC 1224  
 1134 TTGATGCTTGGAGATGGGCTTTCTGTGCGCTTCTGCGCTGATGACACAGACTTCTGG 1193  
 1225 TTGACACCTTCACTGGGCTTCTGTGCTGATTAATTCGCTTATGACCCAGAGACTATGG 1284

1194 GAGATCTGTACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1253  
 1285 GAGAACTTATACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1344  
 1254 GTCAATCATCTTCTAAGTTCAATCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1313  
 1345 TTGTGATCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1404  
 1314 TGTATGCAATGTCAGAAAGAGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1373  
 1405 GCTTATGAGAA---CAGAACAGGCAACTGAGAGAGAGAGAGAGAGAGAGAGAGAG 1457  
 1374 GGTGAAGGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1433  
 1458 CGAGTTCAAGCAATGCTGAGCAACTCAG---AAGCAGAGAGAGAGAGAGAGAGAG 1512  
 1434 CAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1493  
 1513 GCTGCAATGAGCACTGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1569  
 1494 GCCAAGCTCCAGGATTTCTGATCAGCTATGAGCTATTTGTTGGCGGAGAGAGAG 1553  
 1570 GAAAGTGGGTAGGCTCTCCAGAGAGCTTCTGAACTGTCTAACTCAGTTCCAGAGC 1629  
 1554 AACATGACACACAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1613  
 1630 GCGAAGAGCGGCGGAA-----CGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1673  
 1614 GTGAGCTTATTAACAAGACACAGACCTTACACAGACACCAAGCTAACCAAGTTGCT 1673  
 1674 GCTCTGAAAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1720  
 1674 AAAGTGAACGACATCTTATCTTACCTGTTTCACTGTTTCACTGTTTCACTGTT 1733  
 1721 CAGAGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1780  
 1734 GGTATTTCTCAAGTACAGATACAGATACAGAGAGAGAGAGAGAGAGAGAGAGAG 1793  
 1781 GGAAGTTTTCATCATGATCATGATGATGATGATGATGATGATGATGATGATGATG 1840  
 1794 GATGTAAGCCATTTGATTTGTCAACATATGAGATGAGAGAGAGAGAGAGAGAGAG 1853  
 1841 GACATTAACAGAAAGACAGATCTTACAGCTTCCGAGAGAGAGAGAGAGAGAGAG 1899  
 1854 GACGATCGAATGCGCTACCCGAGATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913  
 1900 GGTCTGAGAAATG-----AGTTGCAAGACATGAAACAGACAGCTGAGAGAG 1947  
 1914 TACTATGAGCAATTAAGCTCCGACATCTGATGATGATGATGATGATGATGATGATG 1973  
 1948 AGCAGAGGCGGCTGTGATGCTCTTCAATCCGATCCGAGCGCGCGAGCGCGAGCAG 2007  
 1974 TATACCTCAACATGAGCAATCTACTCGGCGGCAATGAGCGGCTGATGAGCAATGACC 2033  
 2008 TACAGTGGCTACAGCGCTACAGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067  
 2034 AAGGAGAGCAAAATTTGCCCAACCGCAACACGCAATCAATCAATGAGGCGCCACCAATG 2093  
 2068 CCGGCGAGCGTGAAGCGCAA-----CAGCAGCGTG 2097  
 2094 GGCACACCTGTGTGAGACCAATCAAGAGCTGATGATGAGAGAGAGAGAGAGAGAGAG 2153  
 2098 GATGCAACGCGGATGATGATCTCATGAGGCGCGGCTACACATCGGCGGCTCTGCT 2157  
 2154 GATGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2213  
 2158 GAGGCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2217  
 2214 CAGACACAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2273  
 2218 GACCAACTGCTCTCTCAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2267  
 2274 GCGGCTGTGTGAGACATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2333

2268 CGTGTGACAAACACCGCTAGTGGAGAGCTGGAAAGTCTCAGAGAA----- 2314  
QY 2334 GAGAGCAGATGACGAGATGGGCGGACGTTCAAAAGAACAGGCACTCGAAGTATCTCATA 2393  
Db 2315 -----AGTCCCAACCGTGTGGTAAAGTTTGGCCAAACCTTCTCA-- 2356  
QY 2394 GGCATGATGTGTTTTGTGTGGGACTGTGCTGGGGTGTGTTGAATTTCCAGAGTGG 2453  
Db 2357 -----TCTGGAGTGTCAACCCCTAAGTAAACCTGAAAGGAGATC 2397  
QY 2454 GATACGCTACGTCTTCGATCCCTTGTGTGAGCTCTTCATCAACGCTGTGATTTGGTTC 2513  
Db 2398 GTGAACCTTAATCGTCAATGACCCCTTTTGTAGCTTGAACATCAACATCGCATGTCTTG 2457  
QY 2514 AACACAGTGTTCATGGCAATGGATGATCAACGATATGAAACAAAGAGATGAAACGCTGTCTC 2573  
Db 2458 AATACGCTAATTTATGGCAATGAGACACATCCATGACACACAGTTCCAAACGCTTGG 2517  
QY 2574 AAGATGGCAACTATTTCTTCAACCGCAACCTTGGCCATCGAGGCCAATGAAGCTPAATG 2633  
Db 2518 GCGGTAGGAATCGGTGTTCACCGGATCTTCAACGGCGGAAATGTTTCTGAAGCTCATG 2577  
QY 2634 GCCATGAGCCCCAGTACTATTTTCCAGAGAGGCTGGAAACATCTTCACATTCATTCGTG 2693  
Db 2578 GCCATGAGCCCCACTACTATTTATTTCCAAAGAGGCTGGAAACATTTTGAAGATTTATGTC 2637  
QY 2694 GCCCATATCGCATTTGAACTGGGACTCGAGGGGTGTCCAGGGGTGTGTCCTGATTCGCTTC 2753  
Db 2638 TCCCTCAGTTTATGAGCTGATGCTGTGCAATGTGAGAGGGGCTCTCAGTGTGCGGTCT 2697  
QY 2754 TTTGATTTGCTGCGTGTATTTCAAACTGGCAAGCTTGGCCCACTTAATTTACTATTC 2813  
Db 2698 TTCCGATGCTCCGAGCTTCAAGCTGGCAAGCTGCGCCCAACCTGGAACATGTCTGATC 2757  
QY 2814 TCGATTTATGGAGCGCACCATGAGGCGCTTGGGTATCTGAATTTGACTTTGATATATC 2873  
Db 2758 AAGATCACTCGGAACTCCGTTGGGTGCGCTGGCAACCTGAACCTGTGCTGGCCATATC 2817  
QY 2874 ATCTTCATCTTTGGGATGATGGGAATGCAACTGTTCCGAAAGATTAATCAATGA---TCAC 2930  
Db 2818 GTCTTCATCTTCCGCGTGTGGGATGCAAGCTGTTTGGAAAGTTTCAAGAGTGTGCTC 2877  
QY 2931 AAGAGCGCTTTCCGATGGGACTGCGCGCTGGAACCTTCAACCACTTATGACACAGC 2990  
Db 2878 TGTAAATCAACACGAGATGCAAGCTCCGCGCTGGACATGAACGACTTCTTCCACTCC 2937  
QY 2991 TTTCATATCTGTTCCCGGTGCTCTGGGAGATGATTCGAGTCAATGATGGGACTGTGATG 3050  
Db 2938 TTCTCATATGCTTCCGAGTGTCTGTGTGGAGTGAATCGAGACCATGTGGGACTGTGATG 2997  
QY 3051 TACGTG---GGCGATGTCTCTGATTCCTCTTCTTGGCCACCGTTGATCGCAAT 3107  
Db 2998 GAGGTGGCGGCGCAAGGCGATGTCTCATGTCTTCAATGATGTATGTGCTATTTGGCAAC 3057  
QY 3108 CTGTGTGATTTAACTTTTCTTAACTGCTTGTGTTCATTTTGGCTCATCTAGCTTA 3167  
Db 3058 CTGTGTGTGCTGAATCTAATCTGACCTTGTCTTGAAGCTCTTCAAGGCGACACCTTG 3117  
QY 3168 TCAGGCGGCACTGCGGATTAAGATGCAATGAATAATAGCCGAGGCTTCAATCGAATGGC 3227  
Db 3118 GCGGCGACAGACGACGAGCGGGAATGAACA----- 3149  
QY 3228 CGATTTAAAGTTGGGTTAAGCGTAATATGCTGATGTTTCAAGTTAATACGTAAACAA 3287  
Db 3150 ----- 3149  
QY 3288 TTGACAAATCAATTAATGATCAACCATCAAGGTAGAGAGCAACCAACGATGATTTGATT 3347  
Db 3150 -----CTTGCATATCTCAAGTATTC 3168  
QY 3348 TGGAGCGAAGCAGATGTGACAAAGAACTGGAGCTGGGCCAGACGAGATCTCGCCGAC 3407

3169 CGGATCAAGAAAGGCGCTGCGCTGACCAAAAGTGAAGTCAACGCTTCAATGCAAGGCTCAC 3228  
QY 3408 GGCCTCATCAAGAAAGGGGATCAAGAGACAGCACTGAGTGTGGCATGTGGGATGGG 3467  
Db 3229 TTCAAGACCGGGAGCGGATGAAGTGAACCCCTCGACGAGCTGTATGAGAAAGAGCC 3288  
QY 3468 ATGGAATTCAGATTCACGCGGACATGAAGAACAAACAAAGCCGAAAGAAATCCAAATATCTA 3527  
Db 3289 AACTGCATGCGCAACCAACGCGGCTGTGATTCACCGGAACGGGACTTCCAGAAAGAAC 3348  
QY 3528 AATTAAGCAACGATATTTGGCAACTCAATTAACCAACAGACAAATAGAATGGAACAGAG 3587  
Db 3349 GGGAAAGGAACACCAAGGGGATTCGGCAGACGCTGTGAGAAATACATCATGACAGAGAC 3408  
QY 3588 CTAAACATAGAAGTTTGTCTTACAGAGACGACACTGCGCAGATTAATCATATAGGT 3647  
Db 3409 CACA-----TGTCTTCAATTAACA-----CCAAACTGACGCTCGGGT 3449  
QY 3648 AGCCATTAAGATCGAACATTTCAAGGACGAGCCCAAGAGGCGCGGAGACGATGAG 3707  
Db 3450 GCCCATGTCTGTGGGAGTCT---GACTTGAAGACTTCAACAGAGATGTTAGC 3504  
QY 3708 GCGGAGAGAAAGCGGACCGCAGCAAGAGATTAAGTCTGACGAGAACTGACGAG 3767  
Db 3505 AAGGATCAACCTGAAAGGACGAAAGTAA-----ACTGAGCATACAGCTCTCA 3558  
QY 3768 GAGGCGGAATGCGAGAGGAGCCCGCTCGAGCGGTATCATATTCATGCAACGACGAG 3827  
Db 3559 GAAGGAATGACATCGACATCAAGCTGTGAGGAAAGTTCCGTGAGCAACCTGAG 3618  
QY 3828 GATATACGATGAATATCACTGATGCTGCGCCGATTCGTACTAATGAATTTCCG 3887  
Db 3619 GAATATCTGG-----ATCCGACGCTGTCTTACAGAGGTGTGGTCAAGGGTTCAG 3672  
QY 3888 ATCTTACCGGTGACGATGATCTGCGCTTCTGCAAGATGAGGCAATTTAGACCTGAA 3947  
Db 3673 TGCTGCAGGTCAACATCGAGGAAGGACTAGGCAAGTCTGTGTGATCTTGGGAAACCC 3732  
QY 3948 ACTTTTCATTAATTAATAATTAATTTTGAAGAGCTGTATCACTATGAATTTATG 4007  
Db 3733 TGCTTCCGATGTGAGGACAAATGTTTGAAGCTTATCATATCTTCAATGATCTGCTC 3792  
QY 4008 AGTAGCTAGCTTTGGCATTTAGAGATGTACATCTGCCAAGAACCCATCTGACAGAT 4067  
Db 3793 AGCAGTGGCGCCCTGCGCTTTAGAGCATCTACATTTAGACAGAGAAACATCCGACCC 3852  
QY 4068 ATTTTACTATATGACAGATATTTTACGTTATATCTTCTTGGAAATGTTAATCAAG 4127  
Db 3853 ATCTGAGATAGCGGACAAAGGCTTCACTCATCTTCACTGTGAGATGTTGCTCAAG 3912  
QY 4128 TGTGTGGCGCTGGCTTCAAGATGTACTCACCAAGCGCGGTGTGGCTGCAATTCGTG 4187  
Db 3913 TGAACAGCTTACGGCTTGTCAAGTTCTTACCAATGCTGTGTGTGTGACTTCCG 3972  
QY 4188 ATGTGATGTATGCTTATCAACTTGTGCTTCACTGTGTGAGCTGTGTATTCAA 4247  
Db 3973 ATGTGTGTGTCTTATTAATGACCTTAATAGCTAATGCGCTGAGTACTGGAATCAGAT 4032  
QY 4248 GCGCTTAAGACTATGGAAGTTAAGACACTGAGACCACTAGTGCATATGCGGTATG 4307  
Db 4033 GCCATTAAGTCCCTTGAAGCCCTTAAGAGCTTTGAGACCTTAAAGCCTTATACATTT 4092  
QY 4308 CAGGGCAATGAGGAGCGCTTAATGCGTGTGACAGCTTACAGCTTCACTTCAATGTG 4367  
Db 4093 GAAGGATGAGGAGTGTGTGAATGCTGTGTGTGGCGCATCCCTTCATCATGATGTG 4152  
QY 4368 CTATGTGTGTCTAATATTTTGGCTAATTTTGCATTAATGAGTGTACAGCTTTTGTCT 4427  
Db 4153 CTGTGTGTGTCTCAATCTTCTGCTGATTTTCAAGATCAATGGAATTAACCTGTTTGGC 4212  
QY 4428 GAAATATTTTAATGTC---GAGACATGAATGCGACGAAGCTCAGCCGACGAGATCAT 4484  
Db 4213 GGGAAATACCACTACTGCTTAAATGAGACTTGTGAATCCGTTTCAAAATCGATTTGTCT 4272



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Qy 4485 CCAATGCGAATGCTGGAG-----AGGAGAACTACAGTGGTG 4526
Db 4273 AACATTAAGGAGCTGAGAAAGCTCATGAGGGCAACAGACGAAATCGATGAGAG 4332
Qy 4527 AATTCAGCAATGATTTGATCATGTAGGTAAAGGATCTGTGCTTTTCCAAATGGCC 4586
Db 4333 AATGCAAGATCACTTTGACATGTGCGAGAGGGTACCTGGCCCTTCTTCAATGGCA 4392
Qy 4587 ACCTTCAAGGCTGAGTAAATCATGAGACATGCTATCGATTCAAGAGGTGAGCAAG 4646
Db 4393 ACCTTCAAGGCTGAGTAAATCATGATGCGGCTGATGATTCGGAAGCAGACGAG 4452
Qy 4647 CAACCAATTCGTAAGCAACATCTACATGTATTTATTTGATTTCTTCAATATTT 4706
Db 4453 CAGCTGACTACGAGGCAACATCTACATGTATTTCTTCAATCTTCTTCAATCTTC 4512
Qy 4707 GATTCCTTTTCACTCAATCTGTTTCAATGTTTATTTATTTATTTATTTATGAGCA 4766
Db 4513 GGTCTCTTCTTCACTCAATCTGTTTCAATGTTTATTTATTTATTTATTTATGAGCA 4572
Qy 4767 AAGAAAAAGAGGTGATCATTTAGAAATGTTTATGAGAGATCAGAAAAAGTACTAT 4826
Db 4573 AAGAAAAA---GTTGAGGTGAGGACATCTTCAATGACAGAGAACAGAAAGTACTAC 4629
Qy 4827 AATGTAAGAAAAAGATGGGCTCTTAAAAACCTTAAAGCATTCCAAAGCAAGGTGG 4886
Db 4630 AATGCAAGAAAAAGATGGGCTCTTAAAAAGCCATTCAGAGCCCTTGAAC 4689
Qy 4887 CGACCAACAGCAATGTTTGAATATGTAACCGATTAAGAAATGATATATCATATATG 4946
Db 4690 AAAATTCAGAGGATTTGTTGATTTGCTCATCAAGCCTTGAATGATGATCATG 4749
Qy 4947 TTATTCATGATCTGAAATGTTTCAATGACCTGATCTGATGATGATGATGATGATG 5006
Db 4750 ATGCTCATCTGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 4809
Qy 5007 TATTAACGGCTCTAGATATCTCAATGCAATGCAATGCAATGCAATGCAATGCAATG 5066
Db 4810 ATGAGAAACATTTCTTACATGATTAATGCTGCTTCTTCAATCTTCTTCAATCTT 4869
Qy 5067 CTATTAATAATATTCGTTTACATGATATCATATTTATTTATTTATTTATTTAT 5126
Db 4870 GTGCTCAAAATGTTGCTTGAACATCTATTTTCAATTTGCTGAGAAATCTTTTAC 4929
Qy 5127 GTAGTATGTTGATTTATTCATCTTATGATCTTATGATGATGATGATGATGATGAT 5186
Db 4930 TTGATGATGATCTATCTCTCATTTGATGATGATGATGATGATGATGATGATGATG 4989
Qy 5187 TTGATGATGATCTATCTCTCATTTTATGATGATGATGATGATGATGATGATGATG 5246
Db 4990 TTGATGATGATCTATCTCTCATTTTATGATGATGATGATGATGATGATGATGATG 5049
Qy 5247 CTGATGAAGGAGGCAAGGATTCGAGACATGCTTCTGATGATGATGATGATGATGATG 5306
Db 5050 CTGATGAAGGAGGCAAGGATTCGAGACATGCTTCTGATGATGATGATGATGATGATG 5109
Qy 5307 GCTCTGTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5366
Db 5110 GCTCTGTTCAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5169
Qy 5367 ATGTCGTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5426
Db 5170 ATGTCGTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5229
Qy 5427 ACCTTGGCCAGAGATGATCTGCTCTTTCAGATGATGATGATGATGATGATGATGATG 5486
Db 5230 ACATTTGGCAACAGATGATCTGTTTGTTCAGATGATGATGATGATGATGATGATGATG 5289
Qy 5487 GTACTGAGCGCATTTATCA-----TAGAGAGATGCGATCCAGCAGCAGC 5537
Db 5290 CTGCTGTCGCAATCTGAGACCGCCCTGATGATGATGATGATGATGATGATGATGATG 5349

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Qy 5538 AAGGCTATCCGGCAATTTGTTTCAAGCAACCGTTGGAATTAAGTTTCTCTCATAC 5597
Db 5350 AGTGCTTCAAAAGGAGCTGTGGAAACCTCTGGGGGCACTTCTTTTGTGAGTAC 5409
Qy 5598 CTAGTTTAAGCTTTTGTATGATTTATTAATGATACATGCTGATCTTCTGAGAACTAT 5657
Db 5410 ATCAATCATCTCTTCTGATTTGTGATGATGATGATGATGATGATGATGATGATGATG 5469
Qy 5658 AGTCAGGCAACCGAGAGCTGCAAGAGGCTTAAACCGAGCAAGCACTACGATGATCTAT 5717
Db 5470 AGCGTGCCCAACCGAGAGAGCGCCGACCTCTGATGATGATGATGATGATGATGATGAT 5529
Qy 5718 GAGATCTGGAGCAATTCGATTCGAGAGGCAACCGATACATACCTATGATGATGATG 5777
Db 5530 GAGATCTGGAGCAATTTGATTCGAGAGGCAACCGATACATACCTATGATGATGATG 5589
Qy 5778 GAATTCCTGAGAGTACTGAGACCCCGCTGAGATGCAACAAACGAACTACAAAGATC 5837
Db 5590 GACTTTGCGGACGCGCTGAGACACCGCTCCGAGTACCCAGCCCAACATGATGAGCTC 5649
Qy 5838 ATATGATGACATACCATCTGTGCGGATGATGATGATGATGATGATGATGATGATGAT 5897
Db 5650 ATCCCATGAGACTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5709
Qy 5898 GCGCTTACGAAAGCTTCTTGGCGGAGAGGCAATCCGATAGAGAGACGGGTGAGAT 5957
Db 5710 GCTTTCACAAAGCAATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5769
Qy 5958 GGTGAG-----ATAGCGGCGCGCGCGGATACGAGAGGCTTACAGAGCCGCTCATCAAG 6011
Db 5770 GAGAGAGGCTTGTGAGATCAATCAATCTTCAAAAGTCTTACAGAGCTTACAAACACT 5829
Qy 6012 CTGAGGCTGAGAGGATGAGAGTACGAGCCCGGCTTATTCAGACAGCTGCGAAAGAC 6071
Db 5830 CTGCGGCGCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5889
Qy 6072 AAGCGGCGCGCG 6084
Db 5890 TTGGCTAGCGCGG 5902

RESULT 15
ADP71901
ID ADP71901 standard; DNA; 6556 BP.
AC ADP71901;
DT 26-AUG-2004 (first entry)
DE Renal toxin progression gene marker #490.
KW ds; toxic effect; gene expression profile; kidney tissue;
KW differential gene expression; toxicity progression; toxicity marker;
KW drug screening; toxicity assay; kidney pathology; nephritis;
KW kidney necrosis; glomerular injury; tubular injury;
KW focal segmental glomerulosclerosis.
OS Rattus norvegicus.
PN W02004048598-A2.
PD 10-JUN-2004.
PE 24-NOV-2003; 2003WO-US037556.
PR 22-NOV-2002; 2002US-00301856.
RA (GENE-) GENE LOGIC INC.
XX Mendrick DL, Porter WM, Johnson KR, Castle A, Higgs B;
XX Elashoff M;
XX WPI; 2004-460771/43.

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Qy 1794 GATGTAAGCATTTGATGTGCAATATGAGATGCCAGACGACTTGGCCCTATGCC 1853  
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Qy 1854 GACGACTCGAAATGCGCTGACCCCGATGTCCGAAGAATGGGGCCCATATAGTCCCTG 1913  
Db 1900 GGCTCTGAGAAATG-----AGTTCCGAGCAGATGAACACAGACGCTGGAGAG 1947  
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Db 2357 -----TCTGGAGTGTCAACCCCTACTGATTAATGTAAGAGATC 2397  
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Tue May 10 12:01:09 2005

us-08-554-424-7.rng

Page 51

Search completed: May 9, 2005, 04:52:59  
Job time : 3212 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 04:00:40 ; Search time 962 Seconds  
(without alignments)

11078.036 Million cell updates/sec

Title: US-08-554-424-7

Sequence: 1 TCTAGACGTTGGCCGATAG.....ACGCGATTTAGCTCTAGA 6513

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Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 81813859 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
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Listing first 45 summaries

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	6513	100.0	US-08-338-702-7	Sequence 7, Appli
2	6513	100.0	US-08-337-339-7	Sequence 7, Appli
3	6513	100.0	US-08-724-095-7	Sequence 7, Appli
4	6513	100.0	PCT-US95-14262-7	Sequence 7, Appli
5	6513	100.0	US-08-808-793-24	Sequence 7, Appli
6	6163.8	94.6	US-07-998-289B-7	Sequence 24, Appli
7	5233.2	80.4	US-08-808-793-1	Sequence 1, Appli
8	4447.8	68.3	US-08-772-512A-1	Sequence 1, Appli
9	4447.8	68.3	US-09-428-371-1	Sequence 1, Appli
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#### ALIGNMENTS

RESULT 1  
US-08-338-702-7

Sequence 7, Application US/08338702  
Patent No. 555049

GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.

TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE

NUMBER OF SEQUENCES: 7  
TITLE OF INVENTION: PARA SODIUM CHANNEL

CORRESPONDENCE ADDRESS:

ADDRESSEE: John W. Wallen III

STREET: P.O. Box 2000, 126 E. Lincoln Avenue

CITY: Rahway

STATE: New Jersey

COUNTRY: USA

ZIP: 07065-0900

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,702

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Wallen III, John W.

REGISTRATION NUMBER: 35,403

REFERENCE/DOCKET NUMBER: 19338

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-3905

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 6513 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

US-08-338-702-7

Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best local similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTAGACGTTGGCCGATAGCAATGACAGAAAGTTCGACTGATATCTGAGGAAGAC 60  
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QY 901 ATATGAGGCTGTCTACCGAAGAGTGCATCAAGAAAGTTCCGCTGACGCTTCTGCGGCA 960  
| | | | |  
Db 901 ATATGAGGCTGTCTACCGAAGAGTGCATCAAGAAAGTTCCGCTGACGCTTCTGCGGCA 960  
QY 961 ATTCGACGAGAGAACTGGGACTATCAATTCGCAATAGCTTCCAAATTTGATTCGAGG 1020  
| | | | |  
Db 961 ATTCGACGAGAGAACTGGGACTATCAATTCGCAATAGCTTCCAAATTTGATTCGAGG 1020  
QY 1021 ACGAGGAGCTCTATTTCCGTTATGCGGCAATATATCCGTTGCGGCGCAATGCAACGAC 1080  
| | | | |  
Db 1021 ACGAGGAGCTCTATTTCCGTTATGCGGCAATATATCCGTTGCGGCGCAATGCAACGAC 1080  
QY 1081 ATTATGCTGTGCTGAGAGGTTTGTCCGAATCCGAATTTATGCTACACAGCTTCGATT 1140  
| | | | |  
Db 1081 ATTATGCTGTGCTGAGAGGTTTGTCCGAATCCGAATTTATGCTACACAGCTTCGATT 1140  
QY 1141 CGTTGAGATGGGCTTTCTGTCCGCTTCCGCGTGATGACACAGGACTTCTGAGAGATC 1200  
| | | | |

Db 1141 CGTTGAGATGGGCTTTCTGTCCGCTTCCGCGTGATGACACAGGACTTCTGAGAGATC 1200  
| | | | |  
QY 1201 TGTACAGCTGTGTGTGCGCGCGCGGACCATGCGACATGCTGTTCTTATATGATCATCA 1260  
| | | | |  
Db 1201 TGTACAGCTGTGTGTGCGCGCGCGGACCATGCGACATGCTGTTCTTATATGATCATCA 1260  
QY 1261 TCTTCTAGTTCATTTCTATCTTTGGAATTTGATTTTGGCCATTTGGCATGTGATG 1320  
| | | | |  
Db 1261 TCTTCTAGTTCATTTCTATCTTTGGAATTTGATTTTGGCCATTTGGCATGTGATG 1320  
QY 1321 ACGAATTTGCAAGAAAGGCGGCAAGAAAGAGAGTCCGCAAGAGAGGCGATACGTAAG 1380  
| | | | |  
Db 1321 ACGAATTTGCAAGAAAGGCGGCAAGAAAGAGAGTCCGCAAGAGAGGCGATACGTAAG 1380  
QY 1381 CCGAAGAGCTGCGCGCGCAAGCGGCAAGCTGAGAGAGCGGCGCAATGCGCAGGCTTC 1440  
| | | | |  
Db 1381 CCGAAGAGCTGCGCGCGCAAGCGGCAAGCTGAGAGAGCGGCGCAATGCGCAGGCTTC 1440  
QY 1441 AGGACAGACGATGCGGCTGCGCGGAGAGAGCTGCACTGATCCGGAATGGCCAGAC 1500  
| | | | |  
Db 1441 AGGACAGACGATGCGGCTGCGCGGAGAGAGCTGCACTGATCCGGAATGGCCAGAC 1500  
QY 1501 GTCCGACGATTTCTTGCATCAGCTATGAGCTATTTGTTGGCGGCGAAGAGGCGACGATG 1560  
| | | | |  
Db 1501 GTCCGACGATTTCTTGCATCAGCTATGAGCTATTTGTTGGCGGCGAAGAGGCGACGATG 1560  
QY 1561 ACAACAAACAAAGAGATGTCATTCGAGAGCTGCGAGCTGAGTGTGAGAGG 1620  
| | | | |  
Db 1561 ACAACAAACAAAGAGATGTCATTCGAGAGCTGCGAGCTGAGTGTGAGAGG 1620  
QY 1621 TTATACAAAGACAAACGAGACCTTACACAGACACCAACCACTACCAAGTTCTGTAAGTGA 1680  
| | | | |  
Db 1621 TTATACAAAGACAAACGAGACCTTACACAGACACCAACCACTACCAAGTTCTGTAAGTGA 1680  
QY 1681 GCAAGCATCTTATCTTATCTTACCTGTTCAACGTTTAAACATAGCAGAGGATCAGTAGTT 1740  
| | | | |  
Db 1681 GCAAGCATCTTATCTTATCTTACCTGTTCAACGTTTAAACATAGCAGAGGATCAGTAGTT 1740  
QY 1741 CTACAAAGTACAGATACGGAACGAGAGCTGCGGCTTGGTATACCGGATGAGATCGTA 1800  
| | | | |  
Db 1741 CTACAAAGTACAGATACGGAACGAGAGCTGCGGCTTGGTATACCGGATGAGATCGTA 1800  
QY 1801 AGCCATTTGATTTGTCAACATATCAGAGATGCCAGAGACCTTGCCCTATGCGGACGACT 1860  
| | | | |  
Db 1801 AGCCATTTGATTTGTCAACATATCAGAGATGCCAGAGACCTTGCCCTATGCGGACGACT 1860  
QY 1861 CGAATGCGGTACCCCGATGTCCGAAGAGATGGGCGCATATAGTCCCGTATCTATG 1920  
| | | | |  
Db 1861 CGAATGCGGTACCCCGATGTCCGAAGAGATGGGCGCATATAGTCCCGTATCTATG 1920  
QY 1921 GCAATCTAGGCTCCGACACTCATGATATCCCTGCAATGATCCGAATATGCTATACCT 1980  
| | | | |  
Db 1921 GCAATCTAGGCTCCGACACTCATGATATCCCTGCAATGATCCGAATATGCTATACCT 1980  
QY 1981 CACATGCGATCTACTCGCGGAGATGCGGCTGATGAGGCTGACACATGACCAAGAGAGA 2040  
| | | | |  
Db 1981 CACATGCGATCTACTCGCGGAGATGCGGCTGATGAGGCTGACACATGACCAAGAGAGA 2040  
QY 2041 GCAATTTGCGCAACCGCAACACACGCAATATATCAAGTGGGCGCAACAAATGGGCGACCA 2100  
| | | | |  
Db 2041 GCAATTTGCGCAACCGCAACACACGCAATATATCAAGTGGGCGCAACAAATGGGCGACCA 2100  
QY 2101 CCGTCTGAGACACCAATCAACAGCTGATCATGCGCATGAGAAATTTGGCCTGAGATGCA 2160  
| | | | |  
Db 2101 CCGTCTGAGACACCAATCAACAGCTGATCATGCGCATGAGAAATTTGGCCTGAGATGCA 2160  
QY 2161 CGAGCAGAGCTGGCAAGATTTAAACATCATGACATCTTTTATGAGAGCCGCTCAGACAC 2220  
| | | | |  
Db 2161 CGAGCAGAGCTGGCAAGATTTAAACATCATGACATCTTTTATGAGAGCCGCTCAGACAC 2220  
QY 2221 AAACGCTGTTGATATGAAGATGTGATGCTCTGAAATGACATCATGGAACAGGCGGCTG 2280  
| | | | |

Db	2221	AAAGSGTGGTTGATATATGAAGAATGTGAATGTGCTCTGAATGACATCATCGAAGCGCCGCT	228
Qy	2281	GTCCGACACAGTCGGGCAAGCGATCGCGGATGCTCCGTTTACTATTTCCCAACAGAGACG	2340
Db	2281	GTCCGACACAGTCGGGCAAGCGATCGCGGATGCTCCGTTTACTATTTCCCAACAGAGACG	2340
Qy	2311	ATGACAGAGATGCGGCCGACGTTCAAAAGACAGGCACTGMAAGTATCTCAAGGCAATCG	2400
Db	2311	ATGACAGAGATGCGGCCGACGTTCAAAAGACAGGCACTGMAAGTATCTCAAGGCAATCG	2400
Qy	2401	ATGCTCTTTGCTGTGGGACCTGTGCTGGGTTTGGTTGAATTTGACAGAGTGGGATATGC	2460
Db	2401	ATGCTCTTTGCTGTGGGACCTGTGCTGGGTTTGGTTGAATTTGACAGAGTGGGATATGC	2460
Qy	2461	TCATCGCTTCGATCCCTTCGTCGAGCTCTTCATACCGCTGCACTTGCTGTCACACGA	2520
Db	2461	TCATCGCTTCGATCCCTTCGTCGAGCTCTTCATACCGCTGCACTTGCTGTCACACGA	2520
Qy	2521	TGTTTCATGSCAATGGATCACACGATATGAACAAAGAGATGMAAGCGGTCTCAAGATG	2580
Db	2521	TGTTTCATGSCAATGGATCACACGATATGAACAAAGAGATGMAAGCGGTCTCAAGATG	2580
Qy	2551	GCAACTATTTCTTCCACCGCCACCTTTGGCATGAGAGCCACCATGAAGCTAATGGCATGA	2640
Db	2551	GCAACTATTTCTTCCACCGCCACCTTTGGCATGAGAGCCACCATGAAGCTAATGGCATGA	2640
Qy	2641	GCCCCAAGTACTATTTCCAGAGAGGCTGGAACATCTTGACCTTCATATTCGAGGCCATAT	2700
Db	2641	GCCCCAAGTACTATTTCCAGAGAGGCTGGAACATCTTGACCTTCATATTCGAGGCCATAT	2700
Qy	2701	CGCTATTTGGAACCTGGGACTCGAAGGATGTCAGAGGATCTGTCCGATATGCGTTCCCTTCGAT	2760
Db	2701	CGCTATTTGGAACCTGGGACTCGAAGGATGTCAGAGGATCTGTCCGATATGCGTTCCCTTCGAT	2760
Qy	2761	TGCTGCGGTGATTCGAACCTGTGCGCAAGCTTGTGGCCCACTTAATTTACTCATTTGCAATTA	2820
Db	2761	TGCTGCGGTGATTCGAACCTGTGCGCAAGCTTGTGGCCCACTTAATTTACTCATTTGCAATTA	2820
Qy	2821	TGGGACGACCAATGGGCGCTTTGGGTAATCTGACATTTGTACTTGTGATATATCATCTTCA	2880
Db	2821	TGGGACGACCAATGGGCGCTTTGGGTAATCTGACATTTGTACTTGTGATATATCATCTTCA	2880
Qy	2881	TCTTTGCGGTGATGGAATGCACTGTTGGAAGAAATATCATGATCAACAAGACCGCT	2940
Db	2881	TCTTTGCGGTGATGGAATGCACTGTTGGAAGAAATATCATGATCAACAAGACCGCT	2940
Qy	2911	TTCCGGAATGGGACCTGCGCGGCTTGGAACTTCAACGACTTATATGCAAGCTTCATGATCG	3000
Db	2911	TTCCGGAATGGGACCTGCGCGGCTTGGAACTTCAACGACTTATATGCAAGCTTCATGATCG	3000
Qy	3001	TGTTCCGGGTGCTCTGCGGGAAGATGAGTCAGTCATGTGGACATGACATGATCGGGCG	3060
Db	3001	TGTTCCGGGTGCTCTGCGGGAAGATGAGTCAGTCATGTGGACATGACATGATCGGGCG	3060
Qy	3061	ATGTCCTCGTCAATCCCTTCTTCTTGGCACCGCTGTGATATGGCAATCTTGTGTGATCTTA	3120
Db	3061	ATGTCCTCGTCAATCCCTTCTTCTTGGCACCGCTGTGATATGGCAATCTTGTGTGATCTTA	3120
Qy	3121	ACCTTTTCTTAGCCTTGCTTTTGTTCGAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG	3180
Db	3121	ACCTTTTCTTAGCCTTGCTTTTGTTCGAATTTTGGCTCATCTAGCTTATCAGCGCCGACTG	3180
Qy	3181	CCGATTAACGATATCGAATTAATAATAGCCGAGGCTTCATATCGAATTTGGCCGATTTAAAGTT	3240
Db	3181	CCGATTAACGATATCGAATTAATAATAGCCGAGGCTTCATATCGAATTTGGCCGATTTAAAGTT	3240
Qy	3241	GGGTTAAGCCTAATTTGCTGATGTTTCAAGTTATATCGTAACAAATTTGACAAATCAAA	3300
Db	3241	GGGTTAAGCCTAATTTGCTGATGTTTCAAGTTATATCGTAACAAATTTGACAAATCAAA	3300
Qy	3301	TAAAGTATCAACCATCAGGTGAAGAGCAACACAGATCAGTTGGATTTGAGCGCAAGAGC	3360
Db	3301	TAAAGTATCAACCATCAGGTGAAGAGCAACACAGATCAGTTGGATTTGAGCGCAAGAGC	3360

Qy	3361	ATGTGTGACAAAGCAATCTGGAGCTGTGGGCTCCAGACAGATATCTCTGGCCGACGGCTCTATCAAGA	3422
Db	3361	ATGTGTGACAAAGCAATCTGGAGCTGTGGGCTCCAGACAGATATCTCTGGCCGACGGCTCTATCAAGA	3422
Qy	3421	AGGGGATCAAGAGCAGACAGCACTGAGAGTGTGCATCGGGGATTCGATGGAAATTCACGA	3480
Db	3421	AGGGGATCAAGAGCAGACAGCACTGAGAGTGTGCATCGGGGATTCGATGGAAATTCACGA	3480
Qy	3481	TACACGGCGACATGAGAAACAAGCCGAAAGAAATCCAAATATCTAAATATACGACGA	3540
Db	3481	TACACGGCGACATGAGAAACAAGCCGAAAGAAATCCAAATATCTAAATATACGACGA	3540
Qy	3541	TGATTTGGCAACTTAATACCAACCAAGCAATPAGCTGGAAACAAGAGTTAAATCAATPAG	3600
Db	3541	TGATTTGGCAACTTAATACCAACCAAGCAATPAGCTGGAAACAAGAGTTAAATCAATPAG	3600
Qy	3601	GTTTGTCTCTTACAGACACGACACATCTGCACAGATTAACTCATATGTGTATGATCAATCAATC	3660
Db	3601	GTTTGTCTCTTACAGACACGACACATCTGCACAGATTAACTCATATGTGTATGATCAATCAATC	3660
Qy	3661	GACCAATTCAAGACGAGAGCCACAAGGGCAGCGCCGAGACGATGAGGGCCGAGAGAAAC	3722
Db	3661	GACCAATTCAAGACGAGAGCCACAAGGGCAGCGCCGAGACGATGAGGGCCGAGAGAAAC	3722
Qy	3721	GCGAGCCAGCAAGAGAGATTAAAGTCTCGACGAGAACTGGAACAAGAGGGCCGAATTCG	3780
Db	3721	GCGAGCCAGCAAGAGAGATTAAAGTCTCGACGAGAACTGGAACAAGAGGGCCGAATTCG	3780
Qy	3781	AGGAGGGCCCCGTGACGCGTGATTCATTAATTCATGCAACAGACGAGATATCTCGATG	3840
Db	3781	AGGAGGGCCCCGTGACGCGTGATTCATTAATTCATGCAACAGACGAGATATCTCGATG	3840
Qy	3841	AATATCCAGCTGATTCGTCGCCCCGATTCGTAATTAACAATTTCCATTCAGTCCGGTG	3900
Db	3841	AATATCCAGCTGATTCGTCGCCCCGATTCGTAATTAACAATTTCCATTCAGTCCGGTG	3900
Qy	3901	ACGATGACTCGCCGTTCTGCGACAGGATGGGCAATTACGACTGAAAATTTCATTTCAATTTA	3960
Db	3901	ACGATGACTCGCCGTTCTGCGACAGGATGGGCAATTACGACTGAAAATTTCATTTCAATTTA	3960
Qy	3961	TTGAAAAATTAATTTTGTGAAAACAGCTGTATCATTAATTTTAATGATGCTTAAGCTT	4020
Db	3961	TTGAAAAATTAATTTTGTGAAAACAGCTGTATCATTAATTTTAATGATGCTTAAGCTT	4020
Qy	4021	TGGCAATTGAGAGTGTATCATCTGCGCAACAAGCCATCTGACAGATATTTATTAATCTATA	4080
Db	4021	TGGCAATTGAGAGTGTATCATCTGCGCAACAAGCCATCTGACAGATATTTATTAATCTATA	4080
Qy	4081	TGGACAGAAATTTACGGTTATATTTCTTTGGAAATGTTATCAAGTGTGGCGCTCG	4140
Db	4081	TGGACAGAAATTTACGGTTATATTTCTTTGGAAATGTTATCAAGTGTGGCGCTCG	4140
Qy	4141	GCTTCAAGTGTATCTTCAACCAACGGTGTGTTGGCTCGATTTGCTGATTTGCAATGATAT	4200
Db	4141	GCTTCAAGTGTATCTTCAACCAACGGTGTGTTGGCTCGATTTGCTGATTTGCAATGATAT	4200
Qy	4201	CGCTTATCAACTTCGTTGCTTCACTGTTGTGAGCTGTGATTTCAAGCTTCAAGACTA	4260
Db	4201	CGCTTATCAACTTCGTTGCTTCACTGTTGTGAGCTGTGATTTCAAGCTTCAAGACTA	4260
Qy	4261	TGCGAACTTAAAGACACTGAGACACTAGCTGCCATGCCCGTATGCAAGGGCAATGAGGG	4322
Db	4261	TGCGAACTTAAAGACACTGAGACACTAGCTGCCATGCCCGTATGCAAGGGCAATGAGGG	4322
Qy	4321	TGCTGTATTAAGCGGTGTGTACAAGCTATACCGTCACTTCAATGTGCTATTTGTGTGTC	4380
Db	4321	TGCTGTATTAAGCGGTGTGTACAAGCTATACCGTCACTTCAATGTGCTATTTGTGTGTC	4380
Qy	4381	TAAATATTTGGCTAATTTTGGCATTAATGGGTGTACAGCTTTTGTCTGAAAAATATTTTAA	4440
Db	4381	TAAATATTTGGCTAATTTTGGCATTAATGGGTGTACAGCTTTTGTCTGAAAAATATTTTAA	4440

QY 4441 AGTCCAGGACATGATGGCGAAGCTCAGCCAGAGATCATACCAATTCGAAATGCT 4500  
 DB 4441 AGTCCAGGACATGATGGCGAAGCTCAGCCAGAGATCATACCAATTCGAAATGCT 4500  
 QY 4501 GCGAGAGGAGAACTACAGTGGGTGAATTCAGCAATGAAATTCATGATGTAAG 4560  
 DB 4501 GCGAGAGGAGAACTACAGTGGGTGAATTCAGCAATGAAATTCATGATGTAAG 4560  
 QY 4561 CGTATCTGCTCTTTCCAAAGTGGCCACTTCAAAAGCTGATCAAAATCATGAAGATG 4620  
 DB 4561 CGTATCTGCTCTTTCCAAAGTGGCCACTTCAAAAGCTGATCAAAATCATGAAGATG 4620  
 QY 4621 CATGCAATTCAGAGAGGTGAGCAAGCAACCAATTCGTGAAGCAATCTACATGAT 4680  
 DB 4621 CATGCAATTCAGAGAGGTGAGCAAGCAACCAATTCGTGAAGCAATCTACATGAT 4680  
 QY 4681 TATATTCGATCTTCATCATATTTGATGATCTTTTCACTCAATCTGTTCAATGGTG 4740  
 DB 4681 TATATTCGATCTTCATCATATTTGATGATCTTTTCACTCAATCTGTTCAATGGTG 4740  
 QY 4741 TTAATCATGATAATTTAATGAGCAAAAGAAAAGAGGTGATGATTAAGAAATGTTCA 4800  
 DB 4741 TTAATCATGATAATTTAATGAGCAAAAGAAAAGAGGTGATGATTAAGAAATGTTCA 4800  
 QY 4801 TGAAGAGATTCAGAAAAGTACTATATGCTATGAAAAAGATGGGCTTAAGAAATGTTCA 4860  
 DB 4801 TGAAGAGATTCAGAAAAGTACTATATGCTATGAAAAAGATGGGCTTAAGAAATGTTCA 4860  
 QY 4861 TAAAGGCAATTCAGAGCAAGAGTGGGACACAGCAATAGTCTTTGAATAGTAACG 4920  
 DB 4861 TAAAGGCAATTCAGAGCAAGAGTGGGACACAGCAATAGTCTTTGAATAGTAACG 4920  
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 DB 4921 AATAAGAAATTCGATATATATATATGATGATTTATTCATGCTGAAATGTTCAATGACC 4980  
 QY 4981 TCGATGTTACAGAGGTGGGACACGATATAGCGGGCTTGAATCTCAATGCGATAT 5040  
 DB 4981 TCGATGTTACAGAGGTGGGACACGATATAGCGGGCTTGAATCTCAATGCGATAT 5040  
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 DB 5041 TCGATGTTATTTCAAGTTCGAAATGCTATTAATAAATATTCGTTTACATATCACTAT 5100  
 QY 5101 TTAATGAGGCAATGAAATTTATGATGATGATGATGATTTATTCATGCTGAAATGACC 5160  
 DB 5101 TTAATGAGGCAATGAAATTTATGATGATGATGATGATTTATTCATGCTGAAATGACC 5160  
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 DB 5161 TACTAGGCAATTTATGAGAGATCTTCGTTGCGAGCCCTGCTCCAGTGGTGCTG 5220  
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 DB 5341 TCAATGTTCAATCTTTGCAATTTTGGGCAATGCTGCTTCAATGCAATGCAAGAGAGCG 5400  
 QY 5401 GCATTAACGAGCTTACAACTTCAAGCCTTTGGCAGAGCATGATCTCTCTTTTCA 5460  
 DB 5401 GCATTAACGAGCTTACAACTTCAAGCCTTTGGCAGAGCATGATCTCTCTTTTCA 5460  
 QY 5461 TGTGAGAGTCAAGCGGTTGGGATGCTGATGAGCGCATTTATTAAGAGAGAGAGATGCG 5520  
 DB 5461 TGTGAGAGTCAAGCGGTTGGGATGCTGATGAGCGCATTTATTAAGAGAGAGAGATGCG 5520  
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DB 5521 ATCCACCGGACAGGAGCAAAAGGCTATCCGGGCAATGCTGTTCAAGCCTTTGAATTA 5580  
 QY 5581 CGTTTCTCTCTCAATCTAGTTAATGATTTTGAATGTTAATGATGATGCTG 5640  
 DB 5581 CGTTTCTCTCTCAATCTAGTTAATGATTTTGAATGTTAATGATGATGCTG 5640  
 QY 5641 TCAATCTGAGAACTATAGTCAAGGCAAGGAGGATCTAATCCGACGACG 5700  
 DB 5641 TCAATCTGAGAACTATAGTCAAGGCAAGGAGGATCTAATCCGACGACG 5700  
 QY 5701 ACTAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
 DB 5701 ACTAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5760  
 QY 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
 DB 5761 GCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 5820  
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 DB 5821 CGAAGCAAGTACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 5880  
 QY 5881 GCGTGCATCTCTGACAGCGCTTACGAAAGACTTCTTTGCGGGAAGGCAATCCGATG 5940  
 DB 5881 GCGTGCATCTCTGACAGCGCTTACGAAAGACTTCTTTGCGGGAAGGCAATCCGATG 5940  
 QY 5941 AGGAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
 DB 5941 AGGAGAGCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6000  
 QY 6001 TCTCATCAAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 6060  
 DB 6001 TCTCATCAAGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 6060  
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 DB 6061 GCGGAAAGCAAAAGGCGCGGAGGAGGATGATGATGATGATGATGATGATG 6120  
 QY 6121 GCGATGCGGATATCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 6180  
 DB 6121 GCGATGCGGATATCCGATGATGATGATGATGATGATGATGATGATGATGATGATG 6180  
 QY 6181 CGCCGCGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
 DB 6181 CGCCGCGTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6240  
 QY 6241 AGAGTATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
 DB 6241 AGAGTATGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6300  
 QY 6301 CGCGGCGGCGGAGCAAGAGCGGAGGATGATGATGATGATGATGATGATGATG 6360  
 DB 6301 CGCGGCGGCGGAGCAAGAGCGGAGGATGATGATGATGATGATGATGATGATG 6360  
 QY 6361 CGCGGCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6420  
 DB 6361 CGCGGCTTCTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6420  
 QY 6421 ACTGCGATGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6480  
 DB 6421 ACTGCGATGCGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6480  
 QY 6481 CCCTCAAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6540  
 DB 6481 CCCTCAAGATGAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 6540

RESULT 2  
 US-08-337-339-7  
 ; Sequence 7, Application US/08337339  
 ; Patent No. 553864  
 ; GENERAL INFORMATION:

APPLICANT: Warmke, Jeffrey W.  
APPLICANT: Hall, Linda  
APPLICANT: Feng, Gouping  
APPLICANT: Van Der Ploeg, Leonardus  
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
TITLE OF INVENTION: PARA SODIUM CHANNEL  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: John W. Wallen III  
STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0900  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/337,339  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Wallen III, John W.  
REGISTRATION NUMBER: 35,403  
REFERENCE/DOCKET NUMBER: 19332  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-3905  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6513 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-337-339-7

Query Match 100.0%; Score 6513; DB 1; Length 6513;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCTAGAGTTGGCCGCGATGACATGACAGAAAGTTCCGATCTCGATATCTGAGGAAGAC 60  
DB 1 TCTAGAGTTGGCCGCGATGACATGACAGAAAGTTCCGATCTCGATATCTGAGGAAGAC 60  
QY 61 GCAGTTTGTCCGTCCTTTACCCGCGAATCATTTGGTGCATATGGAACAAACGCAATTGCG 120  
DB 61 GCAGTTTGTCCGTCCTTTACCCGCGAATCATTTGGTGCATATGGAACAAACGCAATTGCG 120  
QY 121 CTGAACATGAAAGCAGAGAGAGCTGAAAGAAAGAGCCGAGAGAGAGGTGCGCGAT 180  
DB 121 CTGAACATGAAAGCAGAGAGAGCTGAAAGAAAGAGCCGAGAGAGAGGTGCGCGAT 180  
QY 181 ATGTGCGCAGAAAAAAGAAAGAAATCCGATATGATGACAGAGAGAGATGAGATC 240  
DB 181 ATGTGCGCAGAAAAAAGAAAGAAATCCGATATGATGACAGAGAGAGATGAGATC 240  
QY 241 CACAAACGCGATCTTACCTTGAACAGAGGTGCGCAATCTGTTGATTTGAGAGGAGCT 300  
DB 241 CACAAACGCGATCTTACCTTGAACAGAGGTGCGCAATCTGTTGATTTGAGAGGAGCT 300  
QY 301 TCCCGCGGAAATGGCCCTCCACTCTCTGAGAGATATCGATCTTACTACAGCAATGAC 360  
DB 301 TCCCGCGGAAATGGCCCTCCACTCTCTGAGAGATATCGATCTTACTACAGCAATGAC 360  
QY 361 TGAATTCGTATGTTGTAAGCAAGAAAGATATTTTTCGTTTTCGATCAAAAGCAA 420  
DB 361 TGAATTCGTATGTTGTAAGCAAGAAAGATATTTTTCGTTTTCGATCAAAAGCAA 420  
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DB 421 TGTGATGCTGCATTCATTCGATAGCTGATGAGTTCGATTTACATTTAGTGATC 480

DB 421 TGTGATGCTGCATTCATTCGATAGCTGATGAGTTCGATTTACATTTAGTGATC 480  
QY 481 CATTAATTTTCCCTTATTCATCATCCACAAATTTCTGTCATGATCTGTATGATATGC 540  
DB 481 CATTAATTTTCCCTTATTCATCATCCACAAATTTCTGTCATGATCTGTATGATATGC 540  
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DB 541 CGACAGCCCGCAGGTTGAGTCCACTGAGGTATTTACACCGGAATCTACATTTGAAT 600  
QY 601 CAGCTGTTAAAGTATGAGCAAGAGTTTCATTTTATGCGCGTTTACGTATCTTGAAGATG 660  
DB 601 CAGCTGTTAAAGTATGAGCAAGAGTTTCATTTTATGCGCGTTTACGTATCTTGAAGATG 660  
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DB 661 CATGAAATTTGCTGACCTTCTGATTAATAGCTTTTATGATGATGATGATGATGATG 720  
QY 721 TAGGTAATCTAGCAGCCCTGCGAAGTTTATGAGGTGCGAGCGCTTAAACCGTAGCA 780  
DB 721 TAGGTAATCTAGCAGCCCTGCGAAGTTTATGAGGTGCGAGCGCTTAAACCGTAGCA 780  
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DB 781 TTGTCCAGGCTTGAAGACATCTGCGAGCGCTGATCATGATCGGTGAAGATCTGCGCG 840  
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DB 841 ATGTGATTAATCTGACATGATTTCTCTGTCGTGTTGCGGTTATGAGGCTTACAGATCT 900  
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DB 1861 CGAATCCGTCACCCGATGTCGGAAGAGATGGGCGCATATAGTCCCTGATATG 1920  
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Db	6121	GGCATGGCGGTGATCCGGATCCGCGGAGCCCGCGCCCGATGAAGCAACGACCGCATG	6180
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RESULT 3			
US-08-724-095-7			
Sequence 7, Application US/08724095			
Patent No. 5688917			
GENERAL INFORMATION:			
APPLICANT: Warmke, Jeffrey W.			
APPLICANT: Hall, Linda			
APPLICANT: Feng, Gouping			
APPLICANT: Van Der Ploeg, Leonardus			
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE			
TITLE OF INVENTION: PARA SODIUM CHANNEL			
NUMBER OF SEQUENCES: 7			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: J. Mark Hand - Merck & Co., Inc.			
STREET: P. O. Box 2000 - 126 E. Lincoln Avenue			
CITY: Rahway			
STATE: New Jersey			
COUNTRY: USA			
ZIP: 07065-0907			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: FASTeq, Version #1.ds			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/724,095			
FILING DATE:			
CLASSIFICATION: 536			
ATTORNEY/AGENT INFORMATION:			
NAME: Hand, J. Mark			
REGISTRATION NUMBER: 36,545			

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1 REFERENCE/DOCKET NUMBER: 19332DA
2 TELECOMMUNICATION INFORMATION:
3 TELEPHONE: (908) 594-4305
4
5 TELEFAX: (908) 594-4720
6
7 INFORMATION FOR SEQ ID NO: 7:
8
9 SEQUENCE CHARACTERISTICS:
10
11 LENGTH: 6513 base pairs
12 TYPE: nucleic acid
13 STRANDEDNESS: single
14 TOPOLOGY: linear
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16 MOLECULE TYPE: cDNA
17
18 JS-08-724-095-7

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	Best Local	Similarity	100.0%	Prod. No. 0;			
	Matches 6513;	Conservative	0;	Mismatches	0;	Indels	0;
						Gaps	0;
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DB	1	TCCTAGACGTTGGCCGCATAGCAATGACAGAAAGTTCGACCTCGATATCTGAGAGAAAC	60				
QY	61	GCAGTTTGTCCTGGTCCCTTTACCCGCGCAATATGGTGCATATGGAACAGCATTTGCGG	120				
DB	61	GCAGTTTGTCCTGGTCCCTTTACCCGCGCAATATGGTGCATATGGAACAGCATTTGCGG	120				
QY	121	CTGAACATGAAAGCAGAAAGAGCTGTGAAGAAAGAGCCGAGGAGAGGTGCTCGCAT	180				
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QY	181	ATGTGTCCGAAGAAAAACAAAAAATCCGATATGAGACGAGGACGAGGATGAAGGTC	240				
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QY	241	CACAAACCGGATCTCAACCTTGACAGGGTGTGCCAATACCTTTGATTTGCAAGGACCT	300				
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QY	661	CATGGAATTTGGCTGACCTTCGATGATATAGCTTTAGCTTATGTGACAAATGGGATATGATT	720				
DB	661	CATGGAATTTGGCTGACCTTCGATGATATAGCTTTAGCTTATGTGACAAATGGGATATGATT	720				
QY	721	TAGTAAATCTAGACACCTTCGACAGCTTTAAGGTGTGCGAGCGCTTAAACCGTAGCCA	780				
DB	721	TAGTAAATCTAGACACCTTCGACAGCTTTAAGGTGTGCGAGCGCTTAAACCGTAGCCA	780				
QY	781	TTGTGCCAGGCTTGAAGAACATCGTCGGGCGGTATCGAATCCGGTGAAGATCTCGCG	840				
DB	781	TTGTGCCAGGCTTGAAGAACATCGTCGGGCGGTATCGAATCCGGTGAAGATCTCGCG	840				

QY 841 ATGATATATCTGACATGTTCTCCGTTGCTGCTGTTGATGAGGCGCTACAGATCT 900  
DB 841 ATGATATATCTGACATGTTCTCCGTTGCTGCTGTTGATGAGGCGCTACAGATCT 900  
QY 901 ATATGAGGCTGCTCAACGAGAAAGTGCATCAAGAAATTCCTGAGACGTTCTGAGGCA 960  
DB 901 ATATGAGGCTGCTCAACGAGAAAGTGCATCAAGAAATTCCTGAGACGTTCTGAGGCA 960  
QY 961 ATCTGACCGACGAGAACTGGGACTATCAATTCGCAATAGCTCCAAATTTGATTCGAGG 1020  
DB 961 ATCTGACCGACGAGAACTGGGACTATCAATTCGCAATAGCTCCAAATTTGATTCGAGG 1020  
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DB 1021 ACGAGGCGATCTCAATTCGTTATGCGGCAATATATCCGTTGCGGAGCAATGCGAGCG 1080  
QY 1081 ATTAAGTGTGCTGACGAGGAGTTGTGTCGAAATCCGAATTAATGACTACACAGCTTCGATT 1140  
DB 1081 ATTAAGTGTGCTGACGAGGAGTTGTGTCGAAATCCGAATTAATGACTACACAGCTTCGATT 1140  
QY 1141 CGTTGCGATGGGCTTCTGTCGCGCTTCGCGCTGATGACACAGGACTTCTGAGGAGATC 1200  
DB 1141 CGTTGCGATGGGCTTCTGTCGCGCTTCGCGCTGATGACACAGGACTTCTGAGGAGATC 1200  
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DB 1201 TGTACAGCTGTGTGTGCGCGCGCGGACCATGSCATGCTGTTCTTTATAGCATCA 1260  
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DB 1261 TCTTCTAGGTTCAATCTATCTTGTGAATTTGATTTTGGCCATTTGTTCCCATGTCGATG 1320  
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QY 1381 CGGAAGAGCTGCGCGCGCGCAAGAGGCGCAAGCTGGAAGAGGCGCAATGCGAGCTC 1440  
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DB 1441 AGGAGAGCGGAGTGCCTGCGCGCGGAGAGGCTGCACTGCATCCGAAATGCGCAAGA 1500  
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DB 1501 GTCCGAGCTATCTTGTGATCAAGCTATGAGCTATTTGTTGGCGGCAAGGCGCAAGT 1560  
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DB 1561 ACAACAACAAGAGAAGTGCATTCGAGAGCTGAGAGTGAAGTGCAGAGTGCAGAGC 1620  
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DB 1681 GCACGACATCTTATCTTACCTGCTGACCGTTTAAATAGCGAGGAGTACCTAGATT 1740  
QY 1741 CTCACAGTACAGATACGGAACGAGAGTGGCGCTTGTGATTAACCGGTTGCGATCTGA 1800  
DB 1741 CTCACAGTACAGATACGGAACGAGAGTGGCGCTTGTGATTAACCGGTTGCGATCTGA 1800  
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DB 1801 AGCCATTGTTATTCACATATCAGATGCGCAGACACTTGGCTTATGCGGAGCT 1860  
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DB 1861 CGAATGCCGTCAACCCGATGTCGGAAGAAATGGGCGCATCATAGTCCCGTGTATG 1920  
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DB 1921 GCAATCTAGGCTCCGACATCATGTATACCTGCGATCAAGTCCGGAATATCTATACCT 1980  
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DB 1981 CACATGGCATCTACCTGCGCGGATGCGCTGATGAGGCGTCAAGCAATGACCAAGAGA 2040  
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RESULT 4  
PCT-US95-14262-7  
Sequence 7, Application PC/TUS9514262  
GENERAL INFORMATION:  
APPLICANT: Warmke, Jeffrey W.  
APPLICANT: Van Der Ploeg, Leonardus  
TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
NUMBER OF INVENTIONS: PARA SODIUM CHANNEL  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jack L. Tribble  
STREET: P.O. Box 2000, 126 E. Lincoln Avenue  
CITY: Rahway  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/14262  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Tribble, Jack L.  
REGISTRATION NUMBER: 32,633  
REFERENCE/DOCKET NUMBER: 19338 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908) 594-5321  
TELEFAX: (908) 594-4720  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6513 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
PCT-US95-14262-7  
  
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Matches 6513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1141 CGTTCGATGAGCTTTCTGTCGCTTCGCTTCGCTGATGACACAGACTTCTGAGAGATC 1200  
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QY 1381 CGAAGAGAGCTGCGCGCCGAGAGAGGCGCAAGCTGAGAGAGGCGCAATGAGCAAGCTC 1440  
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DB 2341 ATGACGAGATGAGGCGGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2400



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RESULT 5  
 PCT-US95-14378-7  
 ; Sequence 7, Application PC/TUS9514378  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Warmke, Jeffrey W.  
 ; APPLICANT: Hall, Linda  
 ; APPLICANT: Feng, Gouping  
 ; APPLICANT: Van Der Ploeg, Leonardus  
 ; TITLE OF INVENTION: PROCESS FOR FUNCTIONAL EXPRESSION OF THE  
 ; TITLE OF INVENTION: PARA SODIUM CHANNEL  
 ; NUMBER OF SEQUENCES: 7  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Roy D. Meredith

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1 STREET: P.O. Box 2000, 126 E. Lincoln Avenue
2 CITY: Rahway
3 STATE: New Jersey
4 COUNTRY: USA
5 ZIP: 07065-0907
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: PatentIn Release #1.0, Version #1.25
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: PCT/US95/14378
13 FILING DATE:
14 CLASSIFICATION:
15 ATTORNEY/AGENT INFORMATION:
16 NAME: Meredith, Roy D.
17 REGISTRATION NUMBER: 30,777
18 REFERENCE/DOCKET NUMBER: 19332 PCT
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (908) 594-4678
21 TELEFAX: (908) 594-4720
22 INFORMATION FOR SEQ ID NO: 7:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 6513 base pairs
25 TYPE: nucleic acid
26 STRANDEDNESS: single
27 TOPOLOGY: linear
28 MOLECULE TYPE: cDNA
29 PCT-US95-14378-7

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Query Match	100.0%;	Score 6513;	DB 5;	Length 6513;
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	best	LocalSimilarity	100.0%;	Pred. No. 0;	Mismatches	6513;	Conservative	0;	Indels	0;	Gaps	0
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Db	1	TC	TACACG	TTGGCCCGCATGACATGACGAA	GATTCCGACCTCGAATCTGAGGAAGAAC	60						
QY	61	GCAG	TTGTTC	CGCTCCCTTTACCCGCGAATCA	TGTGTGCAATCGAACACGCAATTGCCG	120						
Db	61	GCAG	TTGTTC	CGCTCCCTTTACCCGCGAATCA	TGTGTGCAATCGAACACGCAATTGCCG	120						
QY	121	CTGAA	CAATGAAAAGAGAAAGAGAGCTG	GAAGAAAGAAAGAACCCGAGGAGGAGATGCCCGAT	180							
Db	121	CTGAA	CAATGAAAAGAGAAAGAGAGCTG	GAAGAAAGAAAGAACCCGAGGAGGAGATGCCCGAT	180							
QY	181	ATG	GTGCGAAGAAAAAACAAGAAATCC	GATATATACGAGACGAGATGAAAGATC	240							
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Db	781	TTGTGTCCAGGCTTGAAGACCAATCGTCGCGCGCGTCATGGAATCGGTGAAGAAATCTGCGCG	840
QY	841	ATGTGATTAATCTGACCAATGTTCTTCCTGTGCGGTGTTCCGGTTGATGAGGACCTTACAGATCT	900
Db	841	ATGTGATTAATCTGACCAATGTTCTTCCTGTGCGGTGTTCCGGTTGATGAGGACCTTACAGATCT	900
QY	901	ATATGAGGCGGTCTCACCGAAGAAAGTCATCAAGAAAGTTCCGCTGGACGGTTCTGAGGGACA	960
Db	901	ATATGAGGCGGTCTCACCGAAGAAAGTCATCAAGAAAGTTCCGCTGGACGGTTCTGAGGGACA	960
QY	961	ATCTGACCGACGAGAACTGGAGACTATCAAAATCGCAATAGCTCCAAATTGTAATTCGAGAG	1020
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QY	1021	ACGAGGGCATCTCAATTCCTGTTAATGCGGCATATATCCGGTGGCGGGCAATCCGACGACG	1080
Db	1021	ACGAGGGCATCTCAATTCCTGTTAATGCGGCATATATCCGGTGGCGGGCAATCCGACGACG	1080
QY	1081	ATTACGTTGCTGTACAGAGGGGTTTGGTCCGAATCCGAATTATGAGCTACACAGCTTCGAAATT	1140
Db	1081	ATTACGTTGCTGTACAGAGGGGTTTGGTCCGAATCCGAATTATGAGCTACACAGCTTCGAAATT	1140
QY	1141	CGTTGCGATGAGGCTTTCTCTGTCCGCTTCCGGCTGATGACACAGGACTTCTGGAGAGATC	1200
Db	1141	CGTTGCGATGAGGCTTTCTCTGTCCGCTTCCGGCTGATGACACAGGACTTCTGGAGAGATC	1200
QY	1201	TGTACGAGCTGTGTGTGGCGCGCGCGGACCATGTGGCAATGTCTGTTTATAGTACATCA	1260
Db	1201	TGTACGAGCTGTGTGTGGCGCGCGCGGACCATGTGGCAATGTCTGTTTATAGTACATCA	1260
QY	1261	TCTTCTTAGTTCATCTTATCTTGTGAATTTGATTTTGGCCATTGTTGCCAATGTGCTATG	1320
Db	1261	TCTTCTTAGTTCATCTTATCTTGTGAATTTGATTTTGGCCATTGTTGCCAATGTGCTATG	1320
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Db	1321	ACGAATTGCAAAAGAAAGGCGCGAAGAAAGGAGGAGGCTGCCGAAGAGAGGCGATACGTGAAG	1380
QY	1381	CGGAAGAAAGCTGCCGCGCCCAAAGCGGCAAGCTGTAGAGAACGGGCCAATGCGCAGGCTC	1440
Db	1381	CGGAAGAAAGCTGCCGCGCCCAAAGCGGCAAGCTGTAGAGAACGGGCCAATGCGCAGGCTC	1440
QY	1441	AGGACGACGCGGATGCGGCTGCGCGCGCAAGAGGCTGCACTGCATTCGGAAATGTGCCAAGA	1500
Db	1441	AGGACGACGCGGATGCGGCTGCGCGCGCAAGAGGCTGCACTGCATTCGGAAATGTGCCAAGA	1500
QY	1501	GTCGGAAGTATCTTGTGCAATCGAGTATAGGCTAATTTGTTGGGCGGAGAAAGGCAACGATG	1560
Db	1501	GTCGGAAGTATCTTGTGCAATCGAGTATAGGCTAATTTGTTGGGCGGAGAAAGGCAACGATG	1560
QY	1561	ACAAACAACAAAGAGAAATGTCATTCGGAAGCTCGAGGTGGAAGTCCGAGTCCGTTGACG	1620
Db	1561	ACAAACAACAAAGAGAAATGTCATTCGGAAGCTCGAGGTGGAAGTCCGAGTCCGTTGACG	1620
QY	1621	TTTATACAAAGCAACCGACACTTACACAGACACCAAGCTAACCAAGTTCTGTAAAGTGA	1680
Db	1621	TTTATACAAAGCAACCGACACTTACACAGACACCAAGCTAACCAAGTTCTGTAAAGTGA	1680

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## RESULT 6

US-08-808-793-24

Sequence 24, Application US/08080793

Patent No. 5858713

GENERAL INFORMATION:

APPLICANT: Soderlund, David M.

APPLICANT: Ingles, Patricia J.

TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS

TITLE OF INVENTION: AND USE THEREOF

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Nixon, Hargrave, Devans &amp; Doyle LLP

STREET: Clinton Square, P.O. Box 1051

CITY: Rochester

STATE: New York

COUNTRY: USA

ZIP: 14603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/808,793

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/034,361

FILING DATE: 24-DEC-1996

CLASSIFICATION: 435

APPLICATION NUMBER: US 60/012,649

FILING DATE: 01-MAR-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Braham, Susan J.

REGISTRATION NUMBER: 34,103

REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 716-263-1636

TELFAX: 716-263-1600  
 INFORMATION FOR SEQ ID NO: 24:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 6519 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 US-08-808-793-24

Query Match 94.6%; Score 6163.8; DB 2; Length 6519;  
 Best Local Similarity 97.7%; Pred. No. 0;  
 Matches 6339; Conservative 0; Mismatches 12; Indels 138; Gaps 3;

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QY 1944 TCGTATACCTTGACATGATCCGGAATATGATTAACCTCAATGAGAGATTAATCTGGGAGC 2003  
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QY 3204 GCCAGAGGCTTCAATCGAATTTGCGGATTTAAAGTTGGTTAAAGCCTAATATTGCTGAT 3263  
Db 3118 GCCAGAGGCTTCAATCGAATTTGCGGATTTAAAGTTGGTTAAAGCCTAATATTGCTGAT 3177  
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Db 3231 -----AGGACATGTGTGCAACGAACTGGAGCTG 3258  
QY 3384 GGCCACGACGAGATCTCGCGGAGCTCATCAAGAGGGAATCAAGAGACAGCGCA 3443  
Db 3259 GGCCACGACGAGATCTCGCGGAGCTCATCAAGAGGGAATCAAGAGACAGCGCA 3318  
QY 3444 CTGAGAGTGTGCTATCGGAGATCGATGGAATTTCAAGATCAAGCGGACATGAAGAAC 3503  
Db 3319 CTGAGAGTGTGCTATCGGAGATCGATGGAATTTCAAGATCAAGCGGACATGAAGAAC 3378

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Db 3379 AAGCCGAAGAAATCCAAATATCTAAATTAAGCAAC----- 3413  
QY 3564 CAAGCAATTAAGCTGGAACAGAGCTAAACATAGAGGTTGTCTTACAGACGAGC 3623  
Db 3414 -----GAGCAACAG 3423  
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Db 3424 ACTGCAGCAATTAATCTATATGTAAGCCATTAAGATTCAGACAGAGCCAC 3483  
QY 3684 AAGGCAAGCCGCGAGACGATGGAAGGCGAGAGAAAGCCGACGACGAAGAAGATTTA 3743  
Db 3484 AAGGCAAGCCGCGAGACGATGGAAGGCGAGAGAAAGCCGACGACGAAGAAGATTTA 3543  
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Db 3724 GGAATGGGCAATTAACGACTGAAATCTTCAATTAATTAAGAAATTAATTTGAACA 3783  
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Db 3964 GCGTGTGTGCTGATTTGCTGATTTGCTATGCTATGCTATCAACTTGTGCTTCA 4023  
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Db 4264 AAGCTCAGCAGAGATCATACCAATGCAATGCTGCGAGAGCGGAATCAACGCTG 4323  
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 DB 4444 AACCAACCAATTCGTGAAAGCAATCATGATATTTATTTTCATTCATCATA 4503  
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 QY 4824 TATATGCTATGAAAAAAGATGGGCTCTAAAAAAACATTTAAAGCCATTCAGAACCAAG 4883  
 DB 4624 TATATGCTATGAAAAAAGATGGGCTCTAAAAAAACATTTAAAGCCATTCAGAACCAAG 4683  
 QY 4884 TGGCGACACACACCAATATGCTTTGAAATAGTAAACCGATTAAGAAATTCGATATATCAT 4943  
 DB 4684 TGGCGACACACACCAATATGCTTTGAAATAGTAAACCGATTAAGAAATTCGATATATCAT 4743  
 QY 4944 ATGTTATTCATTTGCTGACATGTTACATGACATGACCTGATGTTACATGATGTTGAGAC 5003  
 DB 4744 ATGTTATTCATTTGCTGACATGTTACATGACATGACCTGATGTTACATGATGTTGAGAC 4803  
 QY 5004 ACCTATACACGCGTCTAGACATATCTCATGATGATTCGATATTTTCAGTTCCGAA 5063  
 DB 4804 ACCTATACACGCGTCTAGACATATCTCATGATGATTCGATATTTTCAGTTCCGAA 4863  
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 DB 4864 TGTCTATTAATAATATTCGCTTACATGATATCATTTTATTTAGACCATGAAATTTATTT 4923  
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 QY 5184 TACTGCTGTGCGCGACCTGCTCCAGATGATGATGATGATGATGATGATGATGATGATGAT 5243  
 DB 4984 TACTGCTGTGCGCGACCTGCTCCAGATGATGATGATGATGATGATGATGATGATGATGAT 5043  
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 DB 5044 CGACTGTGTAAGGAGGACCAAGGCGATTCGACATCTCTTCGCGTGGCATATGTCGCTG 5103  
 QY 5304 CCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5363  
 DB 5104 CCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5163  
 QY 5364 GCGATGTCGTTCTTCATGACAGTGAAGAGAGAGCGGCTTAAACGATCTCAACTTC 5423  
 DB 5164 GCGATGTCGTTCTTCATGACAGTGAAGAGAGAGCGGCTTAAACGATCTCAACTTC 5223  
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 DB 5224 AAGACCTTTGGCCAGACATGATCTCTCTTCATGATGATGATGATGATGATGATGATGATGAT 5283  
 QY 5484 GGTGATATGAGCGCATTTATCAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5543  
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 QY 5544 TATCCGGGCAATTTGTTGATGAGCGCGTGAATTAAGTTTCTCTCTCATCTAGTT 5603  
 DB 5344 TATCCGGGCAATTTGTTGATGAGCGCGTGAATTAAGTTTCTCTCTCATCTAGTT 5403  
 QY 5604 ATAAAGCTTTTGAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 5661  
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RESULT 8  
 US-08-808-793-1  
 ; Sequence 1, Application US/08080793  
 ; Patent No. 5858713  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soderlund, David M.  
 ; APPLICANT: Ingles, Patricia J.  
 ; TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS  
 ; NUMBER OF INVENTION: AND USE THEREOF  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
 ; STREET: Clinton Square, P.O. Box 1051  
 ; CITY: Rochester  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 14603  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/808,793  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/034,361  
 ; FILING DATE: 24-DEC-1996  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 60/012,649  
 ; FILING DATE: 01-MAR-1996  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Braman, Susan J.  
 ; REGISTRATION NUMBER: 34,103  
 ; REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 716-263-1636  
 ; TELEFAX: 716-263-1600  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6318 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: cDNA  
 ; US-08-808-793-1  
 Query Match 68.3%; Score 4447.8; DB 2; Length 6318;  
 Best Local Similarity 82.0%; Pred. No. 0;  
 Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;  
 QY 24 ATGACGAGAGATTCGACATCGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 83  
 DB 1 ATGACGAGAGATTCGACATCGATATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60  
 QY 84 CGGAAATCATTTGTTGCAATTCGAAACACGATTCGCTGAACATGAAAAAGCAAGAGAG 143  
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 QY 204 GAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 263  
 DB 149 -AGATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 207  
 QY 264 CAGGATGTCGCAATTCATCTGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
 DB 208 CAGGATGTCGCAATTCATCTGTTGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267



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268 CCTCTCGAGATATGATCCCTTCTACAGTATGTACTGACATTTGTTGTAATTAAGTAAA 327  
384 GAAAAAGATATTTTTCGCTTTTCTGATCAAAAAGCAATGTGAGCTCGATCCATTCAT 443  
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868 TGCATTTAAACGATTCCTGCTGAGCGTTCTGCGGCAATCTGACCGAGAGATGAGAC 927  
984 TATACATATGCGATATGCTCCATTTGTTGTTCCAGAGAGAGGAGATCTCATTTCCGTTA 1043  
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1228 GTGATTTGATTTTGGCATTGTTGCAATGCTGATGATGCAATTTGCAAGAGAGCGCAA 1287  
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1288 GAAAGAGAGCTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347

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2065 CCGATGCGATCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2124  
2169 GCTGCGAGAGATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2228  
2125 GCTGCGAGAGATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 2184  
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2281 GATGGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
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Qy	2529	GCAATGGATCAACACGATATGAAACAGAGATGGAAACGCGTGTCAAGATGGCACTAT	2588
Db	2461	GCCATGATCATCAACGACATGATATCCGGAAATTAGAAAGGCTGAAAGGGTAACTAT	2520
Qy	2589	TTCTTCAACCGCACCTTTGGCATGAGAGCCACATGAAAGCTAAAGGCATAGGCCAAG	2648
Db	2521	TTCTTCAACCGCACCTTTGGCATGAGAGCCACATGAAAGCTAAAGGCATAGGCCAAG	2580
Qy	2649	TACTATTTCCAGAGAGGCTGGAAACATCTTCACTTCATTAATCGAGGCCATATCGCTATG	2708
Db	2581	TACTATTTCCAGAGAGGCTGGAAACATTTTGATTTCAATTAATGAGGCTTGCTCTG	2640
Qy	2709	GAACTGGGACCTCGAGGGGTGTCAGAGGGTGTGTCGGTATTTGGCTCTTTCGATTTGCTGGCT	2768
Db	2641	GAATTTGGGCTCGAGAGGGGTGTCAGAGGGCTGTGCGATTTGTAAGATTTTCGTTGCTTCGT	2700
Qy	2769	GTATTTCAAACTGGGCAAGTCTTTGGCCCACTTAATTTATCTCATTTTGGATTAATGGACGC	2828
Db	2701	GTATTTCAAAATTTGGCAAAATCATGCCCCACACTCAATTTACATTTTCGATTAATGGCCGG	2760
Qy	2829	ACCAATGGGCGCTTTGGGTATCTGACATTTTGTACTTTGCAATTAATCATCTTTCATCTTTGGC	2888
Db	2761	ACAAATGGGTGATTTGGGTAACTGACATTTTGTACTTTGCAATTAATCATCTTTCATCTTTGGC	2820
Qy	2889	GTGAATGGGAATGCAACTGTTGCGAAAGAAATATCATATCAACAAGAACCGCTTCCGGAT	2948
Db	2821	GTGAATGGGAATGCAACTTTTGGAAAGAACTATATTGACACAAGAAATCGCTTCAAGAC	2880
Qy	2949	GGCCACCTGCGCGCTGGAACTTCAACCGACTTTATGCAACAGCTTCATGATCGTGTCCGG	3008
Db	2881	CATGAATTAACCGCGCTGGAACTTCAACCGACTTCATGCAACAGCTTCATGATGTGTCCGA	2940
Qy	3009	GTGCTCTGCGGAAATGATTCGAATCCATGTGGGACATGCAATGACATGAGGGGAGATGCTCG	3068
Db	2941	GTGCTCTGCGGAGATGATTCGAATCCATGTGGGACATGCAATGATGAGGGGAGATGCTCG	3000
Qy	3069	TGCATTTCCCTCTCTTTGGCCACCGTGTGTCATGCGCAATCTTGTGATTAATCCTTTTC	3128
Db	3001	TGTATTAACCTCTCTTTGGCCACCGTGTGATTAAGCAATCTTGTGATTAATCCTTTTC	3060
Qy	3129	TTAGCTTGTCTTTGTGCAATTTTGGCTCATCTAGCTTATAGGCGCGACCTGCCGATAC	3188
Db	3061	TTAGCTTGTCTTTGTGCAACCTTGTGCTCATCTAGCTTATAGGCGCGACCTGCCGCAAT	3120
Qy	3189	GATACGAATAAATAGCCGAGGCTCTCATGCAATTTGGCCGATTTAAAGTTGGGTTAAG	3248
Db	3121	GATACGAATAAATAGCGAGGCTCTCATGCTATGCTGCTTTTAAAGATGGGTTAAG	3180
Qy	3249	CGTAAATATGCTGATTTGTTCAAGTTAATCGTAAACAAATTTGACAAATCAAAATAATGAT	3308
Db	3181	CGTAAATATGCTGATTTGTTTAAAGTTAATGCAAAATTTGACAAATCAAAATAATGAT	3240
Qy	3309	CAACCATACAGGTGAGAGGACCAACAGATCAAGTTGGAATGGAGCGAAGACATGCTGAC	3368
Db	3241	CAACCATACAGGTGAGAGGACCAACAGATCAAGTTGGAATGGAGCGAATGCTGAC	3261
Qy	3369	AACGAATCTGAGCTGGGCAACGAGATCTCTGCGCCGACGCTCATCTAAGAAAGGATC	3428
Db	3262	AATGAATCTGAGCTGGGCAACGAGATCTAAGAAATCAATGGGCGATGGCTTGATCAAAAAGGATG	3321
Qy	3429	AAGGAGCAGACGCACTGAGAGTGGCCATCGGGGATGCGAGTGAATTCAGATACAGGC	3488
Db	3322	AAGGCGAGACCCAGCTGAGAGTGGCCATTTGGCAATGGCATGGAGTTCCACATACATGAGC	3391
Qy	3489	GACATGAAGAACCAACAGCCGAAAGAAATCCAAATATCTAAATTAATGCAACAGATGATTTGGC	3548
Db	3382	GATATGAAGAACCAACAGCCGAAAGAAATCCAAATATCTAAGAACCAACAGATGATTTGGA	3441
Qy	3549	AACCTCAATTAACCAACAGCAATAGACTGGAACAGAGCTAAACATAGAGGTTTGTCC	3608

Db	3442	AACTCAATTAACCAACCAAGCAATTAAGCTGAAACATGAGCTTAACCAATAGAGTTGTGTC	3501
Qy	3609	TTTACAGAGCAACGACACTGCGCAGATTTACTCATATATGGTATGCCATTAAGATTCGACCAATTC	3668
Db	3502	ATACAGAGCAAGTAGCACTGCGACGATTTACTCATATATGGTATGCCATTAAGATTCGACCAATTC	3561
Qy	3669	AAGACAGAGAGCCCAAGAGGACAGCGCCGAGACGATGAGGGCGAGAGAGAGCCGACGCC	3728
Db	3562	AAGACAGAGAGCCCAAGAGGAGAGCGCCGAGACCATGAGGGCGAGAGAGAACCGGACGTC	3521
Qy	3729	AGCAAGAGAGATTTAGGCTCTGACGAGGAACGTGACGAGAGGGCCGATTCGAGAGAGGC	3788
Db	3622	AGCAAGAGAGAGCTTCGCGCCTCGACGAGGAACGTGACGAGAGGGCCGAGCGCATGAGAGGC	3681
Qy	3789	CCGCTCGACGGGTGATTCATTTATTCATGCG--ACACAGACGAGTATATCTCGATGGAATAT	3845
Db	3662	CAGCTGGATGGTGACATTTATTCATTCATGCGCAAAACGACGAGATATCGACGACTAT	3741
Qy	3846	CCAGCTGATTCGCTGCCCGCATTCGTACTATTAAGAAATTTCCGATCTTAAAGCCGTGACGAT	3905
Db	3742	CCGGCCGACCTGTTTCCCGCACTCGTACTTAAGAAAGTTTCCGATCTTAAAGCCGTGACGAG	3801
Qy	3906	GATTCGCCGCTTCGAGCAAGATGGGGCAATTTACGATGAAACTTTTCAATTAATTGA	3965
Db	3802	GACTGCGCGTCTGCGCAAGATGGGGCAATTTACGATGAAACTTTTCAATTAATTGA	3861
Qy	3966	AATAAATATTTTGAAGACAGCTGTATCATATGATTTTAATGATAGTACTTAACTTTGGCA	4025
Db	3862	AATAAATATTTTGAAGACCGAGTTATCATATGATTTTAATGATAGTACTTAACTTTGGCC	3921
Qy	4026	TTAGAGATGTACACTGCGCAAAAGCCATCTGACGAGATTTTATATCTATAGAC	4085
Db	3922	TTAGAGAGTGTACTTTAACCGGATCGACTGTCAATGAGATTAATCTGTACTAGAC	3981
Qy	4086	AGAAATTTACGGTTATATCTTTGGAATATGTATCAAGTGTGAGCGCTCGGCTTC	4145
Db	3982	AGGATATTTACGGTGTATCTTTTGGAGATGTATCAAAATGTTGGCCCTGGGCTTC	4041
Qy	4146	AAAGTGTACTTCACCAAGCGGTGTGGCTGATTTGCGTATGTGATGATATGCTT	4205
Db	4042	AAGGTTTACTTCACCAATGCTCGGTGTGGCTGATTTGCGTATGTGATGATATGCTT	4101
Qy	4206	ATCAACTTCGTTGCTTCACTTGTGAGCGTGGTATTAAGGCTTCAGACATATCGA	4265
Db	4102	ATAAATTTGGTTCGCTTGGTGGGCTTAATATATATACCGGTTTATGATCAATGCC	4161
Qy	4266	ACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCGATATGCAAGGCGATGAGGCTGTC	4325
Db	4162	ACACTGGCGCCCTTAAGGCCATTCGTCGTCGTCTGTAGATGGGAGGTATGAAGTTGTC	4221
Qy	4326	GTTAATGGCTGTGATCAAGCTATACCGTCACTTCAATATGCTATGGTGTGCTATA	4385
Db	4222	GTTAATGGCTGTGATCAAGCTATACCGTCACTTCAATATGCTATGGTGTGCTATA	4281
Qy	4386	TTTTGGCTAATTTTGGCATTAATGGGTGTACAGCTTTTGTCTGGAATAATTTTAAATGC	4445
Db	4282	TTTTGGCTAATTTTGGCATTAATGGGTGTACAGCTTTTGTCTGGAATAATTTTAAATGT	4341
Qy	4446	GAGGACATGAATGCAAGAGCTACGACGACGATCATACCAATTCGCATTCGCTGGAG	4505
Db	4342	AAAGATGTTATGACACTGTGCTAGCGCATGAATATCATACCGATCTTAATTCCTGGAAA	4401
Qy	4506	AGCGAGAACTACAGTGGGTGAATTCAGCAATGAATTTGATCTATGTAGAGTAACGCTAT	4565
Db	4402	AGTGAATCTACACTGGGAAATTTGGCAATGAATCTTGATCATGTAGATATGCTAT	4461
Qy	4566	CTGTGCTTTTCCAAGTGGCCACTTCAAAGGCTGATACAAATCATGAACGATGCTATC	4625
Db	4462	CTGTGCTTTTCCAAGTGGCCACTTCAAAGGCTGATACCAATCATGAACGATGCTAT	4521
Qy	4626	GATTCACAGAGGTGTGACAAACCAATTCGTGAACGAACCTTACATGATATTTAT	4685
Db	4522	GATTCACAGAGGTGTGACAAACCGATTCGAAGAAACAATATCTACATGATATTTAT	4581

QY 4686 TTCCGATCTTCATCATATTTGGATCCCTTTTACACATCAATCTGTGATGGTATTC 4745  
 Db 4582 TTCCGATCTTCATCATATTTGGATCCCTTTTACACATCAATCTGTGATGGTATTC 4641  
 QY 4746 ATTGATTAATTTTATGACAAAAGAAAAGAGAGGTGATCATTTGAAATGTTCTGACA 4805  
 Db 4642 ATTGATTAATTTTATGACAAAAGAAAAGAGGTGATCATTTGAAATGTTCTGACA 4701  
 QY 4806 GAAATTCGAAAAGAACTATTAATCTATGAAAAAGATGGGCTCTAAAAACCATTAATA 4865  
 Db 4702 GAAATTCGAAAAGAACTATTAATCTATGAAAAAGATGGGCTCTAAAAACCATTAATA 4761  
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 Db 4762 GCCATTCGAAAGCCAAAGGTGGACACACAGCAATAGTAAATAGTAAACGATAG 4821  
 QY 4926 AAATTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4985  
 Db 4822 AAATTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 4881  
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 Db 4882 CGTTACGATGCGTCGACACGATTAACGCGCTCTAGACATCTCAATGCGATTTGTA 4941  
 QY 5046 GTTATTTTCAGTTCGAAATGCTATTAATAAATTCGCTTACGATACATATTTTAT 5105  
 Db 4942 GTTATTTTCAGTTCGAAATGCTATTAATAAATTCGCTTACGATACATATTTTAT 5001  
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 Db 5002 GAGCATGGAATTTATTTATGATGATGATGATGATGATGATGATGATGATGATGATG 5061  
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 Db 5062 AGCATATTTATGAGAGTACTTCTGTGCGCCGACCTGCTCCGAGTGTGCGTGTGCG 5121  
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 QY 5286 GCGTGGGCGATGCGTCCGCGCCCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTG 5345  
 Db 5182 GCGTGGGCGATGCGTCCGCGCCCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTG 5241  
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 Db 5242 TTCAATCTTTGCGCATTTTCCGAGTGTGCTTTCATGACGTTGAGAGAGAGAGAGAG 5301  
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 Db 5302 AACGACGCTACCACTTCAACACCTTTGGCCAGAGCATGATCTGCTTTCAATGCTG 5361  
 QY 5466 ACCTCAGCGCGTGGGATGCTGTAAGCCATTAATCAATGAGAGAGAGAGAGAGAGAG 5525  
 Db 5362 ACCTCAGCGCGTGGGATGCTGTAAGCCATTAATCAATGAGAGAGAGAGAGAGAGAG 5421  
 QY 5526 CCCGACAGCGCAAAAGGCTATCCGCGCAATTTGTGCTCAGGACCGCTTGAATAACGTTT 5585  
 Db 5422 CCCGACAGCGCAAAAGGCTATCCGCGCAATTTGTGCTCAGGACCGCTTGAATAACGTTT 5481  
 QY 5586 CTCTCTCATACCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5645  
 Db 5482 CTCTCTCATACCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 5541  
 QY 5646 CTCGAGAACTAATGATGAGGACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5705  
 Db 5542 CTCGAGAACTAATGATGAGGACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5601  
 QY 5706 GACATGTAATTAATGATGAGGACCGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5765  
 Db 5602 GATATGTAATTAATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5661

QY 5766 GATCAGCTGTCGGAATTCCTGAGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5825  
 Db 5662 GATCAGCTGTCGGAATTCCTGAGAGTACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5721  
 QY 5826 AAGTACAGATCATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5885  
 Db 5722 AAGTACAGATCATATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5781  
 QY 5886 GATCCTCTGAGCGGCTTACGAAAGATCTTTTGGCGGAGGAGGAGGAGGAGGAGGAGGAG 5945  
 Db 5782 GATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5841  
 QY 5946 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
 Db 5842 ACGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
 QY 6006 TCAACGCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6065  
 Db 5902 TCAACGCTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5961  
 QY 6066 AAGCAAGAGGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6125  
 Db 5962 CGTTACAAAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5994  
 QY 6126 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6185  
 Db 5995 GAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6054  
 QY 6186 GCTGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
 Db 6055 GCTGTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6114  
 QY 6246 AATGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6305  
 Db 6115 AATGTAATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6159  
 QY 6306 GCGGCGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6365  
 Db 6160 GCGGCGGCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6219  
 QY 6366 GTTCTGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6425  
 Db 6220 GTTCTGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6279  
 QY 6426 CGATGCGGAGCATCATGTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6464  
 Db 6280 AGATGCGGAGCATCATGTCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6318

RESULT 9  
 US-08-772-512A-1  
 : Sequence 1, Application US/08772512A  
 : Patent No. 6022705  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Soderlund, David M.  
 : APPLICANT: Knipple, Douglas C.  
 : APPLICANT: Ingles, Patricia J.  
 : TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM  
 : TITLE OF INVENTION: INSECTICIDE-SUSCEPTIBLE AND INSECTICIDE-RESISTANT HOUSE  
 : NUMBER OF SEQUENCES: 19  
 :  
 : CORRESPONDENCE ADDRESSES:  
 : ADDRESSEE: NIXON, HARGRAVE, DEVANS & DOYLE LLP  
 : STREET: P.O. Box 1051, Clinton Square  
 : CITY: Rochester  
 : STATE: New York  
 : COUNTRY: USA  
 : ZIP: 14603  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/772,512A  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/608,618  
;; FILING DATE: 01-MAR-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Braman, Susan J.  
;; REGISTRATION NUMBER: 34,103  
;; REFERENCE/DOCKET NUMBER: 19603/601 (CRPD-1657)  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 716-263-1636  
;; TELEFAX: 716-263-1600  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 6318 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA  
;; US-08-772-512A-1

Query Match 68.3%; Score 4447.8; DB 3; Length 6318;  
Best Local Similarity 82.0%; Pred. No. 0;  
Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;

QY 24 ATGACGAAAGATTCCGATCTCGATATCTGAGAGAAACGCACTTTGTCCTCCCTTACC 83  
DB 1 ATGACGAAAGATTCCGATCTCGATATCTGAGAGAAACGCACTTTGTCCTCCCTTACC 60  
QY 84 CGGATTCATTTGGTGAATAATCGAACAAGCATTCGCGCTGAAACATGAAAAAGAGAG 143  
DB 61 CGGATTCATTTGGTGAATAATCGAACAAGCATTCGCGCTGAAACATGAAAAAGAGAG 117  
QY 144 CTGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 203  
DB 118 CTGGAAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 148  
QY 204 GAATTCGATATGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263  
DB 149 -AGATCGATATGATGACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207  
QY 264 CAGGAGTGCATTAACCTGTTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 323  
DB 208 CAGGAGTGCATTAACCTGTTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 267  
QY 324 CCTCTGAGAGATATGATCCCTTAAGCAATGTAATGATTCGATTCGATTCGATTCGATTC 383  
DB 268 CCTCTGAGAGATATGATCCCTTAAGCAATGTAATGATTCGATTCGATTCGATTCGATTC 327  
QY 384 GGAAGAATTTTGGCTTTTCTGATCAAAAGCAATGATGATTCGATTCGATTCGATTCGATTC 443  
DB 328 GGAAGAATTTTGGCTTTTCTGATCAAAAGCAATGATGATTCGATTCGATTCGATTCGATTC 387  
QY 444 CGCATAGCTGCTGAGCATTTACATTTAGTGCATTCATTTATTTTCCCTATTCATTCATTC 503  
DB 388 CGCATAGCTGCTGAGCATTTACATTTAGTGCATTCATTTATTTTCCCTATTCATTCATTC 447  
QY 504 ACCACAATTCGCTCAACCTGATCTGATGATTAATGCGCAACGCGCCACGCTTGAATTC 563  
DB 448 ACCACAATTCGCTCAACCTGATCTGATGATTAATGCGCAACGCGCCACGCTTGAATTC 507  
QY 564 ACTGAGTGAATTCACCGCAATCTACATTTGAATCAGCTGTTAAAGATGAGAGAGAGAG 623  
DB 508 ACTGAGTGAATTCACCGCAATCTACATTTGAATCAGCTGTTAAAGATGAGAGAGAGAG 567  
QY 624 GGTTCATTTATGCGCGTTTATGATCTTAGAGATGATGATGATGATGATGATGATGATGATG 683  
DB 568 GGTTCATTTATGCGCGTTTATGATCTTAGAGATGATGATGATGATGATGATGATGATGATG 627  
QY 684 GTAATAGCTTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 743

DB 628 GTAATAGCTTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 687  
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DB 688 ACATTTAGGCTGCTCGAGAGCGCTTAAACCGTAGCATTCGCGAGCTTGAAGCATTC 747  
QY 804 GTGCGCGCGCTGATCGAATCGGTGAAGATTCGCGAGATGATGATTCCTGACCATTCCTC 863  
DB 748 GTGCGCGCTGATCGAATCGGTGAAGATTCGCGAGATGATGATTCCTGACCATTCCTC 807  
QY 864 TCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923  
DB 808 TCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867  
QY 924 TGCATCAAGAATTCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 983  
DB 868 TGCATCAAGAATTCGCGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 927  
QY 984 TATCACAATCGCAATGATTCGCAATGATTCGCAATGATTCGCAATGATTCGCAATGATTCG 1043  
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DB 1048 GGTTCGAATTCGCAATGATTCGCAATGATTCGCAATGATTCGCAATGATTCGCAATGATTCG 1107  
QY 1164 GCTTCGCGCTGATGACACAGAGATTCGGAAGATTCGGAAGATTCGGAAGATTCGGAAGATTCG 1223  
DB 1108 GCTTCGCGCTGATGACACAGAGATTCGGAAGATTCGGAAGATTCGGAAGATTCGGAAGATTCG 1167  
QY 1224 GCGGCAATGAGCACTGCTGTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 1283  
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QY 1284 GTGAATTTGATTTGGCTGATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1343  
DB 1228 GTGAATTTGATTTGGCTGATTCGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1287  
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DB 1288 GAAGAAGAGCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347  
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QY 1584 ATTGCAAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643  
DB 1528 ATTGCAAGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1587  
QY 1644 ACCAGAGCAACCAAGCTACCAAGATTCGTAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 1703  
DB 1588 ACCAGAGCAACCC---GTAAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1644  
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DB 1645 GGTTCACATTTAACTACGCGGAGATCAGGATGATCAGGATGATCAGGATGATCAGGATGATCAG 1704  
QY 1764 GGAAGTGGCGCTGTTGATATCCCGTGAAGATTCGTAAGTGAAGAGAGAGAGAGAGAGAGAGAG 1823  
DB 1705 GGAAGTGGCGCTGTTGATATCCCGTGAAGATTCGTAAGTGAAGAGAGAGAGAGAGAGAGAGAG 1764

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1825 GAAGAGATGGGGCCATCATATGTCGCCGTATGATATGCAATCTAGGCTCCGACATCT 1884  
1944 TCGATATCTGCGATCACTCCGAAATATGATATCTGATGCGATCTATCTGCGCGC 2003  
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1945 ATGGGGCCATATGGGGCTGACGACCAATATGACCAAGAGACCAAAATTCGCAACCGCA 2004  
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2065 CCCGATGCCAATCAACAGGAACAAAGGATTTAGAAATGGGTGAGATTTATACAGACGA 2124  
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2289 AGTGGGGCAAGCATGCGGTGCTCTCGTTTATCTATTTCCAAAGAGAGCATGACGAG 2348  
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2409 TGTGATGGGACATGCTGCTGGGTTGTTGAATTTGAGAGTGGGTATCGCTCATGCTC 2468  
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2461 GCATATGATCAACGATATGACAGAGATGACAGCGCTGCTCAAGATGGGTATGAT 2520  
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2521 TTCTTACCGGCACTTTTGCATATGACAGCATGATGATGATGATGATGATGATGATGAT 2580  
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2701 GTATTTCAATGCGCAATCTTGGCCCACTTAACTTACTCATTTGATTTGAGGACG 2760  
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3241 CAACCAT-----AGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3261  
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3322 AAGGAGCAAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3381  
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3502 ATACAGAGCAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 3561  
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3562 AAGGAGCAAGCAACAGGCGCAAGAAATCCAAATATCTTAAATTAACGCAACGATGATGATGATGATGATGAT 3621  
3729 AGCAAGAGATTTAGTCTTCAAGAGAACTGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3788  
3622 AGCAAGAGATTTAGTCTTCAAGAGAACTGACAGAGAACTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3681  
3789 CCGCTGACCGGTGATCATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3845  
3682 CAGCTGATGATGATCATATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3741  
3846 CCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3905  
3742 CCGGCGCAAGTCTTCCGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3801  
3906 GACTGCGCTTCTGCAAGAGTGGGCAATTTAGACTGAATTTAGACTGAATTTAGACTGAATTTAGACTGAAT 3965  
3802 GACTGCGCTTCTGCAAGAGTGGGCAATTTAGACTGAATTTAGACTGAATTTAGACTGAATTTAGACTGAAT 3861  
3966 AATAAATATTTTGAAGAGCTGATATCATATGATTTTAAATGATGATTTAGACTGATTTAGACTGATTTAGACT 4025







QY	1464	GC	GA	AAGGCTG	CA	CTG	CA	TGC	AT	CCG	GA	AATGG	CC	AA	AGTCC	GA	GTG	AT	TTG	CA	TAG	CAG	1523
Db	1408	GC	CGCTGG	CG	CAG	CT	CTG	CA	TCC	GA	TGG	CA	AA	AGT	CC	CA	GT	CA	TT	GC	AT	TAG	1467
QY	1524	TAT	GACTAT	T	T	T	T	T	T	G	CG	GA	AGG	CA	CA	G	AT	GA	CA	CA	A	A	1583
Db	1468	TAT	GA	CA	CT	G	T	T	T	T	T	G	CG	GA	AGG	CA	CA	G	AT	GA	CA	A	1527
QY	1584	ATT	CG	AG	CG	CT	CG	AG	TG	GA	GT	CG	GA	TG	CG	TT	TA	CA	AA	CA	CA	CG	1643
Db	1528	ATT	AG	CG	AG	CG	CT	CG	AG	TG	GA	GT	CG	GA	TG	CG	TT	TA	CA	AA	CA	CA	1587
QY	1644	ACC	A	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	1703	
Db	1588	ACC	A	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	CA	1644	
QY	1704	G	TT	C	A	C	G	T	T	T	A	A	C	G	A	G	G	A	T	T	C	A	1763
Db	1645	G	TT	C	A	C	A	T	T	A	A	C	G	A	G	G	A	T	T	C	A	A	1704
QY	1764	G	GA	G	T	G	CG	CG	CT	T	G	GA	T	CC	G	GA	T	CG	GA	T	CG	GA	1823
Db	1705	G	GA	G	T	G	CG	CG	CT	T	G	GA	T	CC	G	GA	T	CG	GA	T	CG	GA	1764
QY	1824	C	A	G	A	T	G	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	1883	
Db	1765	C	A	G	A	T	G	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	1824	
QY	1884	G	A	A	G	A	T	G	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	1943	
Db	1825	G	A	A	G	A	T	G	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	CG	1884	
QY	1944	T	C	G	A	T	A	C	T	T	G	A	T	A	T	A	T	A	T	A	T	A	2003
Db	1885	T	C	A	T	A	C	T	T	G	A	T	A	T	A	T	A	T	A	T	A	T	1944
QY	2004	A	T	G	C	C	G	T	C	A	T	G	C	A	T	G	C	A	T	G	C	A	2063
Db	1945	A	T	G	C	C	G	T	C	A	T	G	C	A	T	G	C	A	T	G	C	A	2004
QY	2064	C	G	A	A	T	C	A	T	A	G	G	G	G	C	A	C	A	A	T	G	G	2123
Db	2005	C	G	A	A	T	C	A	T	A	G	G	G	G	C	A	C	A	A	T	G	G	2064
QY	2124	C	T	C	G	A	T	-----	C	A	T	G	C	A	T	A	T	A	T	A	T	A	2168
Db	2065	C	C	C	A	T	G	C	A	T	A	T	A	T	A	T	A	T	A	T	A	T	2124
QY	2169	G	C	T	G	C	A	A	G	T	T	A	A	C	A	T	C	T	T	T	T	T	2228
Db	2125	G	C	T	G	C	A	A	A	A	A	A	A	A	A	C	A	C	A	C	A	A	2184
QY	2229	G	T	T	A	T	A	G	A	A	G	T	A	T	A	G	T	A	T	A	G	A	2288
Db	2185	G	T	T	A	T	A	G	A	A	G	T	A	T	A	G	T	A	T	A	G	A	2244
QY	2289	A	G	T	G	G	C	A	G	C	A	T	G	C	G	T	G	T	C	T			

QY	2529	GCATGGATACACACGGTATGAAACAAGAGATGGAAGCGTGCACAGATGGCAATAT	2588
Db	2461	GCCTATGATCATCAACGACATGAATCCGGAAATTAGAGAAAGTGTGAAAATGTGTACTAT	2570
QY	2589	TTCTTCAACCGCACCTTTGCGATCGAGGCCACCATGAAGTAATAGCCATGAGCCCCAAG	2648
Db	2521	TTCTTCAACGGCCACTTTTGGCAATTGAAGCCAGCATGAAACTGATATGGCCATGAGGCCAAG	2580
QY	2649	TACTATTTCCAGAGAGGCGTGGAAACATCTTGACCTCATATATACGGGCCCTATGCGCTATTCG	2708
Db	2581	TACTACTTCCAGAGAGGCGTGGAAACATTTTGATTTCAATATATGTGGCTTGTCTCTGCTG	2640
QY	2709	GAACTGGGACTCGAGGCGTGTCCAGGGCTGTGCTGATATTTGCGTTCTTTTCGATTTGCTGCGT	2768
Db	2641	GAATTTGGCCCTGGAGGGGTGTCCAGGGCGTGTGCGGTGTGAGAAAGTTTTCGTTTGCTTCGT	2700
QY	2769	GTATTTCAAACCTGGCCAAAGTCTTTGGCCCACTTAATTAATTACTCATTTGATTTATGAGGACGC	2828
Db	2701	GTATTTCAAATTTGGCGAAATCATGTGCCACCACTCAATTTACTCATTTTGATTTATGAGGCGCG	2760
QY	2829	ACCAATGGAGCGCTTTGGGTAAATCTGACAAATTTGTACTTGTGACTTAATCATCTTCATCTTTGCG	2888
Db	2761	ACAATGGGTGATTTGGGTAAATCTGACAAATTTGTACTTGTGACTTAATCATCTTCATCTTTGCGC	2820
QY	2889	GTGATGGGAAATGCAACTGTTTCGAAAGAAATATATCATGATCAACAAGAACCGCTTTCGGAT	2948
Db	2821	GTGATGGGAAATGCAACTTTTCGAAAGAAATATATATGACCAACAAGGATTCGCTTCAMAGAC	2880
QY	2949	GGGACCTGCGCGCGCTGGAACTTCACGACCTTAATGACAGCCTTCATGATCGTGTCCGG	3008
Db	2881	CATGAATTTACCGCGCGCTGGAACTTTCACGACCTTCAATGACAGCCTTCATGATTTGTGTCCGA	2940
QY	3009	GTEGCTCTGCGAGAAATGATTCGAGTCCATGTGGGACTGATGTAACGTGGCGGATGTCTCG	3068
Db	2941	GTEGCTGCGGAGAGTGGATCGAGTCCATGTGGGACTGATGTAATGTGGCGGATGTACGC	3000
QY	3069	TGCAATTCCTTCTTCTTGCGCAACGCTGTGATCGGCAATCTGTGGTACTTAACCTTTTC	3128
Db	3001	TGATATCCCTTCTTCTTGCGCAACGCTGTGATGAGCAATCTGTGGTCTTAACTTTTC	3060
QY	3129	TTAGCCTTGTCTTTGTCCAAATTTTGTGCTCATCTAGCTTAATCAGGCCGCACTGCCGATAC	3188
Db	3061	TTAGCTTTGTCTTTGTCCAACTTTCGTTCAATCTAGTTTAATCAGGCCGCACTGCCGCAAT	3120
QY	3189	GATATCGAATTAATATAGCCGAGGCTTCAATCGAATTGGCCGATTTAAAGTTGGGCTTAAG	3248
Db	3121	GATATCGAATTAATTAATGAGGAGGCGCTTCAATCGATTTCTCGTTTAAAGATGGGCTGAAA	3180
QY	3249	CGTAATTTGTGCTATTTTTCAAATTAATCGTAACAATTTGAACAATTAATTAAGTAT	3308
Db	3181	CGTAATTTGTGCTATTTTTCAAATTAATCGTAACAATTTGAACAATTAATTAAGTATGAC	3240
QY	3309	CAACCATTCAGGTGAGAGGACCMACCAAGATCATGTGATTTGGAGCGAAGAGCATGTGAC	3368
Db	3241	CAACCATTC-----AGAACATCGCGAT	3261
QY	3369	AACGAATTCGAGCTGGGCGCAACGAGATCCTCGCGACGGCCTCATCAAGAAAGGGGATC	3428
Db	3362	AATTAACCTGGAGTTGGGTCAATGAGAAATCATGGGCGATGTGCTTGAATCAAAAAGGATATG	3321
QY	3429	AAGAGACGACGCAACTCGAGGTGTGCCATCGGGGATCGATGGAATTCACGATACACGGC	3488
Db	3322	AAGGGCGAGAACCGACTGGAGGTGTGCCATTTGGCGATGGCATGGAGTTCACGATATATGTGC	3381
QY	3489	GACATGAAGACAAACAAGCCGAGAGAAATCCAAATATCTAAATATACGACGATGATTTGGC	3548
Db	3382	GATATGAAGAAACAACAAGCCGAGAGAAATCAAAATTCATGAACAACAACGATATATTTGGA	3441
QY	3549	AACCTCAATTAACGACCAAGCAATATGACTGGGAACAGAGCTTAACCAATAGAGTTTGTGCC	3608
Db	3442	AACCTCAATTAACCAACCAAGCAATATGACTGGGAACAGAGCTTAACCAATAGAGTTTGTGCC	3501
QY	3609	TTTAAAGGACGACGACATGCGCAGATTAATCATATGTATGACCATTAAGATTCGACATTC	3668

Db	3502	ATACGAGACGATGACATCTGCGACGATTAATCTATATGGTAGCCATAAGATGACCATTC	3561
Qy	3669	AAGACGAGAGCCACAAAGGGCAGCGCCGAGACGATGAGGGCGAGAGAAAGCGACGCG	3728
Db	3562	AAGACGAGAGCCACAAAGGGCAGCGCCGAGACCATTCGAGGGCGAGAGAAAGCGACGCG	3621
Qy	3729	AGCAAGAGAGATTATAGTCTCGACGAGAACTGACGAGAGAGGGAATTGCGAGAGGGC	3786
Db	3622	AGCAAGAGAGACTTGGGCTCGACGAGAACTGACGAGAGAGGCGAGAGGCGATGAGGGC	3681
Qy	3789	CCGCTCGACGGGTATATCATTTATGATGC---ACACGACGAGAGATATCTCGATGATAT	3845
Db	3682	CAGCTGAGATGGTGACATTTATCTTATGCGGAAAACGACGACGAGATATGACGACATAT	3741
Qy	3846	CCAGCTGATTCCTGCCCCGATTCGTAATAAGAAATTTCCGATCTTAGCCGGTAGCAGAT	3905
Db	3742	CCGGCGCATGTGTTTCCCGACCTCGTACTACAAAGAAATTTCCGATCTTAGCCGGCGACGAG	3801
Qy	3906	GACTGCGCGTTCTGGCAGAGATGGGGCAATTTACGACTGAAAATTTCATTAATTAATGAA	3965
Db	3802	GACTGCGCGTTCTGGCAGAGATGGGGCAATTTACGACTGAAAATTTCATTAATTAATGAA	3861
Qy	3966	AATAAATTTTGAACACGCTGTATATCTATGATTTTAAATGATGCTTAGCTTAGGCA	4022
Db	3862	AATAAATTTTGAACACGAGTATATCTATGATTTTAAATGATGCTTAGCTTAGCTAGCC	3921
Qy	4026	TTAGAGATGTACATCTGCGACAAAGACCACATCTGACAGATATTTATTAATTAATGAGC	4085
Db	3922	TTAGAGATGTTCATTTACCTGACCTGTGACGAGATATCTGATCTACATGAGAC	3981
Qy	4086	AGATATTTTACGGTATATTTCTTCTTGAAATGTTATATCAAGTGTGGCGCTGCGCTTC	4145
Db	3982	AGATATTTTACGGTATATTTCTTCTTGAGATGTTGATCAATGTTGGCCCTGCGGCTTT	4041
Qy	4146	AAAGTATCTTCCAAAGCGGTGTGTGCTGCGATTTCCGATTTGTCATGATGATACGGTT	4205
Db	4042	AAGTATCTTCCAAAGTGTGTGCTGCGATTTCCGATTTGTCATGATGATACGGTT	4101
Qy	4206	ATCAACTTCGTGCTTCACTTGTGTGAGACTGGTGTATTTCAAGCTTCAAGACTATGCGA	4265
Db	4102	ATTAATTTGTTGCCGTTTGGTCGGGCTTAAATGATATAGCCGTGTTATGATCAATGCGC	4161
Qy	4266	ACGTTAAGAGCACTGAGACCACTACGTGCCATGTCCGATATGACAGGCGATGAGGGTCGTC	4325
Db	4162	ACACTGCGCGCCCTTAAGGCCACTGTGCTGTCTGTATAGTGGAGGATATGAAAGTTGTC	4221
Qy	4326	GTTAATGGCGCTGTACAGCTATACCGTTCATCTTCATATGTGTCTATATGCTGTCTAATA	4385
Db	4222	GTTAATGGCGCTGTCAAGCTATACCGTTCATCTTCATATGTGTCTATATGCTGTCTAATA	4281
Qy	4386	TTTTGGCTAATTTTTGGCATATATGGGTGTACAGCTTTTGTGCGAAAATTTTAAAGTGC	4445
Db	4282	TTTTGGCTAATTTTTGGCATATATGGGTGTACAGCTTTTGTGCGAAAATTTTAAAGTGT	4341
Qy	4446	GAGACATGAATGGCAGCAAGCTCAGCCAGACGATCATACCAATTCGCAATGCTCGAG	4505
Db	4342	AAAGATGATATGACACTGTGCTGAGCCATGAATCATACCGAATCGTAAATGCTCGCAA	4401
Qy	4506	AGCGAAGACTACACGTGGGTGAATTCAGCAATGAATTTTCATCATATGATAGCGGTAT	4565
Db	4402	AGTGAATCTACACTGGGAAAATTTCCGCAATGAATTCGATCATATGATAGTGAATGCCGAT	4461
Qy	4566	CTGTGCTCTTTCCAAAGTGGCCACTTCAAGAGGCTGATACAAATCATGACAAAGATGCTATC	4625
Db	4462	CTGTGCTCTTTCCAAAGTGGCCACTTCAAGAGGCTGATACAAATCATGATAGTGAATGCCGAT	4521
Qy	4626	GATTCACGAGAGTGGACAAAGCAACCAATTCGTGAACGAACATCTACATGATATTAAT	4685
Db	4522	GATTCACGAGAGTGGACAAAGCAACCAATTCGTGAACGAACATCTACATGATATTAAT	4581
Qy	4686	TTGCTATTTCTCATATATTTGGAATCCTTTTTCACATCTCAATCTGTTCAATGGGTATATC	4745

Db	4582	TTGCAATCTTCATTAATTTGGACATATTTTTCACACCAATCTGTTCAATGGTGTTATC	4641
QY	4746	ATTGTAATATTTTAATGAGCAAAAGAAAAAGACAGGTGATCATTAAGAAATGTCATGACA	4805
Db	4642	ATTGTAATATTTTAATGAACAAAAAGAAAGAAAGCTGGTGATCATTAAGAAATGTCATGACA	4701
QY	4806	GAAAGTCAAGAAAAGTACTAATTAAGTCATGAAAAAGATGGGCTCTAATAAAACCATTTAAA	4865
Db	4702	GAAAGTCAAGAAAAGTACTAATTAAGTCATGAAAAAGATGGGCTCTAATAAAACCATTTAAA	4761
QY	4866	GCCATTCGAAGACCAAGGTGGCGACCAACAACATATAGCTTTGAAATGTGAACCGATTAAG	4925
Db	4762	GCCATTCGAAGACCAAGGTGGCGACCAACAACATATAGATTCGAAATAGTTACAGATAAA	4821
QY	4926	AAATTCGATATATATCATTTATGTTATTCATTTGATGTCGAACATGTTCAACATGACCTCGAT	4985
Db	4822	AAATTCGATATATATCATTTATGTTGTCATTTGCTTAACAATGTTTACATGACCTCGAT	4881
QY	4986	CGTTAACGATGGGTGGGACAGCTATAAGCGGTCTTAAGACTATCTCAATGCGATATTGCTA	5045
Db	4882	CGGTAACGACGGCTCCGAGCGGTACAAACATCTCTCGACAAACCTCAATGGGATATTGCTA	4941
QY	5046	GTTATTTTCAGTTCCGAAATGTCATTAATAAATATTCGGTTACGATATACATATTTATTT	5105
Db	4942	GTTATTTTCAGTTCCGCGAATGTCATTAATAAATATTCGGTTACGATATACATATTTCAA	5001
QY	5106	GAGCCATGGAATTTATTTGATGATGATGATGTCATTTATTCATCTTAAGTCTTGTAATT	5165
Db	5002	GAGCCATGGAATTTATTTGATGATGATGATGTCATTTATTCATCTTAAGTCTTGTAATT	5061
QY	5166	AGCGATATTTACGAAAGTACTTGTGTCCGCGACCTGCTCCGAGTGTGTCGTGGCG	5225
Db	5062	AGCGACATCATTTGAAAGATATTTGTATTCGCGCACATGCTCCGTTGTGTGAAGTGGCC	5121
QY	5226	AAAGTGGGCGGTGCTTCGACGTGTGAAGGAGACCAAGGSCATTCGGACACTGCTCTTC	5285
Db	5122	AAAGTGGGCGGTGCTTCGCGTTTATGTCAGAGGTGCCAAGGATATCCGACCTTGCTGTT	5181
QY	5286	GCGTTGGCAATGTCGTGTCGCGCCCTGTTCACATCTGCTGCTGCTGCTGCTGATG	5345
Db	5182	GCGTTAGCGAATGTCGTGTCGCTTATTCACATTTGTCTGTGCTGCTGCTGCTGATG	5241
QY	5346	TTCAATCTTTGCAATTTTGGCATGTGCTTCTTCATGCACTGAAGAGAGAGCGGCATT	5405
Db	5242	TTCAATCTTTGCTATCTTTGGCATGTGCTTCTTCATGATGTCACAAAGAGAGCGGCATA	5301
QY	5406	AAAGCAAGCTTCAACTTCAAGACCTTTGGCCAGACAGATATCCGTCTTTCAATATGTC	5465
Db	5302	AAATCTGTGATTAATTTTAAGACATTTTGGCCAAAGATATGATATTTGCTTTCAATATGTC	5361
QY	5466	ACGTCAAGCCGGTTGGAGTGTGTACTGAGCGCCATTAATCAATGAGAAAGCATGCGATCCA	5525
Db	5362	ACCTCAAGCCGGTTGGAGTGTGTGTAGATGCCATTAATCAATGAGAAAGATTTGGATCCA	5421
QY	5526	CCCGACAGCGCAAAAGGCTATCCGGGCAATTTGTGTTCAAGCAACGTTGGAATACGTTT	5585
Db	5422	CCCGACAAACGCAAGGCGTATCCGGGCAATTTGTGTTCAAGCACTGTTGGAATACGTTT	5481
QY	5586	CTCTCTCATACCTAAGTTATTAAGCTTTTGTATAGTTATTAATATGTAATTTGCTGTCAAT	5645
Db	5482	CTCTCTCATATCTAAGTTATTAAGCTTTTGTATAGTTATTAATATGTAATTTGCTGTCAAT	5541
QY	5646	CTCGAAGAACTATAGTACAGGCCACCGAGAGACGTGCAAGAGGCTTAAACCGACGAGCTAC	5705
Db	5542	CTCGAAGAACTATAGTACAGGCCCTACCGAAGAGATGTACAGAGGGTCTCACCGACGAGCTAC	5601
QY	5706	GACATGTACTATAGATCTGGCAGCAATTCGATCCGAGGGGCAACCCAGTACATACGCTAT	5765
Db	5602	GATATGTACTATAGAGATTTGGCAACATTTGATCCGAGGGGCAACCCAGTACATACGCTAC	5661
QY	5766	GATATAGCTGTCCGAATTCCTGTGAGATCTGTGAGCCCGCGCTGCGAATTCACAAACGAC	5825
Db	5662	GACCAAGCTGTCCGAGTTTCTGTGAGATGTGTGTGAGCCCGCTGCGAATTCACAAACGAC	5721

QY	5826	AAGTACAAAGATCATATGCGATGAGATACCAATCTGTGCGGGTGAACCTCATGTATCTGCGTC	5885
Db	5722	AAGTACAAAGATCATATGCGATGAGATACCAATCTGTGCGGGTGAACCTCATGTATCTGCGTC	5781
QY	5886	GACATCTCTGACGCGCTTTACGAAAGACTCTTTTGCGCGAAGGGCAATCCGATGAGAGG	5945
Db	5782	GATATATTTGATGCGCTTACCAAGACTCTTTTGCGCGAAGGGCAATCCGATGAGAGG	5841
QY	5946	ACGGGTGAGATTTGTGTAGATGACCGCGCCCGGATACGAGGGGTATGAGACCGGTCTCA	6005
Db	5942	ACGGGTGAGATTTGTGTAGATGACCGCGCGGACCGGACACCGAGGGGTATGATCCGTGTGCG	5901
QY	6006	TCAACGCTGTGTGCGCTCAAGCGTGAAGAGTACTGCGCCCGCTTAATTCAGCAAGCGCTTGCGGA	6065
Db	5902	TCAACGCTGTGTGCGCGACGCTGAAGAGTACTGCGCGCAAGCTGATCAAGATGCGTGTGCGG	5961
QY	6066	AAGCAACAAGCGCGCGCGGAGAGGTGGTCTTTGACCGGATACGGAATCATGCGAT	6125
Db	5962	CGTTACAAAGATGCGC-----CCACCCCGAGAGGGTGAT	5994
QY	6126	GGCGGTATCCGGATGCCGGGAGCCCGGCGCCGATGAAGCAACGGAAGCGGATGCCGCC	6189
Db	5995	GAGGCGGAGGCGGCGTGTGCGAAGAGTGTCTGAAGCGGCTGAAGGAGTGAAGAGGCGAGC	6055
QY	6186	GCTGTGTGAGATGAGTGTGTTAACGGTACTGTCAGAGAGAGCTGCCGATGCCGATGAGAGT	6245
Db	6055	GCGCGCGCGCGCGGTGATGTGTGTCTCAGCGACAGGACAGACCGCGCGCGGAGAGC	6114
QY	6246	AATGTAAATAGTCCGGGTGAGAGATGACAGCGCGCGCGAGACAGCAGCAGCAGCGGCG	6305
Db	6115	ACATCACCCCT-----CAATCCAGATGCGCGCGGAGAGAGATGTGTCAGC	6153
QY	6306	GCGCGCGGCGACAGACGACCGCGGGAAGTCCCGGAGCGGGTACGCGCGGCGACAGACCGCC	6365
Db	6160	GTCGCGCGCGCTTTATGTCCGCGCTGTGTATGTGCGCGCATATGCGCGCCAAAGCGCC	6219
QY	6366	GTTCTGTGTGAGAGCGAGCGGGTCTGTGACGAAGACGCGCACAGAGTGTATCATCTCG	6425
Db	6220	GTACTGTGTGAGAGGAGTGTGTTGTACAAAAGCGTCAATAGGTTGTAAATACACTCG	6273
QY	6426	CGATCGCGGAGCATCATCGTCCGCGACCGCGGAGTGTCTGA	6464
Db	6280	AGATCGCGGAGCATTAACATCCAGGACGCGACAGATGTCTGA	6318
RESULT 11			
US-08-808-793-2			
: Sequence 2, Application US/08808793			
: Patent No. 5858713			
: GENERAL INFORMATION:			
: APPLICANT: Soderlund, David M.			
: APPLICANT: Ingles, Patricia J.			
: TITLE OF INVENTION: CALCIUM PERMEABLE INSECT SODIUM CHANNELS			
: NUMBER OF SEQUENCES: 32			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP			
: STREET: Clinton Square, P.O. Box 1051			
: CITY: Rochester			
: STATE: New York			
: COUNTRY: USA			
: ZIP: 14603			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Floppy disk			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: PC-DOS/MS-DOS			
: SOFTWARE: Patentin Release #1.0, Version #1.30			
: CURRENT APPLICATION DATA:			
: FILING DATE: US/08/808,793			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA:			

Query Match	68.1%	Score 4434.2	DB 2	Length 6315
Best Local Similarity	81.8%	Pred. No. 0	Mismatches 1013	Indels 162
Matches 5284	Conservative	0	Gaps	8
<p>APPLICATION NUMBER: US 60/034,361            FILING DATE: 24-DEC-1996            CLASSIFICATION: 435            PRIOR APPLICATION DATA:            APPLICATION NUMBER: US 60/012,649            FILING DATE: 01-MAR-1996            CLASSIFICATION: 435            ATTORNEY/AGENT INFORMATION:            NAME: Braham, Susan J.            REGISTRATION NUMBER: 34,103            REFERENCE/DOCKET NUMBER: 19603/1062 (D-1906A)            TELECOMMUNICATION INFORMATION:            TELEPHONE: 716-263-1636            TELEFAX: 716-263-1600            INFORMATION FOR SEQ ID NO: 2:            SEQUENCE CHARACTERISTICS:            LENGTH: 6315 base pairs            TYPE: nucleic acid            STRANDEDNESS: single            TOPOLOGY: linear            MOLECULE TYPE: CDNA            US-08-808-793-2</p>				
Query	24	ATGACAGAAATTC	CGACTCGATATCTGAGAGAAACGCACTTTGTCCTCCCTTAC	83
Db	1	ATGACAGAAATTC	CGACTCGATATCTGAGAGAAACGCACTTTGTCCTCCCTTAC	60
Query	84	CGCGAATCATTTGGTGC	CAATGAAACAAACGCTTGGCCGTGAAACATGAAACAGAAAGAG	143
Db	61	CGCGAATCATTTGGTGC	CAATGAAACAAACGCTTGGCCGTGAAACATGAAACAGAAAGAG	117
Query	144	CTGGAAGAAAGAGAGCG	AGAGGAGGAGTGCCGATATGCTCCAGAAAAACAAAA	203
Db	118	CTGGAAGAAAGAGAGCG	AGAGGAGGAGTGCCGATATGCTCCAGAAAAACAAAA	148
Query	204	GAAATCCGATATGATG	ACGAGAGAGATGAAGTCCACACCGGATCTTACACTTGAA	263
Db	149	AGATATGATATGATG	ACGAGAGAGATGAAGTCCACACCGGATCTTACACTTGAA	207
Query	264	CAGAGTGGCCAAATAC	CTGTCGATGAGGAGCACTCCCGCCGGAATTTGAGCTCCACT	323
Db	208	CAGAGTGGCCAAATAC	CTGTCGATGAGGAGCACTCCCGCCGGAATTTGAGCTCCACT	267
Query	324	CCTCTCGAGATATGAT	CCCTACTACAGCAATGTATGACATTTGATGTAACAA	383
Db	268	CCTCTCGAGATATGAT	CCCTACTACAGCAATGTATGACATTTGATGTAACAA	327
Query	384	GGAAGAAATTTTGGT	CTTTCGATCAAAAGCAATGAGAGTCTGATCCATCAAT	443
Db	328	GGAAGAAATTTTGGT	CTTTCGATCAAAAGCAATGAGAGTCTGATCCATCAAT	387
Query	444	CCGATAGCTGCTGAG	CCATTTACATTTTCCCTATTTCAATC	503
Db	388	CCGATAGCTGCTGAG	CCATTTACATTTTCCCTATTTCAATC	447
Query	504	ACCAATTTCTGCTCA	CTGATCTGTATATGCCGACACGCCCACAGGTTGATGCC	563
Db	448	ACCAATTTCTGCTCA	CTGATCTGTATATGCCGACACGCCCACAGGTTGATGCC	507
Query	564	ACTGAGGATATTTCA	CCGGAATCTACATTTGATCAGCTGTTAAAGTATGGCACA	623
Db	508	ACTGAGGATATTTCA	CCGGAATCTACATTTGATCAGCTGTTAAAGTATGGCACA	567
Query	624	GGTTTCAATTTTATG	CCGTTTACGATCTTAAAGTATGGCACA	683
Db	568	GGTTTCAATTTTATG	CCGTTTACGATCTTAAAGTATGGCACA	627
Query	684	GTATATGCTTATGAT	GCATGGGTATATGATTTAGGTATATCTAGCAGCCCTTGGA	743

Dh 628 GTATAGCTTATGCTTATGACCATGCGCATATGAGTATGCTGACGCTTTGAGA 687  
Qy 744 ACGTTTGGGTGCTGCGAGCGCTTAAACCGTAGCATTTGCGAGGCTTGAAGCATC 803  
Db 688 ACATTATGGGTACGCGAGCTCTGAAAACCGTAGCATTTGCGAGGCTTAAAAACCAT 747  
Qy 804 GTGGGCGCGGTATCGATCGGTGAGAACTGCGCGCATGATATATCTGACCATGCTC 863  
Db 748 GTGCGGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807  
Qy 864 TCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 923  
Db 808 TCCCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 867  
Qy 924 TGCAATCAAGAGTTCCCGCTGAGAGGTTCTGCGGCGCATCTGACCGAGAACTGGGAC 983  
Db 868 TGCAATCAAGAGTTCCCGCTGAGAGGTTCTGCGGCGCATCTGACCGAGAACTGGGTT 927  
Qy 984 TATCACATCGCAATGAGCTCAATTTGGTATTCGAGAGAGGAGGATCTCATTTCCGTTA 1043  
Db 928 CTACACATGACACAGTTTCAATTTGGTATTCGAGAGAGGAGGATCTCATTTCCGTTG 987  
Qy 1044 TGCGGCAATATATCCGCTGCGGCGCATGCGACAGATTAAGTGTGCTGCGAGGCTTT 1103  
Db 988 TGCGGCAATGATATCCGCTGCGGCGCAATGCGGCAATGATGATGCTGCTGCGAGGCTTC 1047  
Qy 1104 GGTCCGAATCCGAATTTATGCTATACACAGCTTCCGATTTGCTGCTGCTGCTGCTGCT 1163  
Db 1048 GGGCCCAATCCCAATCTGACATACACAGCTTCCGATTTGCTGCTGCTGCTGCTGCTG 1107  
Qy 1164 GCTCTCGGCTGATGACACAGAGCTTCTGAGAGGATCTGACAGCTGCTGCTGCTGCTG 1223  
Db 1108 GCGTTTGTCTGATGACACAGAGCTTCTGAGAGGATCTGATGACAGCTGCTGAGCA 1167  
Qy 1224 GCGGCAATGACACAGCTGCTTATGATGATGATGATGATGATGATGATGATGATGAT 1283  
Db 1168 GCTGACCCCTGCGACATGTTGTTTATGATGATGATGATGATGATGATGATGATGATG 1227  
Qy 1284 GTGATTTGATTTTGGCATTTGTCATGTCGATGATGATGATGATGATGATGATGATGAT 1343  
Db 1228 GTGATTTGATTTTGGCATTTGTCATGTCGATGATGATGATGATGATGATGATGATGAT 1287  
Qy 1344 GAAGAGAGGCTGCGAAGAGAGAGGCGATGATGATGATGATGATGATGATGATGATGAT 1403  
Db 1288 GAAGAGAGGCTGCGAAGAGAGAGGCGATGATGATGATGATGATGATGATGATGATGAT 1347  
Qy 1404 GCGGCAATGATGAGAGAGGCGCATGCGAGCTGACGAGAGCGGATGCGGCTGCC 1463  
Db 1348 GCGGCAATGATGAGAGAGGCGCATGCGAGCTGACGAGAGCGGATGCGGCTGCCGAT 1407  
Qy 1464 GCGGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1523  
Db 1408 GCGGCTGCGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1467  
Qy 1524 TATGAGGATTTTGTGCGGAGAGAGGCGAATGATGATGATGATGATGATGATGATGATG 1583  
Db 1468 TATGAGGATTTTGTGCGGAGAGAGGCGAATGATGATGATGATGATGATGATGATGATG 1527  
Qy 1584 ATTGAGAGGCTGAGAGGAGAGAGGCTGAGAGGCTGATGATGATGATGATGATGATGAT 1643  
Db 1528 ATAGGAGGCTGAGAGGAGAGGAGAGGCTGAGAGGCTGATGATGATGATGATGATGATG 1587  
Qy 1644 ACCGAGAGGCTGAGAGGAGAGGAGAGGCTGAGAGGCTGATGATGATGATGATGATGAT 1703  
Db 1588 ACCGAGAGGCTGAGAGGAGAGGAGAGGCTGAGAGGCTGATGATGATGATGATGATGAT 1644  
Qy 1704 GGTTCACGCTTATACATGAGAGGAGAGGCTGAGAGGCTGATGATGATGATGATGATGAT 1763  
Db 1645 GGTTCACGCTTATACATGAGAGGAGAGGCTGAGAGGCTGATGATGATGATGATGATGAT 1704  
Qy 1764 GGAAGTGGCGCTTTGATATCCCGATGAGAGGCTGATGATGATGATGATGATGATGAT 1823  
Db 1705 GGGGCTGGAGCTTTTGGATATACAGATGAGAGGCTGATGATGATGATGATGATGATGAT 1764

Qy 1824 CAGATGCCAGAGCACTTGCCCTATGCGAGAGCTGATGAGGCTGACCCCGATGCC 1883  
Db 1765 CAGATGCCAGAGCACTTGCCCTATGCGAGAGCTGATGAGGCTGATGAGGCTGATGAGGCT 1824  
Qy 1884 GAAGAGATGGGCGCATATGATGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1943  
Db 1825 GAAGAGATGGGCGCATATGATGCTGCTGATGATGATGATGATGATGATGATGATGATGAT 1884  
Qy 1944 TCGTATACCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2003  
Db 1885 TCGTATACCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1944  
Qy 2004 ATGGCGCTGATGGGCGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063  
Db 1945 ATGGCGCTGATGGGCGTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2004  
Qy 2064 CGCAATCAATCAGTGGGCGGACCAATGCGGCGACCATGCTGACACCAATCACAG 2123  
Db 2005 CGCAATCAATCAGTGGGCGGACCAATGCGGCGACCATGCTGACACCAATCACAG 2064  
Qy 2124 CTGAT-----CATGCGACTACGAAATTTGCTGAGTGCAGGAGCGAA 2168  
Db 2065 CCCGATCCCAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2124  
Qy 2169 GCTGGCAAGTTAAACATGACATGACATGCTTTTATGAGGCGGCTGACAGAGAGAGAG 2228  
Db 2125 GCTGGCAAGTTAAACATGACATGACATGCTTTTATGAGGCGGCTGACAGAGAGAGAG 2184  
Qy 2229 GTTATATGAAGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2288  
Db 2185 GTTATATGAAGATGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 2244  
Qy 2289 AGTGGGCAAGCGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2348  
Db 2245 AGTGGGCAAGCGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2280  
Qy 2349 GATGGGCGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2408  
Db 2281 GATGGGCGAGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2340  
Qy 2409 TGTGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2468  
Db 2341 TGTGTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2400  
Qy 2469 TTGATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2528  
Db 2401 TTGATCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460  
Qy 2529 GCATGATCACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2588  
Db 2461 GCATGATCACCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2520  
Qy 2589 TTCTTACCGGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2648  
Db 2521 TTCTTACCGGCACTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2580  
Qy 2649 TACTATTTCAAGAGGCTGAGACATGCTGATGATGATGATGATGATGATGATGATGATG 2708  
Db 2581 TACTATTTCAAGAGGCTGAGACATGCTGATGATGATGATGATGATGATGATGATGATG 2640  
Qy 2709 GAATGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 2768  
Db 2641 GAATGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 2700  
Qy 2769 GTATTTCAATGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTG 2828  
Db 2701 GTATTTCAATGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTG 2760  
Qy 2829 ACATGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 2888  
Db 2761 ACATGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCTGAGAGGCT 2820

QY	2889	GTGATGGGAATNGCAACTGTTGGGAAAGAAATATCATGATCACAAGGACCGGCTTCCGGAT	2948
Dp	2821	GTGATGGGAATGCAACTTTTGGAAAGAACTATATTGACCAAGAGATCGCTTCAAGAC	2880
QY	2949	GGCGACCTGC CGCGTGGAACTTCCACGACTTTATGCAAGCTTCATGATCGTGTCCGG	3008
Dp	2881	CATGAATATACCGCGCTGGAAATTTCCACGACTTCATGCGACACTTCATGATTTGTTCGGA	2940
QY	3009	GTGCTTCGCGGAGAAATGGAATGGAATGCCATATGAGGACATGTAACGAGGAGATGTCG	3068
Dp	2941	GTGCTGTCGGAAGATGGATCGAGTCATGAGGACATGCAATGATATGAGGAGCATGTCAGC	3000
QY	3069	TGCATATCCCTCTCTTCTGGCCACCGTGTGCATCGGCATCTTGTTGTTACTTAACCTTTTC	3128
Dp	3001	TGTATACCTCTTCTTCTTGCCACCGGTGTGATCGGCATTTTGTGTGTTCTTTAATCTTTTC	3060
QY	3129	TTAGCCTTGCTTTTGTCCAAATTTTGGCTCATCTAGCTTATACAGCGCGCATCGCCGATAC	3188
Dp	3061	TTAGCTTTGTCTTTTGTCCAACTCGGTTCATCTGTTTATATAGCCGCCACATCGCCGACAT	3120
QY	3189	GATACGAATAAATAAGCCGAGGCGCTTCATGGAATGGCCGATTTAAAGTTGGGTTAAG	3248
Dp	3121	GATACGAATAAATAAGCAGAGGCGCTTCATGGAATGCTGTCTTTTAAAGCTGGGTGAA	3180
QY	3249	CGTAATATTTGCTGATTTGTTCAAGTTAATCGTAACAAATTGACAAATCAAAATAATGTCAT	3308
Dp	3181	CGTAATATTTGCGGATTTGTTTAAATTTGGAATAAATTGACAAATCAAAATAATGTCAC	3240
QY	3309	CAACCATAGGTGAGAGGACCAACCAAGATCAGTTGGATTGTGAGGAGACATGGTGCAC	3368
Dp	3241	CAACCATC-----AGAACATGGCGAT 3261	
QY	3369	AACGAATGAGCTGGGCGACGACGAGATCTCGCCGACGGCTCATCAGAAGGGGATC	3428
Dp	3362	AATGAATCTGAGTTGGGTCTAGACGAATTCATGGGCGATGGCTTGATCAAAAAGGATAG	3321
QY	3429	AAGGAGCAGACGGCACTGGAGTGGCCATCGGGGATCGGAATGGAATTCACGATACACGCG	3488
Dp	3322	AAGGCGGAGCCACAGCTGGAGTGGCCATTTGCGATGCGATGAGGTTCCATCATCATGCG	3391
QY	3489	GACATGGAAGAACCAAGCCGAGCAAGAAATCCAAATATCTTAAATTAACGCAACGATATTTGGC	3548
Dp	3382	GATATGAAAAACAAACAGGCCCAAGAAATCAAAATTCATAAACAACACAGATGATTGGA	3441
QY	3549	AACCTAATTAAACCAACAGACAAATBAGCTGGAACAACGACTTAAACATAGAGTTTGTCC	3608
Dp	3442	AACCTAATTAAACCAACAGACAAATBAGCTGGAACATGAGCTTAAACATAGAGTTTGTCC	3501
QY	3609	TTTACAGGACGACGACATCTGCAGCACTTAACTCATATGGTTACCCATTAAGAAATCGACCATTC	3668
Dp	3502	ATTACAGGACGATGACATCTGCAGCACTTAACTCATATGGTTACCCATTAAGAAATCGACCATTC	3561
QY	3669	AAGGACGAGACCCCAAGGCGCAGCGCTCGAGACGATGAGGGCGAGAGAGACGCGCAGCC	3728
Dp	3562	AAGGACGAGACCCCAAGGCGCAGCGCTCGAGACCATCGAGGGCGAGAGAAACGCGACGTC	3621
QY	3729	AGCAAGAGGAGATTTAAGTCTCGACGAGGAACTGGACGAGAGAGGGCGAATGCGAGAGGGGC	3788
Dp	3622	AGCAAGAGGAGCTTCGCGCTCGACGAGGAACTGGACGAGAGGGCCGAGGGCGAGTGAAGGC	3681
QY	3789	CCGCTCGACGGTGAATCATTAATTCATGC-----ACACGACGAGGATATCTCGATGAATAT	3845
Dp	3682	CAGCTGAGTGTGACATCATCAATTCATCCCAAACGACGACGAGATATCGACGACTAT	3741
QY	3846	CCAGCTGATTTGCTGCCCCGATTTGTAATTAAGAAATTTCCGATCTTAGCCGGTGAAGAT	3905
Dp	3742	CCGGCCGACTTTTCCCGACTCGATCAAGAGATTTCCGATCTTAGCCGGCGACGAG	3801
QY	3906	GACTTCGCGCTTCTGGCAAGAGATGGGGCAATTTAGACTGAATACTTTTCATTTAATGAA	3965
Dp	3802	GACTTCGCGCTTCTGGCAAGAGATGGGGCAATTTAGACTGAATACTTTTCATTTAATGAA	3861
QY	3966	AATTAATATTTTGAACAGCTGTATATCATATGATTTTAATGAGTAGCTTAGCTTTGGCA	4025

Db	3862	AAATAAATTTTGAACCGCAGTTTATCATATGATTTTAAAGATAGCTTAGCTTGGCC	3921
Oy	4026	TTAAGATGTACATCTGCCAACAAGACCATACTGCAGATATTTAACTAATATGAC	4085
Db	3922	TTAAGATGTGTCAATTTAACCCGATCGACCTGTCAAGAGGATTAATCTATCATGAC	3981
Oy	4086	AGAAATTTTACGATTAAATTTCTCTGGAAATGTAAATCAAGTGTGGCGCTGCCTC	4145
Db	3982	AGGATTTTACGATGATATTTCTTTTGGAGATGTGATCAAAATGTGGCCCTGGCTTT	4041
Oy	4146	AAAGTGAATCTTCAACCAACGCGTGTGTGGCTGCATTTCTGATGTCAATGCTTT	4205
Db	4042	AAGGTACTACTTCAACCAATGCTGTGTGTGGATTTTCGATTTGTCATCTATCCGTT	4101
Oy	4206	ATCAAACTTCGTGCTTCACTGTGTGGAGCTGTGTGTAAATCAAGCTTCAAGCATATGGA	4265
Db	4102	ATTAATTTGGTGCCTTGTGTGGGCTTAATATATATAGCCGCTTTAGATCAATGCC	4161
Oy	4266	ACGTTAAGACATCAGACCACTACGTGCCATGTCCCGTATGCAAGGCATGAGGCTGTC	4325
Db	4162	ACACTGGCGCCCTTAAGGCCATCTCGTGTGTCTTATAGTGAAGGATGAAGTTGTC	4221
Oy	4326	GTTAATGGCTGTGTACAAAGCTTAATCCGTCCATCTTCAATGTGCTATGTGCTATA	4385
Db	4222	GTTAATGGCTGTGTACAAAGCTTAATCCGTCCATCTTCAATGTGCTATGTGCTATA	4281
Oy	4386	TTTGGCTAATTTTGGCATATAGGATGATACAGCTTTTGGCTGGAAATATTTTAAGTC	4445
Db	4282	TTTTGGCTAATTTTGGCATATATGGAGATACAGCTTTTGGCTGGAAATATTTTAAGTC	4341
Oy	4446	GAGACATGAATGGCAAGAGCTCAGCAGAGATCATACCAATTCGCAATGCTCGCAG	4505
Db	4342	AAATATGTATATGACACTGTGCTGAGCAGCATGAATCATCCGAATCGTAATGCTCGAAA	4401
Oy	4506	AGCAGAACTACACGTGGTGAAATTCAGCAATGAATTTGCATGTATAGGTAAAGCGCAT	4565
Db	4402	AGTGAATATACACTGTGGAAATTTCCGCAATGAATCTTCATCATGTATAGGTAAAGCGCAT	4461
Oy	4566	CTGTGCTTTTCCAAAGTGGCCACTTCAAAAGCTGTGATCAAAATCATGAACGATGTATC	4625
Db	4462	CTGTGCTAATTTCAAGTGGCCACTTTAAGGGCTGTGATTCAGATTAAGAACGATGTATC	4521
Oy	4626	GATTCACAGAGGTGTGACAAAGCAACCAATTCGTGAACGAACATCTCAATATTAAT	4685
Db	4522	GATTCACAGAGGTGTGACAAAGCAACCAATTCGTGAACGAACATCTCAATATTAAT	4581
Oy	4686	TTCTGTAATCTTCAATATTTTGAATTCCTTTTTCACATCATCTGTCATTTGTGTATTC	4745
Db	4582	TTCTGTAATCTTCAATATTTTGAATTCCTTTTTCACATCATCTGTCATTTGTGTATTC	4641
Oy	4746	ATTGATATTTTAAATGACAAAGAAAAAGACAGGTGTATCTTAAAGATTTTATGACA	4805
Db	4642	ATTGATATTTTAAATGACAAAGAAAAAGACAGGTGTATCTTAAAGATTTTATGACA	4701
Oy	4806	GAAATCAGAAAAAGTACTAATATGTATGTAAGAAAAAGTGGCTTAATAAAAAACATTAATA	4865
Db	4702	GAAATCAGAAAAAGTACTAATATGTATGTAAGAAAAAGTGGCTTAATAAAAAACATTAATA	4761
Oy	4866	GCATTTCCAGAACCAAGGTGGCGACCAACAGCAATAGCTTTTGAATATGTAACCGATAG	4925
Db	4762	GCATTTCCAGAACCAAGGTGGCGACCAACAGCAATAGCTTTTGAATATGTAACCGATAG	4821
Oy	4926	AAATTCGATTAATCATTAATGTTATTTCAATGGTCTGAACATGTCCACATGACCTCGAT	4985
Db	4822	AAATTCGATTAATCATTAATGTTATTTCAATGGTCTGAACATGTTCACATGACCTCGAT	4881
Oy	4986	CGTTACAGATGCTGTGACAACGTATATACGCGTCTCTTAAGCTATCTCAATTCGATATTCGTA	5045
Db	4882	CGTTACAGATGCTGTGACAACGTATATACGCGTCTCTTAAGCTATCTCAATTCGTA	4941
Oy	5046	GTTATTTTCACTTCCGAATGTCTATTAATAATTTGGCTTTAGCATATCACTATTTTAT	5105





QY	24	ATGACAGAAATTCGACTCGATATCTGAGGAAGAACGCACTTTGTTCCGTCCCTTTACC	83
Db	1	ATGACAGAAATTCGACTCGATATCTGAGGAAGAACGCACTTTGTTCCGTCCCTTTACC	60
QY	84	CGCGAATCATTTGGTGGCAATCGAACAAACGATTTCCGCTGAACATGAAAGCAAGAGAG	143
Db	61	CGCGAATCATTTGGTGGCAATCGAACAAACGATTTCCGCTGAACATGAAAGCAAGAGAG	117
QY	144	CTGGAAAGAAAGAGCGGAGGAGAGAGTGCCTCCGATATGTTGCGCAAGAAACAAACAAA	203
Db	118	CTGGAAAGAAAGAGCGGAGGAGAGAGTGCCTCCGATATGTTGCGCAAGAAACAAACAAA	148
QY	204	GAAATCCGATATGATGACGAGACGAGATGAAAGTCCACACCCGATCCTACACTTTGAA	263
Db	149	-AGATTCGATATGATGACGAGACGAGATGAAAGTCCACACCCGATCCTACACTTTGAA	207
QY	264	CAGGTTGGCCAAATCCTGTTTCATTTACAGGGGAGCTTTCCCGCCGAAATTTGGCTCCACT	323
Db	208	CAGGTTGGCTTAATCCTGTTTCATTTACAGGGGAGCTTTCCCGCCGAAATTTGGCTCCACT	267
QY	324	CCTCTCGAGATATCGATCCCTTACCTACAGCAATCTACTGACATTCGATTTGTAACAAA	383
Db	268	CCTCTCGAGATATCGATCCCTTACCTACAGATATCTACTGACATTTGTAAGTAAGTAA	327
QY	384	GAAAGATATTTTTCGTTTTCGATTCATCAAAAGCAATGAGATGCTGCATTCATTCAT	443
Db	328	GAAAGATATTTTTCGTTTTCGCTCCAAACCAATGAGGCTGCATTCATTCATTCAT	387
QY	444	CCGATATCGTGGTGGCCATTTAATCTCTAGATGATCCATTAATTTCCATTCATCATC	503
Db	388	CCGATACGTCGTAGCCATTTAATTTTATGATGATCCCTGTTTGTATTCATTCATTC	447
QY	504	ACCACAATTTTCGTCACACTGTCATCCTGTGATGATATGCGCAACAAGCCACGGTTGATCC	563
Db	448	ACCACTATTTCTAATTAATGATTTAATGATATGCGCAACAAGCCACGGTGCATTC	507
QY	564	ACTGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTATGCGACA	623
Db	508	ACAGAGGTGATATTCACCGGAATCTACACATTTGAATCAGCTGTTAAAGTATGCGACA	567
QY	624	GGTTTCATTTAATGCCCGTTTACGATCTTGAAGATGATGAATTTGGCTGGCATTTGTA	683
Db	568	GGTTTCATTTAATGCCCGTTTACGATCTTGAAGATGATGAATTTGGCTGGCATTTGTA	627
QY	684	GTAATAGCTTTAGCTATATGTGACCAATGGATTTAGTTAGTAAATCTAGACCCCTCGA	743
Db	628	GTAATAGCTTTAGCTATATGTGACCAATGGATTTAGTAAATCTAGACCCCTCGA	687
QY	744	ACGTTTACGGTGTCTGCGAGCGCTTAAACCGTAGCCATTTGTGCCAGGCTTGAAACCATC	803
Db	688	ACATTTACGGTGTCTGCGAGCGCTTAAACCGTAGCCATTTGTGCCAGGCTTGAAACCATT	747
QY	804	GTCGCGCCGCTGATCGAATCGGTGAAGAAATCTGGGCCATGTGATTAATCTGACCATGTC	863
Db	748	GTCGCGCTGCTGATCGAATCTGTAAATAATCTACCGCAATGATTAATTTTGAACATGTTT	807
QY	864	TCCCGTGGGTGTTGGCGTGAATGGGCTTACAGATCTAATATGGGCGTCTCACCGAGAG	923
Db	808	TCCCGTGGGTGTTGGCGTGAATGGGCTTACAGATCTAATATGGGCGTCTCACCAAAAG	867
QY	924	TGCATCAAGAAAGTTCCCGCTGAGCGGTTCTGGGGCAATCTGACCGACGAGAACTGGAC	983
Db	868	TGCATTAACAATATCCCGCTGAGCGGATTTGGGGCAATCTGACCGAGTGAATACTGGATT	927
QY	984	TATCAATTCGCAATAGCTCCCAATTTGTATTTCCAGAGACGAGGGCATCTCATTTCCGTTA	1043
Db	928	CTACCAATAGCAAGTTCCCAATTTGTTTACGAGAAACGATGAGGATCATTCCTGGTGG	987
QY	1044	TGCGGCAATATTCGCGTGGGGGCAATGCGACGCAATTAAGTGTGCTCAGGGGCTTT	1103
Db	988	TGCGGCAATATTCGCGTGGGGGCAATGCGGCAATTAAGTGTGCTCAGGGGCTTT	1047
QY	1104	GGTCCGAATCCGAATTAATGCTACCAACAGCTTCGATTCGTTCCGATGGGCTTCTCTGTC	1163

Db	1048	GGCCCCAATCCCACTACGACTACCAAGTTTGACCTCATCTCGTGGGCTTTCGTGTCG	1107
QY	1164	GCCTTCCGGGTGATGACACAGAGCTTCTGGAGAGATCTGTACAGCTGCTGTCGCGCC	1223
Db	1108	GCCTTTGTCTCATGACCCAAAGATTTCTGGAGAGATCTGTATACAGCACGCTGCAAGCA	1167
QY	1224	GCCGGACCAATGGCAATGCTGTTCTTTATAGTCAATCATCTTCCTAGGTTCAATCTAT	1283
Db	1168	GCTGGACCCCTGGCAACATGTTGTTCTTTATAGTCAATCTTCTTAGGTTCAATCTAT	1227
QY	1284	GTAATTTGATTTTGGCATTTGTCATGTCATGTCATACAAATTTGCCAAAGAGCCGAA	1343
Db	1228	GTAATTTGATTTTGGCATTTGTCATGTCATGTCATACAAATTTGCCAAAGAGCCGAA	1287
QY	1344	GAAGAAAGGCTGCCGAAGAGAGAGGCGATACGTGAACGGAGAGAGAGCTGCCGCCAA	1403
Db	1288	GAAGAAAGGCTGCCGAAGAGAGAGGCGATCCGAAGACTGAAGAGCGGACGACCGAAG	1347
QY	1404	GCGGCGAAAGCTGGAAGAGCGGGCCCATATGCGAGGCTACAGCAAGCGGATGGCGTGC	1463
Db	1348	GCGGCGAAAGCTGGAAGAGCGGGCCCATATGAGCACTTAACCGGTCAAGATGCAAGCGAAT	1407
QY	1464	GCGGAAGAGGCTGACATCGCATCCGGAATAGGCCAAGAGTCCGACGATTTCTTGATAGC	1523
Db	1408	GCGGCTGGGAGCTCTGCAATCCGAGATGACAAAGAGTCCCACTACTCTTGATAGC	1467
QY	1524	TATGAGCTATTTGTTGGCGGGGAGAGAGGACGATGACAAACAAGAGAGATGTC	1583
Db	1468	TATGATCTGTTGTTGGCGGGGAGAGAGGACGATGACAAACAAGAGAGATGTCG	1527
QY	1584	ATTGGAGAGCTGCAAGGTGAGAGTCCGAGTCCGTGAGCGTTTATCAAAACAACGAGCACT	1643
Db	1528	ATTGAGAGCGTGAAGGTGAGAGTCCGAGTCCGTGAGCGTTTATCAAAACAACGAGCACT	1587
QY	1644	ACCAAGACACCAAGCTAACCAAGTTCGTAAATGAGACGAGCATCTTATCTTACT	1703
Db	1588	ACCAAGACACCC---GCTACTAAAGTCCGTAAATGAGACGAGCATCTTATCTTACT	1644
QY	1704	GGTTCAACCGTTTAAATATACGAGGGGGATACGTAATTTCTCAAGATACAGATACGAAAC	1763
Db	1645	GGTTCAACATTTTAACTAACGCGGGGGATACAGTATTTCAACAAGTACACAAATCGAAAT	1704
QY	1764	GAGCTGGCGCCTTTGGTATACCCGGTATGCGATCTGTAAAGCATTTGGTATGTCACATAT	1823
Db	1705	GAGGCTGACCTTTTGGTATACAGGTATGAGCATGCAAGCCATTTGTATCTGCAAAACATAT	1764
QY	1824	CAGGATGCCAGAGCACTTGCCCTATGCGGACGATCGAAATGCGGTCAACCCGATGTC	1883
Db	1765	CAGATGCCAGAGCACTTGCCCTATGCGGATCTGCAATGCGGTCAACCCGATGTC	1824
QY	1884	GAAGAGATGGGGCCATCATATGATGCCCGGTATCTATAGGCAATCAAGCTCCGACACTCA	1943
Db	1825	GAAGAGATGGGTGCATATATAGTACAGGCGCTACTATGTAATTTAGTTTACACATTTCT	1884
QY	1944	TCGTATACCTTGCATCAATCCGAAATATCGTATACCTTCAATGCGCATCTTCTGGCGGC	2003
Db	1885	TCATATACCTTGCATCAATCAAGATCTCGTATACATCACTGTGTGATTTTGGGTGGC	1944
QY	2004	ATGCGCGTCAATGGGTGTCAGCAACATAGCAAGAGAGCAAAATTTGCGCAACCGCAACACA	2063
Db	1945	ATGCGCGTCAATGGGTGTCAGCAACATAGCAAGAGAGCAAAATTTGCGCAATGCGCAACACA	2004
QY	2064	CGCAATCATATAGTGGCGCCACCAATGGCGGACCACTTGTGGAACCAATTCACAG	2123
Db	2005	CGCAATCATATAGTGGGTGTCAGCAACATAGTGGCAATGACGCGCGGTGTGGCTAT	2064
QY	2124	CTCGAT-----CATGCGACTACAAATTTGGCTGTGAGTGAACGACGACGAA	2166
Db	2065	CCCGATGCCAATCAACAGAAACAAGGATTTATGAAGAGGTCAAGATTAATACAGCAAA	2124
QY	2169	GCTGGCAAGATTAACATACAGCAATCTTTATCGAGCCGTCACAGCAAAACGGTGT	2228

Db 2125 GCTGGCAAAATTAACACGACGATCTTTTATCGAGCCGCTCAAACTCAACAGTGTG 2184  
Qy 2229 GTTATATGAAAGATGATGATGCTCTGATATGATCATCGAAGCCGCTGCTGGAC 2288  
Db 2185 GTAAACATGAAAGATGATGATGCTCTTAAATGATATCATTTGAACAAGCCGCTGGACAT 2244  
Qy 2289 AGTGGGCAAGCGATCGCGGTGTCTCGTTACTATTTCCAAAGAGAGATGACAG 2348  
Db 2245 AGTGTGCTAGTGAACGAGT-----GAGAGAGATGACAA 2280  
Qy 2349 GATGGGCGGAGCTTCAAGACAGGCACTCGAAGTATCTCAAGGCGATGATGTTT 2408  
Db 2281 GATGGTCCCATTCAGAGCATCGCCTCGAATATATCTTAAAGGATGAAATCTTT 2340  
Qy 2409 TGTGTGGGACTGTGCTGGGTTTGTGTAATTTCCAGAGTGGGTATCGCTACCTC 2468  
Db 2341 TGTGTAGGGAATGTGTGGGTGTGTTAAATTTCCAGAAATGGGTCTCTTTATGTG 2400  
Qy 2469 TTGATCCCTGTCGAGGCTCTTATCAAGGCTGATGTCAGACAGATGTCATG 2528  
Db 2401 TTGATCCATTTGAGAGCTCTTATTAACCTGTATTTGTGTCATTAATGATTCATG 2460  
Qy 2529 GCAATGATCAACAAGATATGAACAGAGATGAAACGCTGCTCAAGAGTGGCACTAT 2588  
Db 2461 GCAATGATCATCAAGATATGAATCCGAATTTGAGAGAGTGTGTAAGATGATAT 2520  
Qy 2589 TTCTTCAACGCACTTTGCAATGAGCCACATGAAGTATGAGCCATGAGCCCAAG 2648  
Db 2521 TTCTTCAAGGCACTTTGCAATGAGCCACATGAAGTATGAGCCATGAGCCCAAG 2580  
Qy 2649 TACTATTTCCAGAGAGGCTGGAACATCTTGAATCTTATCGAGCCCTATCGTATG 2708  
Db 2581 TACTATTTCCAGAGAGGCTGGAACATTTTGAATCTTATGAGCCCTATCGTATG 2640  
Qy 2709 GAATGGGACTCGAGAGGTGTCAAGGCTGTCCGATATGCGTCTTCAATGTCGAT 2768  
Db 2641 GAATGGGCTGAGAGGTGTCAAGGCTGTCCGATATGAGAGATTTTCTGTTGCTGT 2700  
Qy 2769 GTATTTCAACTGGCCAAATCTTTGGCCCACTTTAATTTTCAATTTGATTTGAGAG 2828  
Db 2701 GTATTTCAAAATTTGCAAAATCTATGCGCCACATGAATTTTCAATTTGAGAG 2760  
Qy 2829 ACGATGGGCTTTGGGATCTGACATTTGATCTTGAATTCATTCATTCATTTTCC 2888  
Db 2761 ACGATGGGCTGATGGGATCTGACATTTGATCTTGAATTCATTCATTTTCC 2820  
Qy 2889 GTATGGGAATGCAACTGTTCGAAAGATATATCATGATCAAGAGCCGCTTCCGAT 2948  
Db 2821 GTATGGGAATGCAACTTTTGGAAAGATATATGACACAGAGATCGCTTCAAGAG 2880  
Qy 2949 GGGCACTGCGCGCTGGAACCTTCAAGATTTATGACAGCTTCATGATGCTTCCG 3008  
Db 2881 CATGAATTAACGCGCTGGAATTTTCAAGATTTATGACAGCTTCATGATGCTTCCG 2940  
Qy 3009 GTGCTTCGGAAGATGATGATGATCTGATGTCATGTCGATGTCGAGAGTGTCTG 3068  
Db 2941 GTGCTTCGGAAGATGATGATGATCTGATGTCATGTCGATGTCGAGAGTGTCTG 3000  
Qy 3069 TGCATTCCTCTTCTTGGCAACGCTGTCATCGGCACTTTGTCGATTTAACCTTTT 3128  
Db 3001 TGTATACCTCTTCTTGGCAACGCTGTCATCGGCACTTTTGTGCTTTATCTTTT 3060  
Qy 3129 TTAACCTTCTTGTTCATTTTGGCTCATCTAGCTTATCAAGCGCGAGCTCGATTA 3188  
Db 3061 TTAAGTTTCTTGTTCATTTGGCTCATCTAGCTTATCAAGCGCGAGCTCGATTA 3120  
Qy 3189 GATAGCAATTAATAGCCGAGGCTTCAATGATTTGCGGATTTAAAGTTGGTTAG 3248  
Db 3121 GATAGCAATTAATAGCCGAGGCTTCAATGATTTGCTGTTTAAAGCTGGGTGAA 3180  
Qy 3249 GGTATATTTGCTGATGTTTCAAGTATAGTAAACAATTTGACAAATCAATTAAGTAT 3308  
Db 3181 GGTATATTTGCTGATGTTTCAAGTATAGTAAACAATTTGACAAATCAATTAAGTAT 3240

Qy 3309 CAACATCAGGTGAGAGGACCAACAGATCAGTTGATTTGGAGAGAGATGATGAC 3368  
Db 3241 CAACATC-----AGAACATGCGAT 3261  
Qy 3369 AACGAATGAGCTGGGCAACGAGATCTCGCCGACCGCTCATCAAGAGGGATC 3428  
Db 3262 AATGACTGAGGTTGGGTCAATGAGAAATCATGAGGCGATGGCTTGATCAAAAAGGATG 3321  
Qy 3429 AAGAGCAAGCACTGAGAGTGGCATCGGGATGAGATGAAATTCAGATCAAGGC 3488  
Db 3322 AAGGCGAGAGCCGAGCTGAGAGTGGCATGGCCATGGAGGATTCACATATCAAGGC 3381  
Qy 3489 GACATTAAGAAACAACAGCGAGAAATTCAAATATCTAAATTAAGCAAGATGATGGC 3548  
Db 3382 GATATGAAACCAACAGCCCAAGAAATCAAAATTCATTAACCAACCAAGATGATGGA 3441  
Qy 3549 AACTCAATTAACCAACCAAGATGAGCTGGAACAGAGCTAAACATAGAGTTGTCC 3608  
Db 3442 AACTCAATTAACCAACCAAGATGAGCTGGAACAGAGCTAAACATAGAGTTGTCC 3501  
Qy 3609 TTAAGAGCAAGCACTGCGAGATTAATCTATGATGATGATGATGATGATGATG 3668  
Db 3502 ATACAGAGCAAGTACATGCGAGATTAATCTATGATGATGATGATGATGATGATG 3561  
Qy 3669 AAGAGCAAGCACTGCGAGAGGCGGAGATGATGAGAGGCGAGAGAGGCGGCGC 3728  
Db 3562 AAGAGCAAGCACTGCGAGAGGCGGAGATGATGAGAGGCGAGAGAGGCGGCGC 3621  
Qy 3729 AGCAAGAGATTAAGTCTGAGAGAGATGAGAGAGGCGGAGAGGCGGAGAGGCGC 3788  
Db 3622 AGCAAGAGATTAAGTCTGAGAGAGATGAGAGAGGCGGAGAGGCGGAGAGGCGC 3681  
Qy 3789 CCGCTGAGAGATTAATTAATTAATGATGATGATGATGATGATGATGATGATGAT 3845  
Db 3682 CAGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3741  
Qy 3846 CCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3905  
Db 3742 CCGGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3801  
Qy 3906 GACTGCGGCTTGGCAAGATGAGGCAATTAAGCACTGAAACCTTTCAATTAATGAA 3965  
Db 3802 GACTGCGGCTTGGCAAGATGAGGCAATTAAGCACTGAAACCTTTCAATTAATGAA 3861  
Qy 3966 AATTAATTAATTAAGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 4025  
Db 3862 AATTAATTAATTAAGCAAGATGATGATGATGATGATGATGATGATGATGATGAT 3921  
Qy 4026 TTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4085  
Db 3922 TTAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3981  
Qy 4086 AGAATTAATTAAGATTAATTTCTTGAAGATGATTAATCAAGTGGGCTGCGCTTC 4145  
Db 3982 AGAATTAATTAAGATTAATTTCTTGAAGATGATTAATCAAGTGGGCTGCGCTTC 4041  
Qy 4146 AAGGTACTTCAACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 4205  
Db 4042 AAGGTACTTCAACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 4101  
Qy 4206 ATCAACTTCTGCTTCACTTTGAGAGCTGATGATTAAGCTTCAAGATTAAGTGA 4265  
Db 4102 ATCAACTTCTGCTTCACTTTGAGAGCTGATGATTAAGCTTCAAGATTAAGTGA 4161  
Qy 4266 ACGTTAAGAGCACTGAGACCACTGATGATGATGATGATGATGATGATGATGATGAT 4325  
Db 4162 ACGTTAAGAGCACTGAGACCACTGATGATGATGATGATGATGATGATGATGATGAT 4221  
Qy 4326 GTTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4385  
Db 4222 GTTATATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4281

QY	4386	TTTTGGCTAAATTTTGGCCATATAGGATGGGTGACAGCTTTTGGCGAAAATAATTTAAAGCG	4445
Db	4282	TTTTGGCTAAATTTTGGCCATATATGGAGATACAGCTTTTGGCGAAAATAATTTAAAGGT	4341
QY	4446	GAGGACATGAATGCGACGAGCTCAGCCACGAGATCATACCAATTCGCAATGCTCGAG	4505
Db	4342	AAAGATGGTAATGACACTGTGCTGAGCCATGAATAATCATACCGAATCGTAATGCTCGCAA	4401
QY	4506	AGCGAAGACCTACAGTGGGTGAATTCACAGATGAATTCAGTCAATGTGATGACCGCAT	4565
Db	4402	AGTGAATACTACACTCTGGGAAAATTCGCAATGAACCTTCGATCATGTAGTAATGCGAT	4461
QY	4566	CTGTGCTCTTTCCAAGTGGCCACTTCGAAAGCTGAGTACAAATCATGAACGATGCTATC	4625
Db	4462	CTGTGCTATTTCAAGTGGCCACTTTTAAAGGCTGATCCAGATTAATGAACGATGCCATT	4521
QY	4626	GATTCAAGAGAGGTGCGACAAACCAATTCGTGTAACGAACATCTCAATGTATTTAT	4685
Db	4522	GATTCAAGAGAGGTGCGACAAACCGCATCCGAGAAACCAATTCATCATGTATTTAT	4581
QY	4686	TTGCTATCTTCATCATATTTTGAATCCCTTTTACACTCAATTCGTTCATTGGTGTATTC	4745
Db	4582	TTGCTATCTTCATCATATTTTGAATCATTTTTCACACTCAATTCGTTCATTGGTGTATTC	4641
QY	4746	ATTGATAATTTTATGACCAAAAGAAAAGCAGGTGATCATTTGAATGTTCAAGCA	4805
Db	4642	ATTGATAATTTTATGAAACAAAAGAAAGACAGGTGATCATTTGAATGTTCAAGCA	4701
QY	4806	GAGATCGAAGAAAAGTACTATATATGCTATGAAAAAGTGGGCTGTAAGAAAACATTAATA	4865
Db	4702	GAGATCGAAGAAAAGTACTATATATGCTATGAAAAAGTGGGCTGTAAGAAAACATTAATA	4761
QY	4866	GCCATTCGAAGACCAAGGTGGCGACACACAAACAAATGCTTTGAATATGTAACCGATAG	4925
Db	4762	GCCATTCGAAGACCGAGGTGGCGACACACAAACAAATGTAATCGAAATGTTACAGATTA	4821
QY	4926	AAATTCGATATATCATATATGTTATTCATGCTGTAACATGTTCAACCATGACCACTCGAT	4985
Db	4822	AAATTCGATATATCATATATATGTTATTCATGCTGTAACCATGTTTACCATGACCTCGAT	4881
QY	4986	CGTTACAGTGGGTGGGACACGATATACCGGGTCTTGACTATCTCAATGCGATATTCGTA	5045
Db	4882	CGTTACAGCGCTCGAGGCGGTACAAACATGTCTCGCAAACTCAAGGATATTCGTA	4941
QY	5046	GTTATTTTCAATTCGGAATGTCCTATTAATAAATTCGTTTACATATCATATTTAT	5105
Db	4942	GTTATTTTCAATGGGGAATGTCATTAATAAATTCGTTTACATATCATATTTTCAA	5001
QY	5106	GAGCCATGAATTTATTTGATGTATGATGTATTCATTTATTCATCTTATAGTCTTGTAATT	5165
Db	5002	GAGCCATGAATTTATTTGATGTATGATGTATTCATTTATTCATCTTATAGTCTTGTAATT	5061
QY	5166	AGCGATATTTACGAGAGTACTTGTGTGCGCCGACCTGTCTCCGATGTGTGCGGTGGCG	5225
Db	5062	AGCGACATCATTTGAGAAATATTTGTAATCGCCGACACTGTCTCGTGTGTGAAGTGGCC	5121
QY	5226	AAAGTGGGCGGTGTCCTTCGACTGTGAAGGAGCAAGGGCATTTCCGACACTGCTCTTC	5285
Db	5122	AAAGTGGGCGGTGTCCTTCGCTGTATGTACAGGATGTCCAGGGATATTCGACCTGTGCTTC	5181
QY	5286	GCGTTGGCGATGTGCGTGGCGGCGCCCTGTTCAACATGTGCTGTCTGTTCCTGTGATG	5345
Db	5182	GCGTTAAGCGATGTGCGTGGCTGCTGCTTATTAACATTTGTCTGTGTCTGTTCCTGTGATG	5241
QY	5346	TTTCATCTTTGGCATTTTCGGCATGTGCTTTCTTACATGACGTGCAAGAGAAAGGCGCAT	5405
Db	5242	TTTCATCTTTGCTATCTTTGCGATGCTCTTCTTCATGCAATGTCAAAGAAAGGCGCAT	5301
QY	5406	AACACAGCTTCAACCTTCAGACCTTTGGCCAGACAGATGATCTGCTCTTTCAATGTGCG	5465
Db	5302	AATGCTGTGTAAATTTTAAAGACATTTGGCCAAAGTATGATATTTGTCTGTTCATATGCT	5361
QY	5466	ACGTACAGCGGTTGGAGTGTGTACTGACGCCATTATCAATGAGAAAGCATGCGATCCA	5525

Db	5362	ACCTCAGCCGGTGGATGGTGGTTAGATGCGCATTCATCATGAGAAAGATTGGATCCA	5421
Qy	5526	CCCGACAGCCGACAAAGGCTATCCGGGCAATTGGGTTCACCGACCCGTGGAAATAGGTTT	5585
Db	5422	CCCGACACACGACAAAGGGCTATCCGGGCAATTGGGTTCACCGACTGTGGAAATTAAGTTT	5481
Qy	5586	CTCCTCTCATACCTAGTATTAAGCTTTTGTAGATGTTAATAATGTAATGTCATGTGCTGATT	5645
Db	5482	CTCCTTTCAATCTAGTATTAAGCTTTTGTAGATGTTAATAATGTAATGTCATGTGCTGATT	5541
Qy	5546	CTCGAAGACTTATAGTCAGGCCACCGAGACGTGCAGAGGGTCTTAACCGACGACATCAC	5705
Db	5542	CTCGAAGAACTATAGCCAGGCTACCGAGAGATGTACAGAGGGGTCTCACCGACGACCATAT	5601
Qy	5706	GACATGACTATAGATCTGGGCGCAATTTGGATCCGAGGGGACCCGATCATACGCTAT	5765
Db	5602	GATATGTAACGAGATTTGGCAACAATTCGATCCGAGGGGTACCCAGTCAATAGATAC	5661
Qy	5766	GATCAGCTGTCCGAATTCCTGAGACTGAGAGCCCCCGCTGCAGATCCAAACCGAAC	5825
Db	5662	GACCAGCTGTCCGAGTTCCTGAGAGCTGTGAGAGCCGCGCTGCAGATCCAAACCGAAC	5721
Qy	5826	AAGTACAAAGTCAATTTGATGAGACATACCATCTGTGGCGGTAGACCTCAATGACTGTGTC	5885
Db	5722	AAGTACAAAAATCAATGATGAGACATGCCAATATGTGGGGCGACATGAATGACTGTGTG	5781
Qy	5886	GACATCTCTCAGCCCTTACGAAAGACTTCTTTGCGCGAAGGGCAATCCGATAGAGAG	5945
Db	5782	GATATATTGGATGCGCTGACCAAGAACTTCTTTGCGCGCAAGGGTATCCGATGAGAG	5841
Qy	5946	ACGGGTGAGATTGTGTGATGATAGCGGCCCCCGGANTTCGAGGGCTACGAGCCCTCTCA	6005
Db	5842	ACGGGTAAATTTGTGTGATTTGGCGGCCGACCGACACCAAGGGCTATGATCCGGTGTGCG	5901
Qy	6006	TCAACGCTGTGGGCGCTCAGCGTGAAGAGATACGCGCCCGGCTAATCCAGCAGCCTGGCGCA	6065
Db	5902	TCCACACTGTGTGGCGCCACGCTGAGAGATACCTGCCCAAGCTGATACAGAAATTCGCTGGCGG	5961
Qy	6066	AAGCACAAGGCGCGGGCGAGGGAGGTGGATCCTTTGACCGGATACGATCATGGCGAT	6125
Db	5962	CGTTACCAAGATGGC-----	5976
Qy	6126	GGGGGTATCCGATGCGGGGACCCGGGCGCCCGATGAAACAACGACGGCGATGCGCCC	6185
Db	5977	CCACCCGAGAGGGTGTATGAGGGCGAGGCGGCTGTGGCGAAGATGTGCTGAAGGCGGT	6036
Qy	6186	GCTGTGTGAGATGTGTAGTGTAAACGTTATCTGCAGAAAGAGCTGCCGATGCGATGAGAT	6245
Db	6037	GAGGGTGAAGCGGCGACGGCGGGCGGCGAGATGATGATGTGGCTCAGCGACGCGGGCG	6096
Qy	6246	AATTTAATATAGTCCGGGTGAGATGTCAGCGCGGCGGACACAGACGACGACGCGGGC	6305
Db	6097	GGAACCAATCACCCACAGATCCAGATGCGCGGACAAACAAATGGTGTCAAGCGCCGCAAT	6156
Qy	6306	GCGGCGGGGACAGACGACGGCGGGAATCCGAGCGGGTATGCGCGGGGACAGACCGCC	6365
Db	6157	GATGGCGGCCCCCTTAGTCCGGGCTGTGTTAATGTGGCGGCAATATGSCCCGCAACGGCC	6216
Qy	6366	GTTTCTGTGAGAGCGACGGGTTCTGTGACGAAGAACGGCAACAAGTGTCTCATCTCG	6425
Db	6217	GTACTGTTCGAAAGCGATGTGTTTGTTCACAAAAACCGTCAATAAAGTTGTATATACCTCG	6276
Qy	6426	CGATCGCGGAGCATCATGTCGCGGACGGCGGAGATGTCGA	6464
Db	6277	AGATCGCGGAGCATCATCAAGACGGCGAGATGTCGA	6315

RESULT 13  
US-09-428-371-2  
; Sequence 2, Application US/09428371  
; Patent No. 6800435  
; GENERAL INFORMATION:

APPLICANT: Soderlund, David M.  
 APPLICANT: Knipple, Douglas C.  
 APPLICANT: Ingles, Patricia J.  
 TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM INSECTICIDE-SUSCEPTIBLE AND  
 FILE REFERENCE: 19603/606  
 CURRENT APPLICATION NUMBER: US/09/428,371  
 EARLIER FILING DATE: 1996-03-01  
 EARLIER APPLICATION NUMBER: 08/608,618  
 EARLIER FILING DATE: 1996-12-24  
 NUMBER OF SEQ ID NOS: 19  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 6315  
 TYPE: DNA  
 ORGANISM: Musca domestica  
 US-09-428-371-2

Query Match 68.1%; Score 4434.2; DB 4; Length 6315;  
 Best Local Similarity 81.8%; Pred. No. 0;  
 Matches 5284; Conservative 0; Mismatches 1013; Indels 162; Gaps 8;

QY 24 ATGACAGAAAGATTCGATCGATATCTGAGGAAGACGAGTTGTCGTCCTTACC 83  
 DB 1 ATGACAGAAAGATTCGATCGATATCTGAGGAAGACGAGTTGTCGTCCTTACC 60  
 QY 84 CGCGATCATTTGTCGCAATCGAACAGCATTTGCCGTCGAACATGAAAGAGAG 143  
 DB 61 CGCGATCATTTGTCGCAATCGAACAGCATTTGCCGTCGAACATGAAAGAGAG 117  
 QY 144 CTGGAAGAAAGAGAGCGGAGGAGAGGTCCGCGATATGTCGCAAGAAAAA 203  
 DB 118 CTGGAAGAAAGAGAGCGGAGGAGAGGTCCGCGATATGTCGCAAGAAAAA 148  
 QY 204 GAATTCGATATGATGAGGAGAGGATGAGATGAGATGAGATGAGATGAGATGAG 263  
 DB 149 AGATTCGATATGATGAGGAGAGGATGAGATGAGATGAGATGAGATGAGATGAG 207  
 QY 264 CAGGATGTCGCAATCTGTCGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 323  
 DB 208 CAGGATGTCGCAATCTGTCGATTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 267  
 QY 324 CTTCTCGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 383  
 DB 268 CTTCTCGAGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 327  
 QY 384 GGAAGAAAGATTTTGGCTTTTCTGATCAAAAGAGATGATGATGATGATGATGAT 443  
 DB 328 GGAAGAAAGATTTTGGCTTTTCTGATCAAAAGAGATGATGATGATGATGATGAT 387  
 QY 444 CCGATACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 503  
 DB 388 CCGATACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 447  
 QY 504 ACCAATTCCTGTCACGTCATCTGATGATGATGATGATGATGATGATGATGATGAT 563  
 DB 448 ACCAATTCCTGTCACGTCATCTGATGATGATGATGATGATGATGATGATGATGAT 507  
 QY 564 ACTGAGGATATTCACCGGATCTACACATTTGAAATGAGCTGTTAAAGTATGAGCA 623  
 DB 508 ACTGAGGATATTCACCGGATCTACACATTTGAAATGAGCTGTTAAAGTATGAGCA 567  
 QY 624 GGTTCATTTTATGCGCTTATACGATCTTATGAGATGATGATGATGATGATGATGAT 683  
 DB 568 GGTTCATTTTATGCGCTTATACGATCTTATGAGATGATGATGATGATGATGATGAT 627  
 QY 684 GTAATAGCTTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 743  
 DB 628 GTAATAGCTTTAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 687  
 QY 744 ACGTTTAGGCTGTCGAGCGCTTAAACCGTATGATGATGATGATGATGATGATGATGAT 803

DB 688 ACATTTAGGATCTGCGAGCTCTGAAACCGTATGATGATGATGATGATGATGATGATGAT 747  
 QY 804 GTGCGCGCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 863  
 DB 748 GTGCGCGCTGTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 807  
 QY 864 TCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 923  
 DB 808 TCCCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 867  
 QY 924 TGCAATCAAGATTCGCGCTGAGAGGTCCTGCGGCAATCTGACGAGAGAGAGAGAGAGAG 983  
 DB 868 TGCAATCAAGATTCGCGCTGAGAGGTCCTGCGGCAATCTGACGAGAGAGAGAGAGAGAG 927  
 QY 984 TATCAATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1043  
 DB 928 TATCAATTCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 987  
 QY 1044 TCGCGCAATATATCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1103  
 DB 988 TCGCGCAATATATCCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1047  
 QY 1104 GATCCGAATCCGAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1163  
 DB 1048 GATCCGAATCCGAATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1107  
 QY 1164 GCTTCGCGCTGATGACACAGAGCTTGGAGAGATGATGATGATGATGATGATGATGATGAT 1223  
 DB 1108 GCTTCGCGCTGATGACACAGAGCTTGGAGAGATGATGATGATGATGATGATGATGATGAT 1167  
 QY 1224 GCGGACCATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1283  
 DB 1168 GCGGACCATGTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 1227  
 QY 1284 GTGATTTGATTTTGGCATTTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1343  
 DB 1228 GTGATTTGATTTTGGCATTTGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 1287  
 QY 1344 GAAAGAGAGCTGTCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1403  
 DB 1288 GAAAGAGAGCTGTCGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1347  
 QY 1404 GCGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1463  
 DB 1348 GCGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1407  
 QY 1464 GCGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1523  
 DB 1408 GCGGCAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1467  
 QY 1524 TATGATGATTTTGTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583  
 DB 1468 TATGATGATTTTGTGCGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1527  
 QY 1584 ATTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643  
 DB 1528 ATTGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1587  
 QY 1644 ACCACAGACACCAAGCTACCAAGTTGTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703  
 DB 1588 ACCACAGACACCAAGCTACCAAGTTGTTAAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1644  
 QY 1704 GGTTCACCGTTTAAATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1763  
 DB 1645 GGTTCACCGTTTAAATAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1704  
 QY 1764 GAGAGTGGCGCTTGTGATACCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1823  
 DB 1705 GAGAGTGGCGCTTGTGATACCGGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1764  
 QY 1824 CAGGATGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883

Db	1765	CAGAGATGCCACGACGACATTTGCCCTTATGCCAGTACGTCCGANTGCCGTAAACACCAATGTC	1822
Qy	1884	GAAAGAAATGGGGCCCATCATATAGTGCCTGGTATCTATGGCAATTGAGCTCCGACACTCA	1943
Db	1825	GAAAGAAATGGGGCCCATCATATAGTGCCTGGTATCTATGGCAATTGAGCTCCGACACTCT	1884
Qy	1944	TGCTATATCTGCACATCAGTCCCGAATATCGTATACCTCACATGGGGAATCTACTGGGCGGC	2003
Db	1885	TCATATACCTTGCCATCATCAAGATCTCTGATACATACATGGGATTTATTTGGGTGGC	1944
Qy	2004	ATGCGCGTCATGGGCGTCAGCAACAATGACCAAGAGACAAATTTGCGCAACCGCAACA	2063
Db	1945	ATGCGCGCCATAGGGGCGCCAGCAACATGACCAAAAGAGCAAAATTTGCGCAACCGCAACA	2004
Qy	2064	CGCAATCAATAGAGGGGCGCCAGCAACATGGGCGCACACTGTCTGGGACACCAATTCACAG	2123
Db	2005	CGCAATCAATAGAGGGGCGCCAGCAACATGGGCGCACACTGTCTGGGACACCAATTCACAG	2064
Qy	2124	CTCGAT-----CATCGCACTACGAATTTGGCCTTGGATGACGAGCGAA	2168
Db	2065	CCCGATGCCATTCACAAAGAACAAAGGAGTTATGAATGGGTACAGGATTTATACAGCGAA	2124
Qy	2169	GCTGGCAAGATTTAAACATCAGACAAATCCTTTATCGAGCCCGTCAGACACAAACGGTG	2228
Db	2125	GCTGGCAAAATTTAAACACACGACGACATCTTTTATCGAGCCCGTCAGACACAAACAGTGG	2184
Qy	2229	GTTGATATGAAGAATGTATGATGATCCTGTAATGACATCATCGAACAGGCGCGTGTGCGAC	2288
Db	2185	GTAACATGAAAGATGTATGATGATCTTAATGATATCATTTGAACAAGCCGCGTGTGCGAT	2244
Qy	2289	AGTGGGCGACGCGATCGCGGTGTCTCGCTTACTATTTCCACAGAGGACGATGACGAG	2348
Db	2245	AGTGGTGTACTGAAACGAGGT-----GAGGAGGATGACGAA	2280
Qy	2349	GATGGGCGGAGGTCCTCAAGACAGGCACTCGAAGTACCTCAAGGCGATCGATGTGTT	2408
Db	2281	GATGATCCCATTTACAGACATGCGCTCGAATATATCTTAAAGGACATGGAATCTTT	2340
Qy	2409	TGTGTGTGGGACTGTTCGTGGGTTTGATTGAAATTCAGAGTGGGATTCGCTCATCGTC	2468
Db	2341	TGTGTATGGACTGTGTGTGGGTGGTTAAATTTACAGAAATGGGTCTCTTTATTTGTC	2400
Qy	2469	TTGCATCCCTTCGTGCAAGCTTTTATCATACGCTGCGCATTTGGTGTCAACAGATGTCATG	2528
Db	2401	TTGCATCCCTTCGTGCAAGCTTTTATCATACGCTGCGCATTTGGTGTCAACAGATGTCATG	2460
Qy	2529	GCAATGATTCACACGATATGAAACAAGAGATGGAACCGTGTCAAGAGTGGCACTAT	2588
Db	2461	GCAATGATTCATCACGATGATTCGGAATTCGGAATTTGGAAGGTGCTGAATAAGTGTATCAT	2520
Qy	2589	TTCTTTACCGGACACTTTGGCATCGAGGCGACATGAAGCTTAATGGCCATGAGCCCGAAG	2648
Db	2521	TTCTTTACCGGACACTTTTTGCAATGAGGCGACAGTAAGGAGGCGCATGAGCCCGAAG	2580
Qy	2649	TACTATTTCCAGAGGCGCTGGAACAATCTTCACATTCATTTATCGTGGCCCTATTCGCTATTTG	2708
Db	2581	TACTATTTCCAGAGAGGCTGGAACAATTTTCATTTTATTTATTTGTCCTTGTCTGTGTC	2640
Qy	2709	GAACTGGGACTCGAGGGGTCTCAGGGGTCTGTTCGATTTGCGTTCTTTCGATGCTGTGCT	2768
Db	2641	GAAATTTGGGCTCGAGGGGTCTCAGGGGCTGTTCGATTTGGAAGAATTTTCGTTTGTCTTCGT	2700
Qy	2769	GTAATTCAAACCTGGGCAAGTCTTTGGCCACACTTAATTTACGATTTGATATGGAAGCGC	2828
Db	2701	GTAATTCAAATTTGGCAAAATTCATGCGCCACACTGAATTTACGATTTTCATTTATGGGCGCG	2760
Qy	2829	ACCAATGGGCGCTTGGGTATCTGACATTTGTACTTTGCACTTATCATCTTTCGCTTTGCG	2888
Db	2761	ACCAATGGGTGATTTGGGTATCTGACATTTGTACTTTGCACTTATCATCTTTCGCTTTGCG	2820
Qy	2889	GTCATGGGAATGCACTGTTTGGGAAGAATATCATGATTCACAGAGCCGCTTTCGGAT	2948
Db	2821	GTCATGGGAATGCACTTTTGGGAAGAATATATGATTCACAGAGATCGCTTTCAGAGAC	2880

QY	2949	GGCGACCTGCGCGCGCTGGAACTTACCGGACTTTATGCAACGCTTCAAGATCGTGTCCG	3008
Db	2881	CATGAATTAACCGCGCTGGAAATTTACCGACTTACATGCAACGCTTCAAGATGTGTCCGA	2940
QY	3009	GTGCTCTGCGGAGATGGATGCACTGCATGTGGAGCTGCAATGTACGTGTGGCGATGTCTCG	3068
Db	2941	GTGCTGTGCGGAGAGTGGATGCACTGCATGTGTGGAGCTGCAATGTATGTGTGGCGATGTCTCG	3000
QY	3069	TGCATTTCCCTTCTTCTTGGCCACCGTGTCACTGGGCAATCTTGTGTACTTAACCTTTTC	3128
Db	3001	TGTATACCCCTTCTTCTTGGCCACCGTGTGTATGGCAATTTTGTGTCTTTAACTTTTC	3060
QY	3129	TTAGCCTGTCTTTGTGCCAATTTTGGCTCATCTGTACTATCAGCGCGCACTGCCGATTAAC	3188
Db	3061	TTAGCTTTGCTTTGTGCCAATTTTGGCTCATCTGTACTATCAGTGTATATCAGCCCGCATCAAT	3120
QY	3189	GATACGAATAAATATGCGCGAGGCTTCAATCGAATTTGGCCGATTTAAAGTTGGCTTAAG	3248
Db	3121	GATACGAATAAATAATGAGAGGCGCTTCAATCGTATCTGTCTTTAAAGACTGGGATAA	3180
QY	3249	CGTAAATATGTGTATGTCTTCAACTTAATCGTAAACATGACAAATGACAAATAGTAT	3308
Db	3181	CGTAAATATGTGTATGTCTTCAACTTGTATTAATTCGAATTAATTTGACAAATCAATATAGTATC	3240
QY	3309	CAACCATCAGGTGAGAGGACCAACAGATCAGTTGATTTTGGACGAGAGCATGTGTAC	3368
Db	3241	CAACCATC-----AGAACATGTGGAT	3261
QY	3369	AACGAATCTGAGCTGTGGCCACAGACGAATCTCTGGCCGACGGCTCATCAAGAACGGATC	3428
Db	3262	AATGAATCTGAGTGTGGTCAATGAAGAAATCATGGGCGATGTGTTGAATCAAAAAGGTATG	3321
QY	3429	AAGGAGCAGACGCAACTGAGAGTGTGCATCGGGGATCGATGTGAATTCAGCATCAACGCG	3488
Db	3322	AAGGCGAGACCCACGCTGTGAGGTGGCCATTTGGCGATGTGCATGAGATTCACGATACATGGC	3381
QY	3489	GACATGAAACAACAAGCCGAGAAATCCAAATATCTAAATTAAGCAACGATGATTTGGC	3548
Db	3382	GATATGAAAAACAACAAGCCCAAGAAATTCAAATTTCAATAACAACAACAGATGATTTGA	3441
QY	3549	AACCTAATTAACGCAAAACAAATAGATGTGGAAACAGGAGCTAAACATAGAGGTTTGTCC	3608
Db	3442	AACCTAATTAACGCAAAACAAATAGATGTGGAAACATGACTTAACATAGAGGTTTGTCC	3501
QY	3609	TTACAGAGCGACGACACTGCCAGCATTAACATCATATGTATGTATGACCTAAAGATTCACATTC	3668
Db	3502	ATTACAGAGCGATGACACTGCCAGCATTAACATCATATGTATGTATGACCTAAAGATTCACATTC	3561
QY	3669	AAGGACGAGACCCCAAGGGGAGGCGGAGACGATGAGGGCGAGGAAGCGGACGACGCC	3728
Db	3562	AAGGACGAGACCCCAAGGGGAGGCGGAGACGATGAGGGCGAGGAAGCGGACGACGCC	3621
QY	3729	AGCAAGAGGATTTAGGTCTTCGACGAGAACTGACACGAGGAGGGCGATGTGAGAGAGGC	3788
Db	3622	AGCAAGAGGACCTCGGCGCTGACGAGGAATCTGACGAGGAGGCGCGAGGGGATGAGAGGC	3681
QY	3789	CCGCTCGACGGTGAATCATTAATTCATGCG--ACACGACGAGGATATATCTGCATGAATAT	3845
Db	3682	CAGCTGAGTGTGATCATCATTCATTCATGCGCCAAAACACGACGAGATATATGACGACATAT	3741
QY	3846	CCAGCTGATTTCTGCGCCGATTCGTATCATTAAGAAATTTCCGATCTTAAGCGCGATGACGAT	3905
Db	3742	CCGCGCCAGCTTTTCCCGGACTGCTACTACAGAAAGTTTCCGATCTTGTGCGCGGACGAG	3801
QY	3906	GACTCGCGGTTCTGGCAAGATGGGGCAATTTACACTGAGAAAATCTTTCAATTAATTGAA	3965
Db	3802	GACTCGCGGTTCTGGCAAGATGGGGCAATTTACACTGAGAAAATCTTTCAATTAATTGAA	3861
QY	3966	AATATAATTTTGAACAAGCTGTATACATATGATTTTAAATGATGACTTAAGCTTTGGCA	4025
Db	3862	AATATAATTTTGAACAAGCTGTATACATATGATTTTAAATGATGACTTAAGCTTTGGCC	3921



QY	4026	TTAGAAAGATGTA	CATCTGGCA	AAAAGACCA	CACTGCGAGAA	ATTTTATCTATATGAC	4085
Db	3922	TTAGAGAGATGTC	ATTACCTTAC	CCGATCGA	CTGTGATG	ACGAGATATCTGATCACTACATGAC	3981
QY	4086	AGAAATATTTA	CGGTATATTTCTT	CTTGAAAA	AGTTATCA	CAATGGTGGCGCTCGGCTTC	4145
Db	3982	AGGATATTTAC	GGTGATATTTCTTTT	TGGAGATG	TTGATCAATATG	GTGGCCTGGGCTTT	4041
QY	4146	AAAGTGTA	CTTGACCA	CGCGTGTGTGG	CTCGATTTTC	TGATTTGCAATGATATCGCTT	4205
Db	4042	AAGGTCTACTT	CACCAATG	CTGGTGTGG	CTGGATTTTC	TGATTTGTCATGTATTCGCTT	4101
QY	4206	ATCAACTTC	GTGTCTTCA	CTTGTGGA	CGTGGTGTAT	CAAGCTTCAAGATATGGA	4265
Db	4102	ATMAATTTGG	TTGGTCCG	TTTGGTGG	CTTAAATGATATAG	CGTGTATTAAGATCAATGGCG	4161
QY	4266	ACGTTAAAG	CACTGAGCA	CTAGATG	CAATGTCGGAT	TCAGAGGATAGAGGTCGTC	4322
Db	4182	ACACTGCGG	CCCTTAAG	CCATTTGG	CTGTCTCTAG	TGGAGGGATATGAAATGTGTG	4221
QY	4336	GTTAAATGG	CTGGTACA	AGCTATAC	CCGTTCATCTT	CAATGTGCTATTTGGTGTCTAATA	4385
Db	4222	GTAATGCGG	CTGTTCA	AGCTATAC	CCGTTCATCTT	CAATGTGCTATTTGGTGTCTAATA	4281
QY	4386	TTTGGCTTA	ATTTTGG	CCATTAAT	TGGGTGTAC	AGCTTTTGTCTGAAAAATTTTAAATGTC	4445
Db	4282	TTTTGGCTTA	ATTTTGG	CCATTAAT	TGGGTGTAC	AGCTTTTGTCTGAAAAATTTTAAATGCT	4341
QY	4446	GAGGACATGA	ATGGGACG	AGTCAG	AGCA	CGATCATACCAATTCGAAATGCGTCGAG	4505
Db	4342	AAAGATGTA	TGATGAC	CTGTGTGAG	CCATGAAATCATAC	CGAATCGTAATGCTGCGAAA	4401
QY	4506	AGCGAGAA	CTACAC	CGTGGTGTAA	TTCAGCAATGAATTTTC	GCATGTAGTAAAGCTAT	4565
Db	4402	AGTGAATA	CTACAC	CTGGGAAAT	TTCCGGAATGA	ACTTGATCATGTATGATATGCGAT	4461
QY	4566	CTGTGCTTTT	CCAGTGG	CCACCTT	CAABGGCTG	ATACCAATCATGAAAGATGCTATC	4625
Db	4462	CTGTGCTTA	TTTCAAGTGG	CCACCTT	TAAAGGCTG	ATCCAGATTTATGAACGATGCCAT	4521
QY	4626	GATTACAG	AGGTGAG	CAAGAAC	CAATTCGTGAA	AAGAACTATCATATGATATTTAT	4685
Db	4522	GATTACAG	AGGTGAG	CAAGAAC	CAATTCGTGAA	AAGAACTATCATATGATATTTAT	4581
QY	4686	TTGCAATCTT	CAATATTTG	GCATCTTTT	TTCACACTCAAT	CTGTTCAATGGTGTATC	4745
Db	4582	TTGCAATCTT	CAATATTTG	GCATCTTTT	TTCACACTCAAT	CTGTTCAATGGTGTATC	4641
QY	4746	ATTGATAAT	TTTTATG	CAAAAGAAAA	AGCGATG	ATCATTAAGAAATGTCCATGCA	4805
Db	4642	ATTGATAAT	TTTTATG	CAAAAGAAAA	AGCGATG	ATCATTAAGAAATGTCCATGCA	4701
QY	4806	GAAATCA	GAAGAAAG	TACTATTA	TCTATGAAAA	AGATGGGCTCTAATAAACCATTA	4865
Db	4702	GAAATCA	GAAGAAAG	TACTATTA	TCTATGAAAA	AGATGGGCTCTAATAAACCATTA	4761
QY	4866	GCCATTTCA	AGACCA	AGGTGGG	CAACAAGCAAT	GTCTTGAATATGTAACGATATAG	4925
Db	4762	GCCATTTCA	AGACCA	AGGTGGG	CAACAAGCAAT	GTCTTGAATATGTAACGATATAG	4821
QY	4926	AAATTCGAT	ATATATCAT	TATATGTTAT	TTCATGAT	CGAACATGTTCAACATGACCTCGAT	4985
Db	4822	AAATTCGAT	ATATATCAT	TATATGTTAT	TTCATGAT	CGAACATGTTCAACATGACCTCGAT	4881
QY	4986	CGTTACGAT	TGCGTCG	CAACGTA	TATACGCGG	CTTAAGCTATCTCAATGCGATATTCGTA	5045
Db	4882	CGTTACGAT	TGCGTCG	CAACGTA	TATACGCGG	CTTAAGCTATCTCAATGCGATATTCGTA	4941
QY	5046	GTTATTTTCA	GTTCCG	ATGTCAT	TATTAATAAT	ATCGCTTACATATCACTAATTTAT	5105
Db	4942	GTTATTTTCA	GTTCCG	ATGTCAT	TATTAATAAT	ATCGCTTACATATCACTAATTTAT	5001
QY	5106	GAGCCATGA	ATTTATTTG	ATGATAG	ATGTGTCTAT	TATATCATTTAATCATCTTAAGCTTGTATCTT	5165

Db	5002	GAGCCATGAAATTATTTGATGATGATGATGTCATTTATATCCATTAGATCTTGTACTC	5061
Oy	5166	AGCGATATTATTCGAGAAAGTACTCTGTGCGCCGACCCCTGCTCCGATGGTGGCG	5223
Db	5062	AGCGATATCATTTGAGAAATTTCTGATATCGCCGACACTGCTCCGTGTGGATGGGCG	5122
Oy	5226	AAAGTGGCCGCTGCTCTTCGACTGTGTGAAGGAGACCAAGGCAATTCGACACTGCTCTTC	5283
Db	5122	AAAGTGGTTCGTGCTCTCGTTTGTGTCAAGGGTGCCAAGGGATATCCGACCTTGCTGTTC	5183
Oy	5286	GGTTTGGCATATGTGCTGCGCGCCCTGTTCAAACATCTGCTGCTGTCTGTGTATG	5343
Db	5182	GGTTTGGCATATGTGCTGCGCGCCCTGTTCAAACATTTGCTGTGCTGTCTGTGTATG	5243
Oy	5346	TTCATCTTTGCGATTTTGGGATGTCGTTCTTCATGCGACGTGAAGAGAAAGCGGCAAT	5406
Db	5242	TTCATCTTTGCGATTTTGGGATGTCCTTTCTTCATGCTATGCAAGAAAGAGCGGCAAT	5302
Oy	5406	AACGACGTCTACAACTTCMAAGACCTTTTGGCCAGAGCATGATCTGCTCTTCAGATGTG	5466
Db	5302	AATGCTGTGTATTAATTTTAAGCAATTTGGCCAAAGTATGATATTTCTGTTCAATGTCT	5362
Oy	5466	ACGTATGCGCGTGGGATGCTGTACTGACCGCCATTATCAATGAGAAAGCATGCAATCCA	5522
Db	5362	ACCTGACGCGGTGGGATGCTGTGTATGATGCAATTAATGAGAAAGATTCGCATATCA	5422
Oy	5526	CCCGACAGCGACAAAGGCTATCCGGGGCAATTTGGTTCAGGACCGTTGGAATATCGTTT	5586
Db	5422	CCCGACACGACAAAGGCTATCCGGGGCAATTTGGTTCAGGACCGTTGGAATATCGTTT	5482
Oy	5586	CTCCTCTCATACCTAGTTATAAGCTTTTGTGATGTTATTAATATGATCATTTGCTCAT	5646
Db	5482	CTCCTTTCATATCTAGTTATATAAGCTTTTGTGATGTTATTAATATGATCATTTGCTCAT	5542
Oy	5646	CTCGAAGACTTATGTCAGGCGCACCGAGGACGTGCAGAGGGCTTAACCGACGACATAC	5706
Db	5542	CTCGAAGACTTATGTCAGGCGCTACCGAGGATGTACAGAGGGCTCTCACCGACGACATAT	5602
Oy	5706	GACATGTACTATGATGTCGACAGAAATTCGATCCGAGGGCACCCCATACATATACGCTAT	5766
Db	5602	GATATGTACTACGAAATTTGGCAAAATTCGATCCGAGGGTATCCCATACATATATATAC	5662
Oy	5766	GATCAGCTGTCCGAATTTCTGAGAGTACGAGCCCGCTGCGAGATCCAAACCGAAC	5826
Db	5662	GACACAGCTGTCCGAGTTCTTGAGAGTGTGAGCCCGCTGCGAGATCCAAACCGAAC	5722
Oy	5826	AAGTACAAAGATCATATCGATGAGACATACCATCTGTGCGGTGACTCATGTACTGCGTC	5886
Db	5722	AAGTACAAAAATCATATCGATGAGACATGCGATATGTGCGGGCGCATATGATGTACTGTG	5782
Oy	5886	GACATCTCTGACGCCCTTACGAAAGACTTTCTTTGCGCGAAGGGCAATCCGATAGAGAG	5946
Db	5782	GATATATTTGATATGCCCTTGACCAAGAGACTTTCTTTGCGCGCAAGGGTAAATCCATGAGAG	5842
Oy	5946	ACGGGTGAGATTGTTGAGATAGCGAGCCCGCCCGGATACGAGAGGCTACGACCCGCTCA	6006
Db	5842	ACGGGTGAAATTTGTTGAGATTGCGGCGGACCGGACCCGAGAGGCTATATATCCGTTGTC	5902
Oy	6006	TCAAACGCTGTGGCGTCAAGCGTGAAGAGTACTGCGCCCGGCTAATTCAGACAGCCTTGCG	6066
Db	5902	TCAACACTGTGGCGCGACGTGAGAGATACGTGCGCAAGCTGATACAGAAATGCGTGGCG	5962
Oy	6066	AAAGCAAAAGGCGCGCGGAGAGAGGTGGTCTTTGACCGCGATACGATATATGGCAT	6122
Db	5962	CGTTACAAAGATGCG-----	5976
Oy	6126	GGCGGTATTCGGAATGCGGGGACCCGCGCCCGCATGAAGACGACGCGGATGCGCC	6186
Db	5972	CCACCCGAGAGGGTGTATGAGGGCGAGGCGGCTGTGCGAAAGATGTGTCTGAAGCGCGT	6036
Oy	6186	GCTGTGTGAGATGATGTTAAACGTTATCTGCAGAAAGAGCTGCGATGCGGATGAGAT	6246



QY	1314	CGTATGCGAATTGCGAAAGGAGGCGGAAAGAAAGAGGCGTCCGAAAGAGGAGCGCATTA	1373
Db	1405	GCTTATGAGAA---CAAGAACAGCGAACACTGAGAGAGGAGAGCAAAAAGAGGCG---	1457
QY	1374	CGTGAAGCGGAGAAAGCTGCGCGCGCCAAAGCGGCGCAAGCTGAGAGAGCGGCGCAATCG	1433
Db	1458	CGAGTTCAAGGCATGCTGAGAGCACTCAAG-----AAGCAGCAGAGAGAGGACAGGCT	1512
QY	1434	CAGGCTCAGGCAAGCAGCGGATGCGGCTGCGCGGCAAGAGGCTGCACTGATCCGGAATG	1492
Db	1513	GCTGCAATGCGCACTCAGCGGCGCACTGCTCGAAGA---CGCATTTGAAGAAAGAGG	1565
QY	1494	GCCAAGATCCGACGTAATTTCTTGCAATCAGCTATGAGCTATTGTTGGCGGCGAAGAGGCG	1553
Db	1570	GAAAGTGGGGTAGGCTCTCCAGAGAGCTCTTGTGAATCTGTAACTGATTTCCAAAGGC	1622
QY	1554	AACGATGACAACAAACAAAGAGAGATGTCATTTCGAGCGTGCAGGTGAGTCCGAGTGC	1613
Db	1630	GCGAAGAGCGGCGGAA-----CGAGGAAAGAGAGAGAGCAAGCAAGAA	1673
QY	1614	GTCAGCGTTATACAAAGCAACCCAGCATCTACACAGCAACACAGCATACCAAGTTGCT	1673
Db	1674	GCTCTTGAAAGCGAGAGAAAGGAGACCCCGAGAAAGTGTTTA-----GT	1720
QY	1674	AAAGTGACACGACATCCCTTATCCCTTACCTGGTATCCGTTTAAATATACGAGGAGATCA	1733
Db	1721	CAGAGTCGGAAGACGATATGAGAAAGAGAGGCGCTTCGCGCTGCACACAAAGATAGGGA	1780
QY	1734	CGTAGTTCTCACAGTATACCATATACGAAACGAGCGTGGCGGCTTTGATATCCGCTAGC	1793
Db	1781	GGAAATTTTTCATCATGATCATAGTGCCTCAGCATTCACAGGCTCGGCTTCCTCTCC	1840
QY	1794	GATCGTAAGCCATTGATGTAATGTCACATATACAGATGCGCCAGACACATTCGCGCTATCC	1853
Db	1841	GACATTAACAGCAAAAGACAGCATCTTCAGCTTCGCGGAGCCG-GTCGCTTCGCGGACCC	1899
QY	1854	GACGACTCGAATGCCGTACCCCGATGTCGGAAGAAATGCGGCGCATATGTCGCCGTG	1913
Db	1900	GCGCTTCGGAATG-----AGTTGCGACAGATGAACAACAGACCGTGGAGAG	1947
QY	1914	TACTATGGCAATCTATAGGCTCCCGAACATCATTCGTATACCTGCAATCACTCCCGAATATCG	1973
Db	1948	AGCGAGGCGCGCGTGACTCGTCTTCAATCCGATCGCGCGCGGACGCGCGGACGAGC	2007
QY	1974	TATACCTCACATGCGCATCTACTCGGCGGACATGCGCGCTCATGCGGCGTACAGCAATGACC	2033
Db	2008	TACAGTGGCTACAGGGGCTTACAGCCAGTGCAGCGCGCTGTGGCGTGAATAATGATTAAGGC	2067
QY	2034	AAGGAGACAAATTCGCGACCCGCAACACAGGCAATCAATGATGTCGCGCCACCAATGGC	2093
Db	2068	AGCTAACGACAGCGCATCTTCCCGACGCTGCGCGCACGCTGAAGCGCAACAGCACGCTG	2127
QY	2094	GGCACCACTGTCTGACACCAATCACAAAGCTCGATCATTCGCGATACGAATTTGGCGCTG	2153
Db	2128	GACTGCAACGCGGTATGTCATCTACGCGGCCGCTACACATGCGGCGGCTCTGCTCT	2187
QY	2154	GAGTGCACGAGCGAAGCTGCGCAAGTTAAACATCATGACAAATCTTTTATCGAGCCGCTC	2213
Db	2188	GAGCGAAAGCATGAGGTGAAATTTAAAGAAAGGCGCTGAGTCTTTTATGTTTCTATG	2247
QY	2214	CAGACACAAACGCTGCTTGAATATGAATAATGATGTCCTGAAATGACATCATGGAACG	2273
Db	2248	GACCAACTCGCTCTTACGAGCGAAGGA-----CAGATCAACAGCATTAATAG	2297
QY	2274	GCCGCTGTGTCGACACATGTCGCGGACAGCATGCGGCTGTCTCGTTACTATATTTCCAA	2333
Db	2298	CGTGTTCACAAACACGCTATGAGAAAGACTGGAAGAGTCTCAGAGAA-----	2344
QY	2334	GAGACGATGACAGAGATGGGCGCAAGCTTCAAGACAGAGGCACTGGAAGTATCTTCAAA	2393
Db	2345	-----AGTGCACACCGTGTGATTAAGTTTGGCAACATTTTCTCTCA--	2386

QY	2394	GGCATCGATGATGTTTGTGTGGGCACTGTTCGCGGTTTGTTGAAATTTCCAGGATGCG	245
Db	2387	-----TCTGGAGTGTCAACCCCTACTGATTAATCTGAAGAGATC	242
QY	2454	GTATCGCTCATTCGTTTCGATCCCTTCGTGAGCTCTTCATCAAGCTGTGCAATTTGTGTC	2513
Db	2428	GTGAACCTTAATCGTATGAGACCCCTTTTGTAACTTAGCATCAACATCTGCATCGTTCTG	2487
QY	2514	AACACGATGTTTCATGCGCATGAGATCAACAGATATGAACAAGAGATGAAACGGTGTCTC	2573
Db	2488	AATAGCTATTATTATGCGCATGAGACCATCCATCCATGACCAAGTTCGAAACAGTCTTGTG	2547
QY	2574	AAGAGTGGCACTATTTCTTCAACCGCCACTTTTGCAATCGAGGCCACCATAGAGCTATG	2633
Db	2548	GCCGTAGAAATCTGATGTTCACCGGAGTCTTCAACGCGGAAATGTTTCTAAGCTCATYA	2607
QY	2634	GCCATGAGCCCCCAAGTACTATTTCCAGAGGAGCTGGAACACTCTTCGACTTCATTATCGTG	2693
Db	2608	GCCATGAGACCCCTACTATTAATTTCCAGAAAGCTGGAACATTTTGAACGATTAATTTGTC	2667
QY	2694	GCCCTATGCTATTGGAACGTGGAACTCGAGGATGTCAAGGATCTGTCCGATATGCTTCC	2753
Db	2668	TCCCTCAGTTTAATGAGACTGATGTCTGCAATGTGAGGGGCTCTCAGTCTGTGGGCTCT	2727
QY	2754	TTTGCATTCGCTCGGTGATTTCCAACTGGCCCAAGTCTTGCCCCACACTTAATTTACTATT	2813
Db	2728	TTCCGACGCTCCAGTCTTTCAGCTGTGCAAGTCTGGCCACCTCGAACAATGCTGATC	2787
QY	2814	TCGATTATGGAGCGCACCATGAGGCGCTTTGGGATATCGACATTTGTACTTTCATATTC	2873
Db	2788	AAGATCATCGGAAACTCCGTGGGTGCTCGGAGCACTGACCTGTGCTGGCCATCATTC	2844
QY	2874	ATCTTCATCTTTGCGGTGATGAGGAAATGCAACTGTTTCGAAAGAAATTAATCATGA--TCAC	2930
Db	2848	GTCCTCATCTTCGCGGTGTGGGATGAGCTGTTTGGAAAGATTAACAAGATGCGCTC	2907
QY	2931	AAGACCGCTTTCCGAGATGCGGCACTGCGCGGCTGGAACCTTCAACGATTTATGCAACGC	2990
Db	2908	TGTAAAGATCAACCAAGAGTGTCAACCTCCCGGCTGGCAATGAACGATTTTCCATCTCC	2967
QY	2991	TTTCATGATCGATTTCCGGGTGCTCTGCGGGAATGAGATCGAGTCAATGTGGAGCTGATG	3050
Db	2968	TTCTCATGCTTTCCAGATCTGTGTGGGAGTGGATCGAGCCAAATGTGGGACTGATG	3022
QY	3051	TACGTG---GGCGATGTCCTGTGCATTCCTCTCTTCTGGCACCGTGTGATCGGCAT	3107
Db	3028	GAGGTGCGCGGCGCAGGCCATGTGCTCATGTCTTCATGATGATTAATGTGATTTGGCAAC	3087
QY	3108	CTTGTGTACTTAACTTTTCTTAGCCTGTGCTTTGTTCCAATTTTGCTCATTAAGCTTA	3167
Db	3088	CTGTGTGTCTGAATCTAATTCCTGTGGCTCTTCTGAGTCTCTTCAGGCGCAGAACACTG	3147
QY	3168	TCAGGCGCGCATGCGCGCATTAAGATTAACAATAATACCGAGGCGCTTCATTCGAATTGGC	3227
Db	3148	GCGGCGACAGCGACGAGCGGGAAATGAACA-----	3179
QY	3228	CGATTAAAGATGGGTTAAGCTAATATTTCTGATTTGTTCAAGTTAATACGTAAACAA	3287
Db	3180	-----	3179
QY	3288	TTGACAAATCAATAATAGTATCAACATCAAGTGAAGAGCAACCAAGATCAGTTGGATT	3347
Db	3180	-----CTGCGAGATCTCAGTATC	3198
QY	3348	TGAGAGCAAGCATGTGTGACACAGAACTGAGAGCTGGGCCACACAGATTCCTGGCCGAC	3407
Db	3199	CGGATCAAGAAAGGCGGTGGCTGTGACCAAAATGAAGTGCACGCTTTCATGTCAAGGCTCAC	3258
QY	3408	GAGCTCATCAAGAGGGGATCAAGAGACAGCAACTGAGAGTGTGGCATTCGGGGATTCGG	3467
Db	3259	TTCAAGACAGCGGGAGCGGATGAAGTGAACCTCTCGACGAGCTGTATGAGAAAGAAAGGCC	3318
QY	3468	ATGGAATTCACGATACAGCGCGCATGAAGAACCAAGCCGAAAGAAATTCAAATATCTA	3527

Db 3319 AATCGATCGCCACCAACGAGGGGTGATATCCACCGGAAACGGCCACTTCAGAAAGAAC 3378  
Qy 3528 AATPAGCAACGATGATTGGCAACTAATTAACCAACAGACAAATAGACTGGAACAGAG 3587  
Db 3379 GGGGAACGGAACCAACAGCGGCATCGGACGAGCGTGGAGAATGATCATCATGACGAGAC 3438  
Qy 3588 CTAAACATAGAGGTGTGCTTACAGAGAGACGACCTGCGACATTAATCTATATGT 3647  
Db 3439 CACG-----TGCTCTCATTAACAC-----CGAACTGACCGTCCGGGT 3479  
Qy 3648 AGCCATPAGATCGACCATTCAGAGACGAGCCACAGGCGACGCGGAGAGATGAG 3707  
Db 3480 GCCCATGTGTGGGCGAGTC-----TGACTTGAAGAACTCAACAGAGATGTTAGC 3534  
Qy 3708 GGGGAGAGAGAGCCACCGCAGAGAGAGATTTAGGTCTCGACGAGAACTGAGACGAG 3767  
Db 3535 AGGGAATCAGACCTTGAAAGGACAGAAAGATTA-----ACTGAGCGATACCACTCTCA 3588  
Qy 3768 GAGGGCGAATGCGAGAGGGCCGCTGACGATGATCATTAATTCAGACAGAGAG 3827  
Db 3589 GAAAGAAATGACATCGACATGAACTGAGGTGAGAAAGTTCCCTGAGCAACTGAG 3648  
Qy 3828 GATATACTCGATGAATTCAGCTGATGCTGCCCGCATTCGATATAAGAAATTCG 3887  
Db 3649 GAATPACTGG-----ATCCGAGCGCTGCTTACAGAGGGTGTGCTCCAGCGGTTCAAG 3702  
Qy 3888 ATCTTACCGGTGACGATGACTGCGCTTCTGGCAGAGATGGGCAATTTAGCATGAAA 3947  
Db 3703 TGTCTGCGAGGTCAACATCGAGAGAGACTAGGCAAGTGTGTGATCTTGGCGGAAACC 3762  
Qy 3948 ACTTTCAATTAATGAAATAATTTTGAACAGCTGTATPACTATGATTTAATG 4007  
Db 3763 TGTCTCTCATTTGTGAGCAAAATGTTGAGACCTTCAATCTTCAATGATTTGCTC 3822  
Qy 4008 AGTAGCTTACCTTGGCATTAGAAAGATGATCATCTGACAAAGAACCCATATGACAGAT 4067  
Db 3823 AGCAGTGGCGCCCTGGGCTTTGAGACATCTACATGAGACAGAAAGCAATCCGACCC 3882  
Qy 4068 ATTTTATACATNANGACAGAAATTTTACGGTTATNTCTTGGAAAATGTTAATCAG 4127  
Db 3883 ATCTGAGATGCGAGCAAGGTCTTCACTCACTCACTTCACTGAGATGTTGCTCAAG 3942  
Qy 4128 TGGTTGCGCTCGGCTTCAAGTGTACTTACCAACCGCTGTGTTGCTCGATTCGATG 4187  
Db 3943 TGGACAGCCATCGGCTTCTGCAAGTTCTTACCAATGCTGTGTGTTGAGACTTCTC 4002  
Qy 4188 ATTTGATGATGCTTATCACTTGTGCTTCACTTGTGAGAGCTGTGTATTCAA 4247  
Db 4003 ATTTGCTGTCTCTTATGCTACGCTTAATGCTAATGCTGAGGCTAATCGGAATAGGT 4062  
Qy 4248 GCTTCAAGCTATGCGAAGCTTAAGACCTGAGACCACTAGTGCATGTCCTGATG 4307  
Db 4063 GGCATTAAGTCCCTTAGAGACCTTAAGAGCTTGAAGCCCTTAAGAGCTTATACAAAT 4122  
Qy 4308 CAGGCGATGAGGCTGCTGTTAATGCGCTGTACCAAGTATACCTTCATCTCAATG 4367  
Db 4123 GAGGAGATGAGGCTGTGTGATGCTGCTTGTGGGCGCCATCCCTTCATCATGAAATG 4182  
Qy 4368 CTATGCTGTCTAATATTTTGGCTAATTTTTCATAATGAGGTGACAGCTTTTGTCT 4427  
Db 4183 CTCTGTGTGTCTCATCTTCTGCTGATTTTCAAGATCATGAGAGTAACTGTTTGGC 4242  
Qy 4428 GGAATAATTTTAAGTC-----GAGGACATTAATGACAGAGCTCAGCCGAGATCATA 4484  
Db 4243 GGGAAATPACCACTACTGCTTAAATGAGACTTGAATTCGATTCGAATGATTTGTC 4302  
Qy 4485 CCAATTCGAATGCTGCGAG-----AGCAGAACTACAGTGGAGT 4526  
Db 4303 AACAAATTAACGAGCTGTGAGAGCTCATGAGAGGCAACGACAGAGATCCGATGGAAG 4362  
Qy 4527 AATTCAAGCAATGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 4586

Db 4363 AATGCAAGTCAACTTTGACATGTCGAGAGAGGTACCTGACCTTCTTCAAGTGGCA 4422  
Qy 4587 ACCTTAAAGGCTGGATATCAATCATGAAAGATGCTATGATTTACAGAGAGTGGACAG 4646  
Db 4423 ACCTTAAAGGCTGGATATCAATCATGAAAGATGCTATGATTTACAGAGAGTGGACAG 4482  
Qy 4647 CAACCAATTCGTAACGAAACATCTACATGATTTATATTTGATTTCTTCAATATTT 4706  
Db 4483 CAGCTGACTCAGAGGCAACATCTACATGATCATCTTGTGATCTTCAATCTTTC 4542  
Qy 4707 GATTCCTTTTCACTCAATCTGTTCAATGTTGTTATCATGATTAATTAATGACAA 4766  
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DB 5920 TTGGCTAGGCGGG 5932

## RESULT 15

US-09-425-043-43

Sequence 43, Application US/09425043

Patent No. 6335172

GENERAL INFORMATION:

APPLICANT: DELGADO, STEPHEN G.

APPLICANT: DIETRICH, PAUL S.

APPLICANT: FISH, LINDA M.

APPLICANT: HERMAN, RONALD C.

APPLICANT: SANGAMESWARAN, LAKSHMI

TITLE OF INVENTION: NOVEL CLONED TETRODOTOXIN-SENSITIVE

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESS: JANET PAULINE CLARK

STREET: 3401 HILLVIEW AVENUE, MS A2-250

CITY: PALO ALTO

STATE: CA

COUNTRY: U.S.A.

ZIP: 94304-1397

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/425,043

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/024,020

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APPLICATION NUMBER: US 60/039,447

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ATTORNEY/AGENT INFORMATION:

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REGISTRATION NUMBER: 34,799

REFERENCE/DOCKET NUMBER: R0020B-REG

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TELEPHONE: (650) 852-3097  
TELEFAX: (650) 855-5322  
INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 6586 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-425-043-43

Query Match 15.7%; Score 1021.4; DB 3; Length 6586;  
Best Local Similarity 52.5%; Pred. No. 1.9e-272;  
Matches 3125; Conservative 0; Mismatches 2486; Indels 342; Gaps 27;

QY 186 CGCAAGAAAAAAGAAATCCGATATGATACGAGAGCGAGATGAAGTCCACA 245  
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QY 246 CCGGATCCTACCTGAACAGGGGTGCAATACCTGTGATTCAGGGGAGCTCCG 305  
DB 328 AAGCAAAACAGTACCTGAGGCTGGAAGGTTGCTTCACTACGAGGACATCCG 387  
QY 306 CCGAATTTGGCTTCACCTCTCTGAGATATGATCTTACTACAGCAATGTACTGCA 365  
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QY 366 TTGTGATTTGTAAGCAAGAAAGATATTTTCTTTCTTTCGATCAAAAGCATGTGG 425  
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2005, 04:13:21 ; Search time 3369 Seconds  
(without alignments)  
11820.771 Million cell updates/sec

Title: US-08-554-424-7

Perfect score: 6513  
Sequence: 1 TCTGACGCTTGCGCGCATAG.....ACGGGAGTATAGCTCTAGA 6513

Scoring table:

IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5654200 seqs, 3057283753 residues

Total number of hits satisfying chosen parameters: 11308400

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
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- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq.\*
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- 19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 20: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 21: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*
- 22: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4447.8	68.3	6318	10	US-09-428-371-1
2	4434.2	68.1	6318	10	US-09-428-371-2
3	1019.4	15.7	6586	17	US-10-152-319A-1723
4	1019.4	15.7	6586	18	US-10-377-139-14
5	974	15.0	6503	18	US-10-377-139-16
6	944.8	14.5	7052	16	US-10-202-824-5
7	941	14.4	6027	17	US-10-297-022-40
8	940.6	14.4	8491	17	US-10-333-191-3
9	940.6	14.4	6048	18	US-09-896-994-1
10	940.2	14.4	6048	18	US-10-685-237-1
11	940.2	14.4	6048	18	US-10-852-840-1

12	939.4	14.4	6048	9	US-09-840-125-3	Sequence 3, Appli
13	939.4	14.4	6048	18	US-10-914-133-3	Sequence 3, Appli
14	939.4	14.4	8490	15	US-10-101-610-617	Sequence 617, App
15	938.4	14.4	8491	17	US-10-333-191-1	Sequence 1, Appli
16	937.8	14.4	6172	18	US-10-632-342-1	Sequence 1, Appli
17	937.8	14.4	6172	18	US-10-632-342-3	Sequence 1, Appli
18	936.6	14.4	6091	16	US-10-077-054-1	Sequence 1, Appli
19	936.6	14.4	6169	18	US-10-632-342-5	Sequence 1, Appli
20	936.6	14.4	6169	18	US-10-632-342-7	Sequence 7, Appli
21	936.4	14.4	8380	19	US-10-482-834-1	Sequence 1, Appli
22	935.4	14.4	5922	9	US-09-930-871-13	Sequence 13, Appli
23	935.4	14.4	5922	19	US-10-925-369-13	Sequence 11, Appli
24	935.4	14.4	6030	9	US-09-930-871-11	Sequence 11, Appli
25	935.4	14.4	6030	19	US-10-925-369-11	Sequence 11, Appli
26	934.6	14.3	8381	18	US-10-451-126A-8	Sequence 8, Appli
27	934.6	14.3	8381	18	US-10-451-126A-9	Sequence 9, Appli
28	933	14.3	8379	18	US-10-806-899-53	Sequence 53, Appli
29	933	14.3	8380	18	US-10-806-899-15	Sequence 15, Appli
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31	933	14.3	8381	18	US-10-451-126A-11	Sequence 11, Appli
32	933	14.3	8381	18	US-10-451-126A-11	Sequence 89, Appli
33	933	14.3	8381	19	US-10-482-834A-8	Sequence 8, Appli
34	933	14.3	8381	19	US-10-482-834A-9	Sequence 9, Appli
35	933	14.3	8381	19	US-10-482-834A-20	Sequence 20, Appli
36	932.6	14.3	8380	18	US-10-806-899-18	Sequence 18, Appli
37	931.4	14.3	8381	18	US-10-451-126A-1	Sequence 1, Appli
38	931.4	14.3	8381	18	US-10-451-126A-3	Sequence 3, Appli
39	931.4	14.3	8381	18	US-10-451-126A-7	Sequence 7, Appli
40	931.4	14.3	8381	18	US-10-806-899-1	Sequence 1, Appli
41	931.4	14.3	8381	18	US-10-806-899-2	Sequence 2, Appli
42	931.4	14.3	8381	18	US-10-806-899-3	Sequence 3, Appli
43	931.4	14.3	8381	18	US-10-806-899-4	Sequence 4, Appli
44	931.4	14.3	8381	18	US-10-806-899-5	Sequence 5, Appli
45	931.4	14.3	8381	18	US-10-806-899-6	Sequence 6, Appli

#### ALIGNMENTS

RESULT 1  
US-09-428-371-1  
; Sequence 1, Application US/09428371  
; Publication No. US20030096336A1  
; GENERAL INFORMATION:  
; APPLICANT: Sodellund, David M.  
; APPLICANT: Knipple, Douglas C.  
; APPLICANT: Ingles, Patricia J.  
; TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM INSECTICIDE-SUSCEPTIBLE AND  
; TITLE OF INVENTION: INSECTICIDE-RESISTANT HOUSE FLIES  
; FILE REFERENCE: 19603/606  
; CURRENT APPLICATION NUMBER: US/09/428, 371  
; CURRENT FILING DATE: 1999-10-28  
; EARLIER APPLICATION NUMBER: 08/608, 618  
; EARLIER FILING DATE: 1996-03-01  
; EARLIER APPLICATION NUMBER: 08/772, 512  
; EARLIER FILING DATE: 1996-12-24  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 6318  
; TYPE: DNA  
; ORGANISM: Musca domestica  
US-09-428-371-1  
Query Match 68.3%; Score 4447.8; DB 10; Length 6318;  
Best Local Similarity 82.0%; Pred. No. 0;  
Matches 5298; Conservative 0; Mismatches 1002; Indels 159; Gaps 9;  
QY 24 ATGACAGAAAGTTCCGATCTGAGAGAGACGACGTTGTCCTTCAC 83  
DB 1 ATGACAGAAAGTTCCGATCTGAGAGAGACGACGTTGTCCTTCAC 60  
QY 84 CGGATCATTTGGTGAATGAACACGATTCGCGTGAACATGAAGAGAG 143

Db 61 CGGATTCATGTTTACAAATCGAACAACGAT---CGCTGACATGAAAAACAAAGAG 117  
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Qy 204 GAATCGATATATATGACGAGAGCGAGATGAAGTTCACAAACCGATCTTACACTTGA 263  
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Qy 264 CAGGATGTCCTTACCTGTTTCATGTCAGAGGAGCTTCCCGCGAATTGGCTCCACT 323  
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Qy 324 CTTCTGAGGATATCGATCCCTTACATGACGAAATGTAAGTACTGATTTGTAAGCAA 383  
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Qy 384 GAAAGATATTTTGTGCTTTCTGATCTAAAGCAATGAGATGCTCCATTCATCAAT 443  
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Qy 444 CCGATACGTCGTGAGCATTTTACATTTAGTCATTCATTTATTTCCCTATTCATC 503  
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Qy 504 ACCAATATTCGTCAATGTCATCTGATCTGATATATGCGCAACGCCCGATGAGTCC 563  
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Qy 564 ACTGAGGATATTTACCGGATCTACATTTGAATCAGCTGTAAAGGATGAGGACGA 623  
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Qy 1764 GAGCGTGGCGGCTGCTGATACCGGATGACGATGATGATGATGATGATGATGATGAT 1823  
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QY 2829 ACCAATGGGCGCTTGGGTAATCTGACATTTGACTGCTGCTGCTGCTGCTGCTGCTG 2888  
DB 2761 ACCAATGGGCGCTTGGGTAATCTGACATTTGACTGCTGCTGCTGCTGCTGCTGCTG 2820  
QY 2889 GTATGAGGATGCACTGCTGGAAGAAATTAATCATGATCAACAAGACCGCTTCCGAT 2948  
DB 2821 GTATGAGGATGCACTGCTGGAAGAAATTAATCATGATCAACAAGACCGCTTCCGAT 2880  
QY 2949 GGGCACTGCGCGCTGGAATCTTCAACGATTTATGCAACGCTTCATGATGCTGCTG 3008  
DB 2881 CATGAAATTAACGCGCTGGAATCTTCAACGATTTATGCAACGCTTCATGATGCTGCTG 2940  
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DB 2941 GTGCTCGGAGGAAATGATGAGATGATGATGATGATGATGATGATGATGATGATG 3000  
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DB 3181 CGTAAATATGCTGATGTTTCAAGTATATGTAACAATTTGACAAATCAATATAGTAT 3240  
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DB 3241 CAACCATC-----AGAACATGCGCAT 3261

QY 3369 AACGAATGAGCTGGGCGACAGAGATCCCTGCGCGAGGCTTCATCAAGAGGGATC 3428  
DB 3282 AATGATCTGAGGTTGGTCAATGACGAATCATGGCGATGGCTTGATTAAGAGGATAG 3321  
QY 3429 AAGGAGCAGACGCACTGAGGTTGGCCATCGGGATCGGATGATTAATCAACATACCGGC 3488  
DB 3322 AAGGAGCAGACGCACTGAGGTTGGCCATCGGGATCGGATGATTAATCAACATACCGGC 3381  
QY 3489 GATCATGAAGAACACAGCCGAGAAATCCAAATATCTAAATTAACGAAATGATGGC 3548  
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DB 3502 ATACGAGCAGATGACATGCGAGATTAATCAATATGATGATGATGATGATGATGATG 3561  
QY 3669 AAGGAGCAGACGCAAGAGGCGAGCGAGATGAGGCGAGAGAGAGAGAGAGCGCC 3728  
DB 3562 AAGGAGCAGACGCAAGAGGCGAGCGAGCGAGATGAGGCGAGAGAGAGAGAGCGCC 3621  
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QY 3846 CCACTGATGCTGCGCCGATGCTGATTAAGAAATTTCCGATCTTACCGGTCGAT 3905  
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QY 3906 GACTCGCGGCTTGGGCAAGATGAGGCAATTTAGAGCAAGAACTTTCAATTAATGAA 3965  
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QY 3966 AATTAATTTTGAAGAGCTGATATCACTATGATTTTAAATGATGATGATGATG 4025  
DB 3862 AATTAATTTTGAAGAGCTGATATCACTATGATTTTAAATGATGATGATGATG 3921  
QY 4026 TTAAGATGATCACTGCGCAAGAAACCATCTGAGATATTTATATATATGAGAC 4085  
DB 3922 TTAAGATGATCACTGCGCAAGAAACCATCTGAGATATTTATATATATGAGAC 3981  
QY 4086 AGAATATTTACGTTATATCTTCTGGAATGTTAATCAAGTGTGGCGCTGCGCTTC 4145  
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QY 4146 AAGGTACTTCAACCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4205  
DB 4042 AAGGTACTTCAACCAAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4101  
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DB 4222 GTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4281  
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QY 4446 GAGGATGATGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATG 4505

Db 4342 AAGATGATATACCTGCTGAGCCATGAAATCATACGATGTATGCTGCTGAAA 4401  
 Qy 4506 AGGAGAACTACACGTGGTGAATTCAGCAATGATTTGATCATGTAGTAAAGCGGTAT 4565  
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 Qy 4686 TTGCTATTTCTTCAATTTGATTCCTTTTCACTCATCTGTCATGCTGTTATC 4745  
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 Db 4762 GCCATTCAGAACCAAGGTGGGAGCAAGCAAGCATAGTATTCGAAATAGTAAACCAATAG 4821  
 Qy 4926 AATGTGATTAATCATTTATGATTTATCATTTGATGCTGAAAGTGTTCACATGACCCCGAT 4985  
 Db 4822 AATGTGATTAATCATTTATGATTTGATTTGCTTTAAACATGTTTACCATGACCCCGAT 4881  
 Qy 4986 CGTTAAGATGCTGAGCAACGTATTAACGCGGTCTTGAAGTCTCATATGAGATATTCGTA 5045  
 Db 4882 CGGTACGAGCCCTCCGAGGCGTACAAAGTCTCTGCAAACTCATATGAGATATTCGTA 4941  
 Qy 5046 GTTATTTTCAAGTCCGATGTCTATTTAAATTTGCTTTAGCATATCATTTTAT 5105  
 Db 4942 GTTATTTTCAAGTCCGATGTCTATTTAAATTTGCTTTAGCATATCATTTTCAA 5001  
 Qy 5106 GAGCCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5165  
 Db 5002 GAGCCATGGAATTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5061  
 Qy 5166 AGGATATTAATGAGAAATCTTCTGTCGCGAGCCCTGCTCGAGTGTGCGTGTGCGG 5225  
 Db 5062 AGGATATTAATGAGAAATCTTCTGTCGCGAGCCCTGCTCGAGTGTGAGAGTGTGCGG 5121  
 Qy 5226 AAGTGGGCGGCTCTTCTGATGAGTGAAGGAGCAAGGCGATTTGGGACATGCTCTTC 5285  
 Db 5122 AAGTGGGCGGCTCTTCTGATGAGTGAAGGAGCAAGGCGATTTGGGAGTGTGCTTC 5181  
 Qy 5286 GCGTTGGGCGATGCTGTCGCGGCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTG 5345  
 Db 5182 GCGTTGGGCGATGCTGTCGCGGCGCTGTTCAACATTTGCTGCTGCTGCTGCTGCTGCTGCTG 5241  
 Qy 5346 TTTCATTTTTCATTTTTCGAGATGCTGCTTTCATGACGTGAAGAGAGAGCGGCAAT 5405  
 Db 5242 TTTCATTTTTCATTTTTCGAGATGCTGCTTTCATGACGTGAAGAGAGAGCGGCAAT 5301  
 Qy 5406 AAGGAGGTGACAACTTCAAGACCTTTGGCGAAGATATCTGCTTTTTCAGATGCTG 5465  
 Db 5302 AAGGAGGTGATATTTTAAAGATTTGGCGAAGATATTTGCTGTTTCAGATGCTG 5361  
 Qy 5466 AGCTGACCGGTTGGAGTGGTACTGAGCGCCATTCATGATGAGAGAGAGAGAGAGAGAGAGAG 5525  
 Db 5362 AGCTGACCGGTTGGAGTGGTACTGAGCGCCATTCATGATGAGAGAGAGAGAGAGAGAGAGAG 5421  
 Qy 5526 CCGGACAGCAGCAAGGCTATCCGGGCAATGCTGTTACGCGAGCGTTGGAATTAACGTTT 5585

Db 5422 CCGGACAGCAGAGGCGTATCCGGGCAATGCTGTTGAGCAGCTGTTGGAATTAACGTTT 5481  
 Qy 5586 CTCTCTCATACCTTACTTATTAAGCTTTTGAATGTTATTAATGATACATTTGCTGCTAT 5645  
 Db 5482 CTCTCTCATATCTATGTTATTAAGCTTTTGAATGTTATTAATGATACATTTGCTGCTAT 5541  
 Qy 5646 CTCTGAGAACTATATGTCAGGCGACCGGAGAGCTGCAAGAGGCTTAAACGAGCAGCAGTAC 5705  
 Db 5542 CTCTGAGAACTATATGTCAGGCGTACGAGAGATGTCAGAGAGGCTTCAACGAGCAGATTA 5601  
 Qy 5706 GACATGATCTATGATGATCTGAGCAATTCATTCGAGAGGAGCCGAGTATCATATGCTAT 5765  
 Db 5602 GATATGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5661  
 Qy 5766 GATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5825  
 Db 5662 GATGATGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5721  
 Qy 5826 AAGTCAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5885  
 Db 5722 AAGTCAAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5781  
 Qy 5886 GACATCTGAGCGCTTTCAGAAAGCTTTTTCGCGAGAGAGGCAATCCGATTAAGAGAG 5945  
 Db 5782 GATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5841  
 Qy 5946 AGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6005  
 Db 5842 AGGAGTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5901  
 Qy 6006 TCAACGCTGTCGTCAGAGGAGTACGTCGCGCGGCTATTCAGCAGCCTGTCGCA 6065  
 Db 5902 TCAACGCTGTCGTCAGAGGAGTACGTCGCGCGGCTATTCAGCAGCCTGTCGCA 5961  
 Qy 6066 AAGCAGAGGCGCGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6125  
 Db 5962 CGTTACAGAAATGAGC-----CAACCCGAGAGGAGTAT 5994  
 Qy 6126 GCGGATGATCCGAGTCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6185  
 Db 5995 GAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6054  
 Qy 6186 GCTGTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 6245  
 Db 6055 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6114  
 Qy 6246 AATGTAATATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6305  
 Db 6115 ACATGACCT-----CAGATCCAGATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6159  
 Qy 6306 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6365  
 Db 6160 GTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6219  
 Qy 6366 GTTCTGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6425  
 Db 6220 GATGATGTCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6279  
 Qy 6426 CGATGCGCAGATCATGCTGCGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6484  
 Db 6280 AGATGCGCAGATCATGATCCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 6318

RESULT 2  
 US-09-428-371-2  
 ; Sequence 2: Application US/09428371  
 ; Publication No. US20030096336A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Soderlund, David M.  
 ; APPLICANT: Knipfle, Douglas C.  
 ; APPLICANT: Ingles, Patricia J.  
 ; TITLE OF INVENTION: INSECT SODIUM CHANNELS FROM INSECTICIDE-SUSCEPTIBLE AND  
 ; TITLE OF INVENTION: INSECTICIDE-RESISTANT HOUSE FLIES



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; FILE REFERENCE: 19603/606
; CURRENT APPLICATION NUMBER: US/09/428,371
; CURRENT FILING DATE: 1999-10-28
; EARLIER APPLICATION NUMBER: 08/608,618
; EARLIER FILING DATE: 1996-03-01
; EARLIER APPLICATION NUMBER: 08/772,512
; EARLIER FILING DATE: 1996-12-24
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 6315
; TYPE: DNA
; ORGANISM: Musca domestica
; US-09-428-371-2

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Query Match	68.1%;	Score 4434.2;	DB 10;	Length 6315;
Best Local Similarity	81.8%;	Pred. No. 0;		
Matches 5284; Conservative	0;	Mismatches 1013;	Indels 162;	Gaps 8

OY	24	TTGACAGAAAGATTCCGACCTCCGATATCTGAGAGAAAGACGATGTTGTCCGTCCCTTAC	83
Db	1	ATGACAGAAAGATTCCGACCTCCGATATCTGAGAGAAAGACGATGTTGTCCGTCCCTTAC	60
OY	84	CGCGAATCATTTGGTCCAAATCGAACAACGATATGCGCTGGAACTGAAAAGCAGAAAGAG	143
Db	61	CGCGAATCATTTGTTCAATTCGAACAAAGTAT--CGCTGAACATGAAAACAAAAGAG	117
OY	144	CTGGAAGAAAGAGAGCCGAGGAGAGAGGTGCTCCGATATGTCGTGCAAGAAAAACAAAA	203
Db	118	CTGGAAGAAAGAGAGAGCCGAGAGAGAGC-----	148
OY	204	GAATCCGATATGATGACGAGAGCAGAGATGAAGGTCCAACAACCGAATCTACACTTGA	263
Db	149	AGATACATATGATGACGAGAGCCGAAGATGAAGGTCCAACGCCGATCCCACTTGA	207
OY	264	CAGGTGAGCAATACCTGTTCCATTTGACAGGCACTTCCGCGCGGAATGGCTCCACT	323
Db	208	CAGGTGAGCTTAATCCTGTTGAAATGACGGCACTTCCGCGCGGAATGGCTCCACT	267
OY	324	CCTCTCGAGATATGATGATCCCTACATACAGCAATGTATGACATTTGTATGTAAGCAA	383
Db	268	CCTCTCGAGATATGATGATCCCTTACAGTATATGATGACATTTGTATGTAATGTA	327
OY	384	GGAAAGATATTTTTCGCTTTTCTGCATCAAAAGCAATGTGAGTCTGCATCATTCAT	443
Db	328	GGAAAGATATTTTTCGTTTTTCTGCTCAAAAGCAATGTGAGTCTGCATCATTCAT	387
OY	444	CCGATACGTCCGTGGCCATTTACATTTCTAGTGCATCCATATTTTCCCTATTCATATC	503
Db	388	CCGATACGTCCGTGAGCCATTTATTTTATGATATCCCTGTTTTGTTATTCATTTATC	447
OY	504	ACCACAATTCCTCGTCACTGCATCTGTGATGATTAATGACGCAACGCCACGGTTAGTCC	563
Db	448	ACCACTATTTCTAACATTTATTTATTAATGATATGCCGACAACGCCACGGTCAATCC	507
OY	564	ACTGAGTGATATTCACCGGAATCTACACATTTGATCAGCTGTTAAAGTATGACGA	623
Db	508	ACAGAGTGATATTCACCGGAATCTACACATTTGATCAGCTGTTAAAGTATGACGA	567
OY	624	GGTTTCATTTATGCCCCGTTTACGTATCTTGAAGATGCATGGAATTTGCTGGACTTGTA	683
Db	568	GGTTTCATTTATGCCCCGTTTACGTATCTTGAAGATGCATGGAATTTGCTGGACTTGTA	627
OY	684	GTAATAGCTTATGCTATATGACACATGGGATATGATTAAGTAATCTATGACGCCCTGGA	743
Db	628	GTAATAGCTTATGCTATATGACACATGGGATATGATTAAGTAATCTGACGCTTGA	687
OY	744	ACGTTTAAAGGTGCTCGAGCGCTTAAACCGTATGCAATGTGCCAGGCTTGAAGACATC	803
Db	688	ACATTTAAGGTATCTCGAGGCTCTGAAAACCGTATGCAATGTGCCAGGCTTAAACCATTT	747
OY	804	GTCGGCGCGTCAATCGAATCGGTGAAGATCTGCGGATGTGATTAATCTGAACATGTTT	863

Db	748	GTCCGTCCTGTCATTGGAATCTGTAAAAAATCTACGCCGATGTGATATATTTTGACATGTTT	807
QY	864	TCCCTGTGCGTGTTCGCGTTGATGGGCTTACAGATCTATATGCGGTCTCACCGAAG	923
Db	808	TCCCTGTGCGTGTTCGCGCTGATGGGCTTACAAATCTATATGGGTGTTCTAACAACAAAG	867
QY	924	TGCATCAAGAAAGTTTCCCGCTGGAAGGTTCTCTGGGGCAATCTGACCGACGAGAACTGGGAC	983
Db	868	TGCATTTAAACGATTTCCCTCTGAGCGGCGAGTTGGGGCAATCTGACCGAAGAAACCTGGTTT	927
QY	984	TATCAACATTCGCAATAGCTCCCAATTTGGATTTCCGAGACGAGGGGATCTCATTTCCGTTA	1043
Db	928	CTACCAATAGACACAGTTTCCAAATTTGGTTTACGAGAAACGATGGCGAATCATATCCGGTG	987
QY	1044	TCCGCAATATATCTCCGTCGCGGGCAATCGACGACGATTAAGTGTGCTCGCAGGGGTTT	1103
Db	988	TCCGGGAATGTATCCGTGTGCGGGACAATGGCGGCAAGTTACGTCTCGTCAAGGGCTTC	1047
QY	1104	GCTCCGAATCCGAATTTATGGCTACACAGCTTCCGATTTGTTCCGATGGGCTTTCTGTCC	1163
Db	1048	GGCCCAATCCCACTACGACCTACACCGATTTCCATTTCCGTTTGGCTTTCTCTGTCC	1107
QY	1164	GCTTCCGGCTGATGACACAGAGCTTGGGAGATCTGTACCGAGCTGCTGTGGGGCC	1222
Db	1108	GCGTTTCTCTCATGACCCAAAGATTTCTGGAGGATCTGTATCGACAGCTGTCTGAAGCA	1167
QY	1224	GCCGACCATGGACATGCTGTTCTTTATGATCATCTTCTAGTTCATTTCTATCTT	1283
Db	1168	GCTGACCTTGGCAATGTTGTTCTTTATGATCATCTTCTAGTTCATTTCTATCTT	1227
QY	1284	GTGAATTTGATTTTGGCCATTGTTGCCATGTCTGTATGACGAATTCGAAAGGAAGGCCGAA	1343
Db	1228	GTGAATTTGATTTTGGCCATTGTTGCCATGTCTGTATGACGAATTCGAAAGGAAGGCCGAA	1287
QY	1344	GAAAGAAAGCTTCGCGAAGAGAGAGGCCATATGTTAAGCGGAAGAACTGCCCGCCGCAAA	1400
Db	1288	GAAAGAAAGCTTCGCGAAGAGAGAGGCCATATGTTAAGCTGAAGAAAGCGGACAGCCGAA	1347
QY	1404	GCGGCAAGCTGAGAGAGAGCGGGCCAAATCTCGAGGCTCAGGACGACGCGATGCGGCTCC	1463
Db	1348	GCGGCAAACTGAGAGAGCGGGCCAAATGACACTCAAGGGCTCAGAGATGACCGGAT	1407
QY	1464	GCCGAAAGGCTGCATCTGCATCCGAAATGGCCAAAGTCCGACGATTTCTTGATCAGC	1523
Db	1408	GCCGCTGCGGAGCTCTGCATCCGAGATGCAAAAGTCCGACGATTTCTTGATCAGC	1467
QY	1524	TATGAGCTATTTGTTGGCGCGAAGAGGGGCAAGATGACACACAAAGAAAGATGTCC	1583
Db	1468	TATGAACTGTTGTTGGCGCGAAGAGGGGCAAGATGACACACAAAGAAAGATGTCC	1527
QY	1584	ATTGCGAGCGTTCGAGTGGAGTCCGAGTCCGTTGAGCGTTATACAAAGAACACACGACCT	1643
Db	1528	ATTGCGAGCGTTCGAGTGGAGTCCGAGTCCGTTGAGCGTTATACAAAGAACACACGACCT	1587
QY	1644	ACCAAGACACCAAGCTTACCAAAATTCTGTAAGTGAACGACATCTTATCTTAACTT	1703
Db	1588	ACCAAGACACCC---GCTATTAAGTCCGTAAAGTTAGCAGACTTCTTATCTTAACTT	1647
QY	1704	GCTTCAACGTTTAACATTCGAGGGGATCACGTAGTTCTCAACAGTACGATACGAAAC	1763
Db	1648	GCTTCAACCATTTTAACATTCGAGGGGATCACGTAGTTCTCAACAGTACGATACGAAAT	1707
QY	1764	GAGGTGGCGCTTTGGTATACCGGGTATCGATGCTTAAGCAATTTGGTATTTGTCAACATAT	1823
Db	1708	GAGGTGGCGCTTTTGGTATACCGGGTATCGATGCTTAAGCAATTTGGTATTTGTCAACATAT	1767
QY	1824	CAGATGCCCAGACACTTGCCTTATGCCGACGACTGAAATGCCGTCAACCCCGATGTC	1883
Db	1768	CAGATGCCCAGACACTTGCCTTATGCCGATGACTGAAATGCCGTCAACCAATGTCC	1827
QY	1884	GAAAGAAATGGGGCCATCATATGTGCCCGGTATCTATGGCAATCTAAGGCTCCGACACTCA	1943
Db	1828	GAAAGAAATGGGGCCATCATATATGTACACAGCCCTACATTTGTATTTAGTTCTAGACATCT	1887

1944 TGGTATACCTCCGATAGTCCGAAATGTGATACCTCAGATGGCGATCTACTCGCGGC 2003  
1885 TATATACCTCCGATACATCAAGAAATCTGTATATACATCATGTGATATATATGGGTGCG 1944  
2004 ATGGCGGTATGGGCGGTCCAGACATGACCAAGAGAGCAAAATTTGGCAACGCAACAA 2063  
1945 ATGGCGGTATGGGCGGTCCAGACATGACCAAGAGAGCAAAATTTGGCGATGGCAACAA 2004  
2064 CGCAATCAATCAATGAGCGCCACCAATGGCGGACCACTGTCTGACCAATCAACAA 2123  
2005 CGCAATCAATCAATGAGCGGTCCAGACATGAGCGGAGTACGAGCGCGGTGTGCTAT 2064  
2124 CTGAT-----CATCGGACTAGCAAAATTTGGCGGTGAGAGTGCACGAGCA 2168  
2065 CGCAATGCGCAATCAAGAAACAAAGGATATGAAATGGGTGAGATTAATACAGCA 2124  
2169 GCTGGCAAGATTAACATCATGACAAATCTTTATCGAGCGCGTCCAGACAAACGATG 2228  
2125 GCTGGCAAAATTAACACCAAGCAATCTTTATCGAGCGCGTCCAACTCAACAGT 2184  
2229 GTTATATGAAGAGATGATGTCTGATGACATCATGACAGCGCGGTGTGCGCAC 2288  
2185 GTGATCATGAAATGATGTATGTCTTAATGATATCATGACAAAGCGCGGTGTGCGCAT 2244  
2289 AGTGGCGCAAGCATGGCGGTGTCTCGTTACTATTTCCACAGAGAGCGATGACGAG 2348  
2245 AGTGGTCTAGTGAACGAGT-----GAGGACGATGACGAA 2280  
2349 GATGGCGCGACGTTCAAGACAGAGCACTGAGATGATCTCAAGAGCATCATGATGTT 2408  
2281 GATGGTCCCATTTCAAGACAGATCGCGCTCGAATATATCTTAAGAGCATCGAAATCTT 2340  
2409 TGTGTGGGAGCTGTGTGGGTGTTGTTGAAATTTCAAGAGTGGGTATCGTCAATGTC 2468  
2341 TGTGTGGGAGCTGTGTGGGTGTTGTTGAAATTTCAAGAGTGGGTATCGTCAATGTC 2400  
2469 TTTGATCCCTTCTCCAGCTCTTATCAACGCTGTGATGTGTCACACAGATGTTCATG 2528  
2401 TTTGATCCATTTGTGGAGCTTTCATTAACCTGTGTATGTGGTCAATTAAGATGTCATG 2460  
2529 GCATGATCATCACCATGATGAACAGAGATGAAAGCGTGTCTCAAGATGGCAACTAT 2588  
2461 GCATGATCATCACCATGATGAACAGAGATGAAAGCGTGTCTCAAGATGGCAACTAT 2520  
2589 TTTCTTACCGCCACTTTTCCATCGAGGCAACATGAAAGTATTTGGCATGAGCCCCAG 2648  
2521 TTTCTTACCGCCACTTTTGAATGAGGCGACATGAACTGATGGCATGAGCCCCAG 2580  
2649 TACTATTTTCAGAGGCGTGAACATTTGCACTTATCGTGGCCCTATGCTATTG 2708  
2581 TACTATTTTCAGAGGCGTGAACATTTGCACTTATTTGAGGCTGTGTCTGCTG 2640  
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2641 GAACTGGGCTCGAGGCTGTCAAGGCTGTGTCCGATTTGAGAGTTTTGTGCTTGTGCT 2700  
2769 GTATTTCAACTGGCCAAATCTTTGGCCCACTTATTTACTCATTTTGGATTTAGGAGCG 2828  
2701 GTATTTCAAAATTTGGCAAAATCATGCCCCCACTGAAATTTACTCATTTTGGATTTAGGAGCG 2760  
2829 ACCATGGGCGCTTTGGGTATTTGACATTTGATCTTTGATTTATCATTTTCACTTTGCG 2888  
2761 ACATGGGCTGTATGGGTATTTGACATTTGATCTTTGATTTATCATTTTCACTTTGCG 2820  
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2821 GTATGGGAATGCAACTTTTGGAAAGAAATTAATTAACCAAGAGATGCTTTCAAGAGC 2880  
2949 GGGGAGCTGGCGGCTGGAACCTTACCGATTTATGACAGCTTTCATGATCGTGTTCGG 3008  
2881 CATGAATTAACGCGCTGGAATTTCAACGACTTCATGACAGCTTTCATGATGTGTTCGA 2940

3009 GTGCTCTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3068  
2941 GTGCTCTGGGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3000  
3069 TGCATTTCTTTCTTTGCGCACGTTGTATCGGCAATCTTTGGTACTTAACTTTTTC 3128  
3001 TGTATACCTTTCTTTGCGCACGTTGTATCGGCAATCTTTGGTACTTAACTTTTTC 3060  
3129 TTAAGCTTCTTTTTCACATTTTGGCTCATCTTACTTATGAGGCGGCTGCGATAC 3188  
3061 TTAAGCTTCTTTTTCACATTTTGGCTCATCTTACTTATGAGGCGGCTGCGATAC 3120  
3189 GATACGAATTAATATAGCGGAGCTTTCATCGAATTTGCGGATTTAAAGTTGGTTAG 3248  
3121 GATACGAATTAATATAGCGGAGCTTTCATCGAATTTGCGGATTTAAAGTTGGTTAG 3180  
3249 CGTAAATTTGCTGATTTGTTTCAAGTTAATGCTAAATTAATTAATTAATTAAT 3308  
3181 CGTAAATTTGCTGATTTGTTTCAAGTTAATGCTAAATTAATTAATTAATTAAT 3240  
3309 CAACCTTCAGTGAAGAGACCAACGATCACTTGGATTTGAGGAGAGAGATGATGAC 3368  
3241 CAACCATC-----AGAACATGCGAT 3261  
3369 AACGAATGAGCTGGGCGACAGAGATCTCGCGCACGCGCTCATCAAGAGGAGATC 3428  
3262 AATGAATGAGTGTGGGTATGACGAATCATGGGAGATGGCTTATCAAAAGGATATG 3321  
3429 AAGGACAGACGCAACTGAGGTGGCATCGGGATCGGATGGAATTCAGATACAGGC 3488  
3322 AAGGCGGACACCGATGAGGTGGCATCGGGATCGGATGGAATTCAGATACAGGC 3381  
3489 GACATGAAGAAACAAAGCGGAGAAATCCTAATTAATTAATTAATTAATTAATTAAT 3548  
3382 GATATGAAGAAACAAAGCGGAGAAATCCTAATTAATTAATTAATTAATTAATTAAT 3441  
3442 AACTCAATTAACCAACCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAAT 3501  
3609 TTAAGAGAGAGACACTGCGCATTTAATCTATGATGATGATGATGATGATGATGATG 3668  
3502 ATACAGAGAGAGACACTGCGCATTTAATCTATGATGATGATGATGATGATGATGATG 3561  
3669 AAGGACAGAGACCAAGGAGCGGCGGAGAGATGAGAGGCGGAGCGGCGGCGC 3728  
3562 AAGGACAGAGACCAAGGAGCGGCGGAGAGATGAGAGGCGGAGAGGAGAGAGAGAG 3621  
3729 AGCAAGAGAGATTTAGTCTGACAGAGAACTGACAGAGAGGCGATGCGAGAGGCG 3788  
3622 AGCAAGAGAGACCTCGGCTCGACAGAGAACTGACAGAGAGGCGGAGAGGCGGAG 3681  
3789 CGGCTGAGAGGATGATTAATTAATGCTGCGGCTGCGACAGAGAGGCGGAGAGGCG 3845  
3682 CAGCTGAGAGGATGATTAATTAATGCTGCGGCTGCGACAGAGAGGCGGAGAGGCG 3741  
3846 CAGCTGAGAGGATGATTAATTAATGCTGCGGCTGCGACAGAGAGGCGGAGAGGCG 3905  
3906 GACTCGCGCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3965  
3802 GACTCGCGCTTTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3861  
3966 AATTAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4025  
3862 AATTAATTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3921  
4026 TTAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4085  
3922 TTAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3981  
4086 AGAATATTAACGTTAATTTCTTTGGAATGTTAATCAAGTGTGGCGCTGCGCTTC 4145

Db	3982	AGGATATTACGGTGAATATCTTTTGGAGATGTGAATCAATGATGGCCCTTGCGCTTT	4041
Oy	4146	AAAGTCTACTTCAACCAAGCGGTGGTGGCTCGATTTTCGTGAATGTCAATGGATATCGCTT	4205
Db	4042	AAAGCTACTTTCACCAATGCCCTGGTGGTGGCTGGATTTTCGTGAATGTCAATGGATATCGCTT	4101
Oy	4206	ATCAACTTCGTGCTTCACTGTGGAGCTGGTGGATTCAGACCTTCAGACATATGCGA	4265
Db	4102	ATAAATTTGGTTGCGTTTGGTCGGGGCTTAAATGATATAGCCGTGTTAGATCAATGGCC	4161
Oy	4266	ACGTTAAGACACTGAGACCACTACGTGCCATGTCCGTATGACAGGCATGAAGGTGCTC	4322
Db	4162	ACACTGCGCGCCCTTAAGGCCATGTGGTCTGTCTTCAATGAGGAGGTATGAATTTTATC	4222
Oy	4316	GTTAATGGCTGGTCAAGCTATACCGTCCATCTTCATGTGCTATTTGGTGTGTATTA	4388
Db	4222	GTGAATGGCTGGTTCAGACCTATACCGTCCATCTTCATGTGCTATTTGGTGTGTATTA	4281
Oy	4386	TTTTGGCTAATTTTTCGCAATAATGGGTGACGCTTTTGTCTGAAAAATTTTAAGTGC	4445
Db	4282	TTTTGGCTAATTTTTCGCAATAATGGGTGACGCTTTTGTCTGAAAAATTTTAAGTGT	4341
Oy	4446	GAGACATGATATGGACGGAAGTCCACGAGATCATACCAATTCGCAATGCCCTGCGAG	4505
Db	4342	AAAGTGGTAATGACACTGTGTGAGCCATGAATCAATCCGAATCGTAATGCCGCAAA	4401
Oy	4506	AGCGAGACTCTACAAGTGGGTGTAATTCAGCAATGAAATTCGATCATGTAGTAAACGCTAT	4565
Db	4402	AGTGAATACTACACTCGGAAAAATTCGCAATGAACCTTCGATCATGTAGTAAATCGAT	4461
Oy	4566	CTGTGCCCTTTTCCAAGTGGCCACTTCGAAAGGCTGGATACAAATCATGAAACGATCTATC	4625
Db	4462	CTGTGTCTATTTCGAAGTGGCCACTTCGAAAGGCTGGATACCAATCATGAAACGATCTAT	4521
Oy	4626	GATTTCAGAGAGGTGGAACAAGCAACCAATTCGTGAAGAACATCTTACATGTATTTAAT	4688
Db	4522	GATTTCAGAGAGGTGGAACAAGCCGATCCGAGAAACCAATTCATCATGTATTTAAT	4581
Oy	4686	TTGCAATCTTCATCATATTTGGATCCCTTTTCAACCTCAATCTGTTCATTGGTGTATC	4745
Db	4582	TTGCAATCTTCATCATATTTGGATCATTTTTCACACTCAATCTGTTCATTGGTGTATC	4641
Oy	4746	ATTGATAATTTTAATGACAAAGAAAAAGCAGGTGATCATTAAGAATGTTCAATGACA	4805
Db	4642	ATTGATAATTTTAATGACAAAGAAAAAGCAGGTGATCATTAAGAATGTTCAATGACA	4701
Oy	4806	GAAATTCAGAAAAAGTACTATTAATGCTATGAAAAAGATGGGCTCTAATAAACCATTAATA	4865
Db	4702	GAAATTCAGAAAAAGTACTATTAATGCTATGAAAAAGATGGGCTCTAATAAACCATTAATA	4761
Oy	4866	GCCATTTCCAAACCAAGGTGGCACCAAGAGCAATGCTTTGAAATGTATAACGATTAAG	4925
Db	4762	GCCATTTCCAAACCAAGGTGGCACCAAGAGCAATGATTAATGCAATATGTTACGATTAATA	4821
Oy	4926	AAATTCGATTAATCATTAATGCTTATTCATGGTCTGAACATGTTCAACCATGACCTCGAT	4985
Db	4822	AAATTCGATTAATCATTAATGCTTATTCATGGTCTGAACATGTTCAACCATGACCTCGAT	4881
Oy	4986	CGTTACGATGGGTGGGACACGTAATACGGCGTCTTAAGCTATCTCAATGCGATTTGCTA	5045
Db	4882	CGTTACGACGGCTCGAGGCGGTACAAACATGTCTTCGCAAACTCAAGGGAATTTGCTA	4941
Oy	5046	GTTAATTTTCAGTTCGGAATGTCTAATAAAATATTCGTTTACGATATCACATTTTAAT	5105
Db	4942	GTTAATTTTCAGTTCGGAATGTCTAATAAAATATTCGTTTACGATATCACATTTTAATA	5001
Oy	5106	GAGCCATGAAATTAATGATGATGATGATGTCATTTATTCATCATCTTAAGTCTTGATCT	5165
Db	5002	GAGCCATGAAATTAATGATGATGATGATGTCATTTATTCATCATCTTAAGTCTTGATCTC	5061
Oy	5166	AGCGATATTATCGAAGTACTTGTGTGCGCGACCTGCTCTCCAGTGTGTGTGTGCGC	5223

Db	5062	AGCGACATCATTTGAGAAAGTATTTTGGTATCGCCCAACTCTGCTCCGTGCTGACAGATGCC	5121
QY	5226	AAAGTGGGCGCTGTGCTCTTTCGACTGTGAGAGGAGCCAAAGGACATTTGGACACTGCTCTTC	5285
Db	5122	AAAGTGGGTGCTGTCTCTGCGTTTATGTCAAGGATGCCAAAGGATATCCGAGCGTTGCTGTTC	5181
QY	5286	GCGTTGGCCATATGTGCTGCGCGGCCCTGTTCAACATCTGCTGCTGCTGTTCTTGATCATG	5345
Db	5182	GCGTTAGCCCATGTGGTTGCGCTGCTTATTCAACTTTGTCTGTGCTGTTCTTGATGATG	5241
QY	5346	TTCAATCTTTGGCATTTTTCGCAATGTCGTCTTCATGCAACGGGAAGGAAGGAGGCAATT	5405
Db	5242	TTCAATCTTTGCTATCTTTGGCATGTCTCTTCTTCATGCAATGCAAGAAAGAGGGACATA	5301
QY	5406	AACGACGCTCTCAACTTCAAGACCTTTTGGCCAGACATGATCCGTGCTCTTTCAGATGTGC	5465
Db	5302	AATGCTGTATTAATTTTAAACATTTGGCCAAAGTATGATTTGCTGTTTCAATGTCT	5361
QY	5466	ACGTACGCGGTTGGGATGTGTACTGGAAGCCATTTATCAATGAGAAACATGCGATATCA	5525
Db	5362	ACCTCAGCGGTTGGGATGTGTGTATGATGCCATTTATCATGTAGGAAGATTTGGATATCA	5421
QY	5526	CCCGACAGCGCAAAAGGCTATCCGAGGCAATTGTGAGTCAAGCAACGTTGAAATACGTTT	5585
Db	5422	CCCGACACGCAAAAGGCTATCCGAGCAATTGTGTATCAGCACTGTTGAAATATCGTTT	5481
QY	5586	CTCCTCTCATCTACATGATTAATAGCTTTTGTGATGATTAATATGATCATTTGCTGTCAAT	5645
Db	5482	CTCCTTTTCAATCTAGTTATTAAGTTATTAAGCTTTTGTATTAATTAATGATCATTTGCTGTCAAT	5541
QY	5646	CTCGAAGACTATTAAGTCAAGGCCACCGAAGACGTGCAGAAAGGCTCTAACCGACGACATAC	5705
Db	5542	CTCGAAGACTCTACCCAGGCTTACCGAAGATGTACAGAGGGGTCTCACCCGACGACGACTAT	5601
QY	5706	GACATGTACTATGAGATCTGCGACACATTTGCAATCCGAGGGCCACCCGATCATATGCGTAT	5765
Db	5602	GATATGTACTACGAGATTTTGGCAACAATTTGCATCCGAGGGGTACCCAGTATCATTAAGTATAC	5661
QY	5766	GATCAGCTGTCCGAAATTCCTTGGAAGTACTGGAAGCCCCGCTCGAGATCCAAACCGAAC	5825
Db	5662	GACCAAGCTGTCCGAGTTCTCTGGAAGTGTGTGAGAGCCGCGCTCGAGATCCAAACCGAAC	5721
QY	5826	AAGTACAAAGATCATATCGATGAGACATACCATCTGTGCGGGTGAAGCTATGATCTGCGTC	5885
Db	5722	AAGTACAAAAATCATATCGATGAGACATGCGCATATGTGCGGGCGCAGATGATGATCTGTGTG	5781
QY	5886	GACATCTCTCCAGCGCCCTTACGAAGAATCTTTTCCGCGGGAAGAGGCATTCGATAGAGAG	5945
Db	5782	GATATATTGTGATGCTCGACCAAGAACCTCTTTTCCGGCCAAAGGGTAAATCCGATAGAGAG	5841
QY	5946	ACGGGTGAGATTTGGTGTAGATATGCGGGCCGCGCCCGGATATCGAGAGGCTCTACGACCCTGTCA	6005
Db	5842	ACGGGTGAAATTTGGTGTAGATTTGCGGCGCGACCGGACACCGAGGGCTATGATCCGCTGTGCG	5901
QY	5902	TCGACACTGTGTGCGCCAGCGGTGAGAGATACGCGCAAGCTGATACAGAAATGCTGTGCGGG	5961
Db	6006	AAAGCAAAAGGCGCGCGCGAGAGAGTGTGTCTTTGACCGGATATGAGATCATGTGGCAT	6125
QY	5962	CGTTTACAAAGATGCG-----	5976
Db	6126	GGCGGTGATCCGAGATGCGCGGGAGCCCGGCGCCGATGAAGACGGAACGCGCGATGCGCC	6185
QY	5977	CCACCCCAAGAGGGTATGAGAGGGCGAAGCGGCTGTGTGGCAAAAGTATGTGTGTAAGAGGGGT	6036
Db	6186	GCTGTGTGAGATGTGATGTATTACGTATCTGCAGAGAGAGCTGCCGATGCGATG	6245
QY	6037	GAGGGTGAAGCGGCAACGCGCGCGCGCGAGATGATGTGTGATCTAGCGACGCGCGCG	6096
Db	6246	AATGTAAATAGTCCGGGTGAGATGTCAGCGCGCGCGGCAACAGACAGACGACGACGCGCG	6305
QY	6097	GGAGCCCATCATCCCAAGATCCAGATGTCGGGCGAACAAGATGTGTGCAGCGCGCGCAAT	6156

Accession	Gene	Protein	Accession	Gene	Protein
Qy	6306	GCGCGGGCAAGACGACGGCGGAAAGTCCCGAGGGGTACCGCGGCGACAGACGCC	Db	6157	GATGCGGGCCCCCTTAGTACCGGGGTGTGTATGTGGCGGCAATATGCGCGCAAAAGCGC
Qy	6366	GTTCTCGGAGACGACGACGGGTTGTGTGACGAAAGCGGCGCAGAGTGTATCCATCG	Qy	6217	GTTACTGGTCGAAAGCGATGATTTGTTCACAAAAAGGTCATTAAGTTGTATATACATCG
Db	6277	AGATCGCCGACGATPACATCCAGACGGCAAGTGTCTGA	Qy	6426	CGATGCCGAGCATCATCGTCGGCGACGGCGGAGTGTCTGA
		6315			6464

RESULT 3  
US-10-152-319A-1723

; Sequence 1723, Application US/10152319A  
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APPLICANT: Mendrick, Donna  
APPLICANT: Porter, Mark

APPLICANT: Castle, Arthur  
; Higgs, Brandon  
APPLICANT: Cornsby, Kelly

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; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular
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; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925

PRIOR APPLICATION NUMBER: US 60/303,810  
PRIOR FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US 60/303,807  
 ; PRIOR FILING DATE: 2001-07-10  
 ; PRIOR APPLICATION NUMBER: US 60/303,808

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; PRIOR FILING DATE: 2001-07-10  
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; PRIOR APPLICATION NUMBER: US 60/315,047  
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PRIOR APPLICATION NUMBER: US 60/324,928  
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; PRIOR APPLICATION NUMBER: US 60/330,867  
 ;  
 ; PRIOR FILING DATE: 2001-11-01  
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 ;

;; PRIOR FILING DATE: 2001-10-22  
;; Remaining Prior Application data removed - See File Wrapper or PALM

SOFTWARE: Pat  
: SEO ID NO 1723

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; LENGTH: 6586
; TYPE: DNA
;

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OTHER INFORMATION: n = a or c or g or t  
US-10-152-319A-1723

D	b	328	AAGCCAAACAGTGA		CTGGAGGCTGGGGAAGAGTTGGCTTTCATCTACAGGGGACATCCG	387
Q	y	306	CCGGAAATTG		CTCCTCGAGATATGATCCCTATCTACAGCATATGACTGA	365
D	b	388	CAAGGCTGTGGT		CTCCCTGGAGAGCTTTGACCTTATCTATTGACGCAAGAAACC	447
Q	y	366	TTGCTAGTTGA		CAAGAAAGATATTTTGGCTTTTCTGATCAAAAGCAATGNG	425
D	b	448	TTTGTAGTATTA		ACAGGGAAACTCTTCAGATTTTAGTGGCAACCTGCCTTGAC	507
Q	y	426	ATGCTGATCC		CAATCCGATACGTCGTGTGCCATTACATTTCTATGATCATTAT	485
D	b	508	ATTTTAAGCC		TTTAACTGATAGAAAGAAATACCTTTTAAATTTTGATACACTGATT	567
Q	y	486	TTTTCCCTAT		TATCATACACAAATCTGTGTAACGTACCTGATGATTAATGCCGA	545
D	b	568	TTTACGATGAT		CATCATGTGCACATCTTGACCACTGTGTTCATGACCTTTAGTAA	627
Q	y	546	ACGCCCA		CGGTTGAGTCCACTGAGTG---ATATTCAACCGGAATCTACATTTGAATCA	602
D	b	628	CTTCAGAAAT		GTGCCAAGAAATGTGAGTACACATTCACAGGGAATTTCACATTGAAATCA	687
Q	y	603	CGTGTAAAG		TGATGACAGAGTTTCAATTTATGCCCCGTTTAGTATCTTAGAGATCA	662
D	b	688	CTATGTAAAT		CATCGCAAGAGTTTGTGATACAGGCTTCACCTTCTTGCGAGAACCG	747
Q	y	663	TGGAATGG		CTGCACTCTGATTAATAGCTTTAGCTTATGTGACCATGAGTATGATTTA	722
D	b	748	TGGAACTGG		TTAGCTTCAGTATCATATATGACATATGTGACAGAGTTTGTGGACCTG	807
Q	y	723	GGTATCTAG		ACGCTTCGCAAGCTTTAGGGTGTGGAGGCTTTAAACCGTACCATT	782
D	b	808	GGCAATCT		CAAGGCTGAGAACATTCAGAGTTTCCGAGCTTTGAAACATATCTGTGA	867
Q	y	783	GTGCAAG		CTTGAAGCATCTGTGGGCGCGTCAATCGATCGAGAAATCTGCGCAT	842
D	b	868	ATTTCAGG		CTCGAAGACATGTGTGGGCGCTTATTCAGTCCGTAAGAGACTGTGGAC	927
Q	y	843	GTGATTA		ATCTGACATGTTCTCCCTGTGCGGTGTGCGTTGATGGGCTTACAGATCTAT	902
D	b	928	GTGATGAT		CTCTGACAGTGTCTGTGCTGATGATTTTCCCGGATTTGGCTCTCACTCTTC	987
Q	y	903	ATGGCG		TGCTCACCCGGAAGTGAT-----CAAGAACTCCGCTGGAGCGGTTCC	953
D	b	988	ATGGGGA		ACTTTGAAACAAAGTGTGTGTGGCCCTTAACCTTCAACGAGACTGACTG	1047
Q	y	954	TGGGCA		TGTGAACGAGAACTGGAGCTATCACATGCAATAGCTCCAAATTTGAT	1013
D	b	1048	GAGAAC		GGCACAGAGGCTTTGACTGGAGGAATATATCAACATTAACAAACTTTTAC	1107
Q	y	1014	TCCGAG		ACAGAGGCACTCTATTTCCGTTATGCGGCAATATATCCGGTGGCGGCAATGC	1073
D	b	1108	ATGGTT		CTCGCATGTAGAACCTTCTCTGCGGGAACGTTTGTGATGTGGGCGCAATGC	1167
Q	y	1074	GACACAT		TAAACGTCCTGACAGGGGTTTGTGTCGAATCCGAATTTATGGCTTACACAGC	1133
D	b	1168	CCAGAG		GGATTCACAGTGCATGAAG---CAGGAAGAAACCCAACTACGGTTACACAGC	1224
Q	y	1134	TTGATTC		GTTCGGATGGGCTTCTGTCCGCTTCCGGCTGATGACACAGGACTTCTGC	1193
D	b	1225	TTTGA		CACTTCAGCTGGGCTTCTTGTGGCAATATTCGCGCTTATGACCCAGGACTATTTGG	1284
Q	y	1194	GAGGAT		CTGTACACAGCTGTGTGCGGCGCGCGGACCATGGGCAATGCTGTTCTTATA	1253
D	b	1285	GAGAACT		TATTAACAGCTTACGACCTTACGAGCGGCTGGAAAACGTACATGATTTCTTTGT	1344
Q	y	1254	GTGATCAT		CTTCTCAGGTTCAATCTATCTTGTGATTTGAATTTTGGCATTTGTGCCATG	1313
D	b	1345	TTGGTAT		CTTTTCGGGTTCTTTCTATCTGTGTGAATTTGAATCTTGGCTGTGTGGCATG	1404
Q	y	1314	TCTGAT		ACGATTTGCAAGAGGCGGAAGAAAGAGCTGCCGAAGAGAGCGGATA	1373

Db 1405 GCTTATGAGAA---CAGAACGAGCAACCTGAGGAGGAGAGCAAAAGAGGCG--- 1457  
Qy 1374 CGTGAAGGGAAGAGCTGCGCGCGCAAGCGGCAAGCTGAGAGAGCGGCGCAATGCG 1433  
Db 1458 CGAGTTCAAGCAATGCTGAGAGCACTCAG---AAGCAGAGAGAGAGGACACAGGCT 1512  
Qy 1434 CAGGCTCAGGAGCAGCGAGATGCGGCTGCGCGCAAGAGAGCTGCACTGCTCGGAATG 1493  
Db 1513 GCTGCAATGGCCACTTCAGCGGCGACTGCTCGGAGAG---CGCATGAGAGAGAGAGG 1569  
Qy 1494 GCCAAGACTCCGACCTATTCTTGCACTGAGCTATGAGCTATTTGTTGGCGGAGAGGCG 1553  
Db 1570 GAAGATGGGTAGGCTCTCCAGAGAGCTCTTCTGAATGCTTAACCTGATTCAGAGGCG 1629  
Qy 1554 AACCATGCAACAAAGAGAGATGTCATTCGAGAGCTGAGAGTGAAGTCCGAGTGC 1613  
Db 1630 GCGAAGGAGCGGCGAA-----CCGAGGAGAGAGAGAGAGCAAGAGAGAG 1673  
Qy 1614 GTGAGCGTTATCAAAAGCAACAGCACTTACACAGAGACCAAGCTAACCAAGTTGCT 1673  
Db 1674 GCTCTGAGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1720  
Qy 1674 AAGAGAGCAGACCTCTTATCTTACCTGCTGCTTACCGTTTAACTACGAGGAGATCA 1733  
Db 1721 CAGAGTCGAGAGAGCGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1780  
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Qy 1794 GATCGTAAAGCATTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1853  
Db 1841 GACATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1899  
Qy 1854 GACAGCTGGAATGCGCTGACCCGAGATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAG 1913  
Db 1900 GGCTCTGAGAAATG-----AGTTCCAGAGAGATGAACAGAGAGAGAGAGAGAG 1947  
Qy 1914 TACTATGCAATCTAAGCTCCGACACTCATCTGATCTGATCTGATCTGATCTGATCTGAT 1973  
Db 1948 AGCAGAGGCGCGGCTGATCTGCTCTTATCTGATCTGATCTGATCTGATCTGATCTGAT 2007  
Qy 1974 TATACCTCAACATGAGCTCTACTCGGCGGAGTGGCGCTGATGAGAGAGAGAGAGAGAG 2033  
Db 2008 TACAGTGGCTACAGCGGCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2067  
Qy 2034 AAGAGAGCAAAATGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2093  
Db 2068 CGGCGAGCGTGAAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2109  
Qy 2094 GGCACCACTGTCTGAGACCAATCAAGCTCGATCTGCGGAGTACGAAATGGCTG 2153  
Db 2110 G-----TAGTGTCACTCATCGGCGCGGCTGACATCTGCG 2144  
Qy 2154 GAGTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2213  
Db 2145 GCGGCTCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2193  
Qy 2214 CAGACCAAAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2270  
Db 2194 ACGACTGAGGTGAATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2253  
Qy 2271 CAGGCGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2330  
Db 2254 CTCGCTCTCTACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2313  
Qy 2331 ACAGAGAGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2390  
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Qy 2391 AAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2449  
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Qy 2450 GTGGATTCGCTCATTCGCTTTCATTCCTTGTGAGAGCTTTCATCACGCTGTGATGCT 2509  
Db 2424 GATGTGAATTAATTCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2483  
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Db 2484 TGTGAATTCGCTATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2543  
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Db 2544 CTGGCGGTAGAGATCTGAGTGTACCGGAGATCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 2603  
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Db 2604 CATAGCCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2663  
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Qy 2810 CATTTGATTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2869  
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Qy 2870 TATCATCTTCATCTTTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2926  
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Qy 2927 TCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2986  
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Db 3024 CATGAGAGTGGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3083  
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Db 3084 CAATCTTGTGATCTTAACCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3143  
Qy 3164 CTATTCAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3223  
Db 3144 CTGAGCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3179  
Qy 3224 TGGCGATTTAAAGTTGAGGTTAAGCTAATGCTGATTTTCAAGTTAATACGTA 3283  
Db 3180 ----- 3179  
Qy 3284 CAATGTAACAAATCAAAATGATGATCAACATCAGGTGAGAGAGAGAGAGAGAGAGAGAGAG 3343  
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Qy 3344 GATTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3403  
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Qy 3404 CGAGCGCTCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3463  
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Qy 3464 TCGAGTGAATTCAGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3523  
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QY 3524 TCTAAATTAACGACATGATTGGCACTCACTTAATTAACCAACGAAACATTAATGATGGAACA 3583  
DB 3375 GAAACGGAAACGGAACCAACGACGCGCATCGGACGACGCTGGAGAAATATCATCATCAACA 3434  
QY 3584 CGAGCTAAACCATAGAGGTTTGTCTTACGAGACGACACACTGCGAGCATTAATCATATA 3643  
DB 3435 GGAACACA-----TGTCTTCACTTAACAA-----CCAAACCTGACCGTCC 3475  
QY 3644 TGTAGCCATTAAGATTCGACCATTCAGAGCAAGAGCCACAGGAGGAGCGCCAGACGAT 3703  
DB 3476 GGGTGGCCATTTGCTGTGGCGAGTC-----TGACTTCAGAGAACCTTCAACACAGAGATGT 3530  
QY 3704 GGAAGGCGAGAGAAAGCGGACCCGACGACAGAGAGATTAGTCTCGACGAGAACTGGA 3763  
DB 3531 TAGACGATTCAGACCCCTGAGAGGACAAAGATTA-----ACTGACCATTAACGACTC 3584  
QY 3764 CGAGGAGGCGAATGCGAGGAGGCGCGCTCGACGCGTATCATTAATTCATGACACGA 3823  
DB 3585 CTGAGAGAGAGATTCATCGACATCAAGCTTGAGTGAGAGAAAGTTCCCGTGAAGCAAC 3644  
QY 3824 CGAGATATATCTCGATGATATTCAGCTGATGCTGCCCGCATTCGTAATAAGAAAT 3883  
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QY 3884 TCCGATCTTACCGGTGACGATGATCGCGCTTCTGCGAAGANTGGGCGAATTTAGACT 3943  
DB 3699 CAAGTGTCCAGGTCAACATCGAGAGAGACTAGGAGAGTCTGTGGGATCTTGCGAA 3758  
QY 3944 GAAACCTTTCAATTAATTAATAAATAATTTTGAACAGCTGTTATCATTAATTAAT 4003  
DB 3759 AACCTGCTTCTCATTTGTGAGACAAATGTTTGAAGCTTTCATCATATCTTAATGATTC 3818  
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DB 3819 GCTCAGAGATGGCGCCCTGGCCCTTTGAGACATCTACATGAGACAGAGAAACCATCCG 3878  
QY 4064 GGAATTTTATATATATGACAGAAATTTTACGTTATATCTCTTGGAAATGTTAAT 4123  
DB 3879 CACCATCTGAGATGACGACAGAGTCTTCACTTACATCTTAATCTTGAAGATGTTCT 3938  
QY 4124 CAAGTGTGGCGCTCGGCTTCAAAAGTATCTTCAACCAACGCGTGTGTGCTCGATT 4183  
DB 3939 CAAGTGAACAGCCACGCTTCTGCAAGTTCTTCAACCAAGCGCTGTGTGGAATT 3998  
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DB 3999 CCTCATTTGGCTGTCTCTTTAGCAGCTTATAGCTAATGCCCTGGGCTACTCGAATC 4058  
QY 4244 TCAAGCTTCAAGATGATGGAAGCTTAAGAGCACTGAGACCACTAGTGCATGTCGCG 4303  
DB 4059 AGGTGCATTAAGTCCCTTAGAGACCTTAGAGCTTGAACCTTAAAGCCTTATACG 4118  
QY 4304 TATGACGAGGATGAGGTCGTCGTTAATGCGCTGTTCAAGCTATACCTTCATCTTCAA 4363  
DB 4119 ATTGGAAGGATGAGGTCGTTGATGATGCTTGTGTGGGCGCATCCCTTCATCATGAA 4178  
QY 4364 TGTGCTATGCTGTCTATATTTTGGCTTAATTTTGGCTTAATGAGGTGACGCTTT 4423  
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DB 4239 TGGCGGGAATACCACTATGCTTTTAATGACATTTCTGAATTCGGGTTCGAATCGATAT 4298  
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DB 4299 TGTCAACAATTAACGAGCTGTGAGAGCTCATGAGGAGGACAGACGAGATCCGATG 4358  
QY 4523 GGTGAATTCAGCAATGAATTTGATCATGATGATGATGATGATGATGATGATGATGAT 4582  
DB 4359 GAAAGATGTCAAGATCACTTTCAGATGTCGAGACGAGGTACTGCGCTTTCTTCAAGT 4418  
QY 4583 GGCACACTTCAAAGGCTGATATGAATCATGACGATGCTATCATTCACGAGAGTGA 4642

DB 4419 GGAACCTTCAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4478  
QY 4643 CAAGCAACCAATTCGTGAACGACATCTCATGATTAATTTTTCGATTTCTTATCAT 4702  
DB 4479 CGAGGACCTGACTAGAGGCGACATCTACATGATCACTTCACTTCTGATCTTATCAT 4538  
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QY 4763 GCAAAAGAAAAAGAGAGGTGATCTTAAGATGTTCAATGACAGAAATCAGAAAAAGTA 4822  
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QY 4823 CTATAATGCTATGAAGATGAGGCTTAAAGAACATTTAAAGCATTTCCAGACCAAG 4882  
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QY 4883 GTGGGACCAACAGCAATGCTTTGAATAAGTAACCGATTAAGAAATCGATATATCAT 4942  
DB 4716 GAACAAAATCGAAGGATGCTTTGATTTGCTCACTCAACAGCTTTGACATTTGAT 4775  
QY 4943 TATGTTATTCATGCTGAGACATGTTCACTGACCTCGATCGTTACGATGCTGGA 5002  
DB 4776 CATGATGCTCATCTGCTTAAATGATGATGATGATGATGATGATGATGATGATGAT 4835  
QY 5003 CACGATTAACGCGGCTTACATCTCAATGCAATGCAATTCGATGATTTTCAAGTCCGA 5062  
DB 4836 CGAGATGAGAAACATTTCTTATGATTAATCTGCTTGTGATCTTCTTCACTGCGA 4895  
QY 5063 ATGCTATTAATAAATATGCTTTACATATCATATTTTATGAGCCATGAAATTAAT 5122  
DB 4896 GTGTGTCTCAAAATGTTTGTCTTGAACACATCAATTTTCAATTTGCTGGAACATCTT 4955  
QY 5123 TGAATGATGATGATGATTTTATTCATCTTGAATCTTGAATGATGATGATGATGAT 5182  
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QY 5183 GATCTTGTGTGCGGACCTCTGCTCCGATGATGATGATGATGATGATGATGATGATGAT 5242  
DB 5016 GATCTTGTGTGCGGACCTCTGCTCCGATGATGATGATGATGATGATGATGATGATGAT 5075  
QY 5243 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5302  
DB 5076 GCTGTGATCAAGGAGGCGCAAGAGATCCGACCTGCTTGTGCTTATGATGATGATGAT 5135  
QY 5303 GCCGCGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5362  
DB 5136 GCCGCGCTGTTCAACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5195  
QY 5363 CGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5422  
DB 5196 TGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5255  
QY 5423 CAAGACCTTTGCGAGAGCATGATCTGCTTTCAATGATGATGATGATGATGATGATGATGAT 5482  
DB 5256 CGAGACATTTGCGAGAGCATGATCTGCTTTCAATGATGATGATGATGATGATGATGATGAT 5315  
QY 5483 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5533  
DB 5316 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5375  
QY 5534 CGACAAAGGTATCCGCGCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5593  
DB 5376 AGGAGATGCTTCAAAAGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5435  
QY 5594 ATACCTAGTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5653  
DB 5436 CTATCATCATCATCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5495  
QY 5654 CTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5713



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Db 5496 CTTGAGCGTGGCCACCGAGAGCGCCGACCTCTGAGTAGATGACTTTCGACACTTT 5555
Qy 5714 CTTAGAGATCTGGAGCAATTCGATCCGAGGAGCCACAGTACATACGCTATGATCACT 5773
Db 5556 CTAAGAGATCTGGAGAGAGTTTGGACCGACGCCACCGATTCATCGATCTGTAAGCT 5615
Qy 5774 GTCCGAATTCCTGGAGCTACTGAGAGCCCGCTGAGATCCACAAACGAAACAGTACAA 5833
Db 5616 GCGAGACTTTGGCCAGCGCCCTGAGACACCCGCTCGAATACCCAGGCCACACATGGA 5675
Qy 5834 GATCATATGATGAGCATATCCCATCTGTGCGGATGACCTCATGTACTGCTGACATCT 5893
Db 5676 GCTCATCCCATGAGCTGCGCATGATGAGAGATGCAATCCACTCTTGGAATCCT 5735
Qy 5894 CGAGCCCTTACGAAAGACTTTTGGCGGAGAGGCGCAATCCGATAGAGAGAGGGTGA 5953
Db 5736 TTTGGCTTTCACAAAGCAGATCTGGGAGACAGTGGGAGTTCATCTGCGGACACA 5795
Qy 5954 GATTGTGAG-----ATAGCGGCGCCCGGATACGAGAGGGCTACGAGCCGCTCATC 6007
Db 5796 GATGAGAGAGCGGCTTCGTCGATTCATCTTCCAAAGTCTTACGAGCCTATACAC 5855
Qy 6008 AACGCTGTGCGTCAAGCTGAGAGTACTGCGCCCGCTAAATCCAGCAGCGCTGCGGAA 6067
Db 5856 CACTCTGGCGGCAAGAGAGAGTGTCTGCAATGCTCTGAGAGCGTGCCTACAGGGG 5915
Qy 6068 GCACAGCGCGCGCGG 6084
Db 5916 ACACCTTGCTGAGCGGG 5932

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## RESULT 4

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US-10-377-139-14
; Sequence 14, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: Mackinnon, Roderick
; APPLICANT: Jjiang, Youxiong
; APPLICANT: Lee Mackinnon, Alice
; APPLICANT: Rutea, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; FILE REFERENCE: Seg. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 6586
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6535)..(6579)
; OTHER INFORMATION: n is any nucleotide: a, c, g, t (u)
US-10-377-139-14

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Query Match 15.7%; Score 1019.4; DB 18; Length 6586;
Best Local Similarity 52.8%; Pred. No. 1.5e-272;
Matches 3146; Conservative 0; Mismatches 2461; Indels 350; Gaps 30;

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Qy 186 CGGAGAGAGAGAGAGAGAGATCCGATATGATGACGAGAGAGAGATGAGATTCACAA 245
Db 268 CTCAAGAGAGAGAGAGAGAGAGATGAGAGAGAGAGAGAGAGATGAGAGAGAGAGAG 327
Qy 246 CCGATCTCTACATTTGAACAGGATGTGCAATATCTGTTTCATTTGACAGGAGAGCTTCCG 305
Db 328 AAGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 387
Qy 306 CCGAGATTTGCTCTCACTCTCTCTGAGAGATGATGATTCCTTACAGAGATGATCTGCA 365
Db 388 CAGAGCTGTGTTGGGTTCCCTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 447

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Qy 366 TTCCAGATTTGATAGAGAGAGAGAGATATTTTGGCTTTTGCATGACAGAGAGATGAG 425
Db 448 TTTTGTATTTTAAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 507
Qy 426 ATGCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 485
Db 508 ATTTTAAAGCCCTTTTAACTGATTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 567
Qy 486 TTTTCCATTTATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 545
Db 568 TTTCAAGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 627
Qy 546 AGCGCCAGAGTGAATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 602
Db 628 CTTCAAGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 687
Qy 603 GCTGTTAAAGATGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 662
Db 688 CTTAGTAAATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 747
Qy 663 TGAATTTGCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 722
Db 748 TGAATTTGCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 807
Qy 723 GGTATATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 782
Db 808 GGCATGCTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 867
Qy 783 GTGCGAGCTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 842
Db 868 ATTCAGAGCTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 927
Qy 843 GTGATTTATCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 902
Db 928 GTGATTTATCTGATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 987
Qy 903 ATGGGCGGTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 953
Db 988 ATGGGAGAGCTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1047
Qy 954 TGCGGCAATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1013
Db 1048 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1107
Qy 1014 TCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1073
Db 1108 ATGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1167
Qy 1074 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1133
Db 1168 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1224
Qy 1134 TTTGATTTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1193
Db 1225 TTTGATTTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1284
Qy 1194 GAGATCTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1253
Db 1285 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1344
Qy 1254 GTATCATCTTTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1313
Db 1345 TTTGATTTGATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1404
Qy 1314 TCGATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1373
Db 1405 GCTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1457
Qy 1374 CTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1433
Db 1458 CAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1512
Qy 1434 CAGGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1493

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1513 GCTGCATGCGCCCTCAGCGGCGCATGTCGGAAGA---CGCATTTGAAGAAGAGG 1569  
QY 1494 GCCAAGATCCGACGTAATCTTGCATCACTATAGCTATTGTGGCGGAGAGGCG 1553  
Db 1570 GAAGATGGGGTAGGCTCTCCGAGAGCTCTTGAAGTGTAACTCAGATTCAGAGC 1629  
QY 1554 AACGATGACAAACAAGAGAAATGTCCATTCCGAGCGTCGAGGTGAGTCCGAGTGC 1613  
Db 1630 GCCAAGGAGCGGAGAA---CCGACGGAAGAAAGAGAGAGAGGA 1673  
QY 1614 GTGAGGCTTATACAAAGACAACAGCACCTACACAGACACCAAGCTTACAAAGTTCCG 1673  
Db 1674 GCTCTTGAAGGAGAGAGAAAGGAGACCGGAGAAAGTCTTAA-----GT 1720  
QY 1674 AAAGTAGACGACATCTTATCTTATCTGTTCACCGTTTAACTAGCAGAGGATCA 1733  
Db 1721 CAGAGTCGGAAGCGGATGAGAAAGGCTTCGCGCTGCAGACAACAGGATAGGGA 1780  
QY 1734 CTTAGTTTCACAAAGTACAGATAGGAGACGAGCGCGCTTGTGTATACCCGATAGC 1793  
Db 1781 GGAAGTTTTCATCATGAATCAGTCGCTGCTCAGCATTTCCAGGCTGCGCTTCTCTCC 1840  
QY 1794 GATCGTAAGCATTTGATTTGTCACATATCAGATGCGGACGACGACTTGCCTATGCG 1853  
Db 1841 GACATTAACGCAAAAGACGATCTTACGCTTCGCGGAGCCCG---GTGCTTCGCGAGCCC 1899  
QY 1854 GACGACTCGAATCCGTCACCCGAGTGTCCGAAGAAATGGGCGCATCATAGTCCCGTG 1913  
Db 1900 GGTCTGAGAAATG-----AGTTGCGAGACGATGACACAGCACCGTGGAGAG 1947  
QY 1914 TACTATGGCATTTAGGCTCCCGACACTATCGTATACCTCGATCAGTCCCGAATATCG 1973  
Db 1948 AGGAGAGCGCGGCTGATCTGCTTATCTCCATCCGCGCGCGACGCGCACGAC 2007  
QY 1974 TATACCTCAATGAGCATCTACTCGCGGCGATGCGCGTCATGAGCGCTCAGACATAGAC 2033  
Db 2008 TACAGTGGCTACACGCGGCTACACGAGTGAAGCGCGCTCGCGCATCTTCCCAAGCTG 2067  
QY 2034 AAGGAGACAAATTTGGCGAACCGCAACACACGCAATCATCACTGCGCGCCACCAATGCG 2093  
Db 2068 CGCGCAGCGCTGAAGCGCAACAGCA-----CGGTGAGCTCTCAACGCGC 2109  
QY 2094 GGACACACCTGTGTGACACCATCAACAGCTGATCATGCGAGCTACGAATTTGCGCTG 2153  
Db 2110 G-----TAGTGTACTTCATCGGCGCGGCTCAACATCGG 2144  
QY 2154 GAGTGCACGACGACGAGCTGCGAAGATTTAAACATCATGACATCTTTATCGAGCCGTC 2213  
Db 2145 GCGGCTCTGCTGAGAGGTGAATA-----GATTAAGCAGCTACGACAGCGCA 2193  
QY 2214 CAGACACAAACGCTGTTGATATGAAG---ANGTATGCTCTGTAATGACATCATCGAA 2270  
Db 2194 ACACATGAGGTGAATAATTAGAAGAAAGCGCTGAGTCTCTTTAGTTTATAGACAA 2253  
QY 2271 CAGGCGCGTGTGGACACATCGGCGCAAGGATCGCGGTGTCTCCGTTTATATTTCCCA 2330  
Db 2254 CTGCGCTCTTACGAGCGAGAGGACAGATCAACAGTAATGACGCTGTCACAAACAG 2313  
QY 2331 ACAGAGCAGATACGAGATGAGCGCAGCTTCAAAAGACAAGGCACTCGAATGATCTTC 2390  
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QY 2391 AAAGGACATGATGTGTTTGT---GTGTGGAAGTGTGTGTGTTGTTGAATTTCAAGA 2449  
Db 2364 TAAGTTTGCACAACTTCTCTCATCTGAGGTGTACCCCTACTGATTAATCTGAAGGA 2423  
QY 2450 GTGGGATGCTCATGCTTTGATCTCTTGTGAGCTCTTATCATACGCTGTGCATTT 2509  
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QY 2510 GGTCAACACAGATGTCATGAGCATGATCACCAGATATAGACAAGAGATGGAACGCGT 2569

2484 TCTGAATACGCTATTATGATGAGACCATCCATGACACCAAGTGGAAACGCT 2543  
QY 2570 GCTCAAGATGGCACTATTTCTTCAACCGCCACCTTTGGCATCGAGCCACCATAGAGT 2629  
Db 2544 CTTGGCCGTAGGAATCTGGTGTTCACCGGATCTTCAAGCGGGAATGTTTCTGAAGCT 2603  
QY 2630 AATGGCATGAGCCCAAGTACTATTTCCAGAGGAGTGAACATCTTGCATTCATAT 2689  
Db 2604 CATAGCATGAGACCCCTATCTATTTCCAGAGAGCTGGAACATTTTGAAGGATTAAT 2663  
QY 2690 CGTGGCCCTTATGCTATTGGAACCTGGGACTCGAGGCTGTCCAGGCTGTCCGTAATTGG 2749  
Db 2664 TGTCTCCCTCAGTTTATGAGACTGATGCTCCAGATGTGAGGGGCTCTCAGTGTGCG 2723  
QY 2750 TTCTTTGATTTGCTGCGGTATTCAAATGGCCAAAGTGTGGCCACATTAATTTACT 2809  
Db 2724 GTCTTTCGACGCTCCGAGTCTTCAAGTGCACAGTCTGGCCACCTGAACATGCT 2783  
QY 2810 CATTTGATTTATGGGACGACCATGAGCGCTTTGGGTAATCTGACATTTGTAATTGCA 2869  
Db 2784 GATCAAGATCATCGGAATCTCGTGGGTGCTCGGCAACCTGACCTGTGTGCGCAT 2843  
QY 2870 TATCATCTTCACTTTGCGGTATGGAATGCAACTGTTGGAAGATTAATCATGA--- 2926  
Db 2844 CATGCTTCACTTGTGCGGTGTGGGATGACGCTGTTGGAAGATTAACAGAGTGT 2903  
QY 2927 TCACAGAGACCGCTTTCGGAATGGGCACTGCGCGCTGGAATTTACCGCATTAATGA 2986  
Db 2904 CGTCTGTAAATCAACAGAGATGCAAGTCCCGGCTGCAATGAAAGACTTCTTCA 2963  
QY 2987 CAGCTTCATGATCGATGCTCCGGGTGCTGCGGAGATGATGAGTCCATGTGGAGCTG 3046  
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Db 3024 CATGAGATGAGCGGCGACGACATGCTCATTTGCTTCAATGATGATATGCTATTTGG 3083  
QY 3104 CATCTTGTGTACTTAACCTTTCTTACGCTTGTGTCATTTTGGCTCATCTAG 3163  
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QY 3164 CTTATCAGCGCGACCTGCGATACATACGATTAATAATAGCGAGCCCTTCAATCGAAT 3223  
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QY 3224 TGGCGATTTAAAGTTGGGTTAAGCTAATATGCTGATTTGTTCAAGTTAATACGTA 3283  
Db 3180 ----- 3179  
QY 3284 CAAATTGACAAATCAATAAGTATCAACATCAAGTGAAGAGCAACCATCATGTTG 3343  
Db 3180 -----CTGCAAGTCTCAGT 3194  
QY 3344 GATTGGAGCGAAGACATGTGTGACAAACGACTGAGCTGGCGACAGAGATCTTCG 3403  
Db 3195 GATCGGATCAAGAGGCGGTGTGCTGAGCAAAAGTGAAGTGAAGCGCTTATCAGAGG 3254  
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Db 3255 TCACTTCAAGAGCGGAGGCGGATGAAGTGAACCCCTCGACGAGCTGTATAGAGAA 3314  
QY 3464 TCGGATGAAATTCAGATACAGGCGACATGAAAGAACCAAGCCGAGAAATTCGAATA 3523  
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QY 3524 TCTTAATTAAGCAAGCATGATTGGCAACTCAATTAACCAAGCAATATGACTGAGACA 3583  
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QY 3584 CGAGCTTAAACATAGAGGTTGTCTTACAGAGCAGACGACTGCGAGCATTAATCATATA 3643  
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QY 3644 TGGTAGCCATTAAGATCGACATTCAGAGGAGAGCCCAAGAGGAGCGCCGAGACAT 3703  
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QY 3704 GAGAGGCGAGAGAGAGCGCGAGCCAGCAGAGAGATTGAGTCTGACAGAGAACTGGA 3763  
Db 3511 TAGCAGCAATCGACCTGAAAGGCGAGAAAGATA-----ACGGAGATACAGAGCTC 3584  
QY 3764 CGAGAGGCGCAATCGAGAGAGGCGCTGACGCTGATATCATTTATGACACAGA 3823  
Db 3585 CTCAGAGAGAGATCATCGACATCAAGCTGAGTGAAGAGTTCCTGAGCAAC 3644  
QY 3824 CGAGATATATCGATGAATATCGAGTATGCTGCCCGATGCTATTAAGAAAT 3883  
Db 3645 TGAGAAATACCTGG-----ATCCGAGCGCTGCTTTACAGAGGTTGCTCACCGTT 3698  
QY 3884 TCCGATCTTAGCCGAGATGATGACTCGCGTTCTGCAAGAGATGGGCAATTTACAT 3943  
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QY 3944 GAAATCTTTCAATTATTTGAAATTAATTTTGAACAGCTGTTATCATATGATTT 4003  
Db 3759 AACCTGCTTCATTTGAGAGCAGCAATTTGATGACCTTCATCATCTTCATGATCT 3818  
QY 4004 AATGATGCTTAGCTTGGCATTTAGAGATGATGATGATGATGATGATGATGATGAT 4063  
Db 3819 GCTCAGAGTGGCGCTGCGCTTTGAGAGACATTCATGAGCAGAGAGAGACATGCT 3878  
QY 4064 GATATTTTATATATATGAGCAGAAATTTTACGTTATTTCTTTGAAATGTAAT 4123  
Db 3879 CACATCTGAGATGAGGAGCAAGTCTTCACTCAATCTTCACTGAGAGATTTGCT 3938  
QY 4124 CAAGTGTGGCGCTGCGCTTCAAGATGATCTTCAACAGCGTGTGTGCTGATTT 4183  
Db 3939 CAAGTGTGACAGCTTACGCTTCTGCAAGTCTTCAACAGCTGCTGCTGATGATCT 3998  
QY 4184 CGTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4243  
Db 3999 CTTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4058  
QY 4244 TCAAGCTTCAAGATATGAGCAGATGAGCAGATGAGCAGATGAGCAGATGAGCAG 4303  
Db 4059 AGTGTCCATTAAGTCCCTTAAGACCTTAAGACCTTAAGACCTTAAGACCTTAAG 4118  
QY 4304 TATGAGGAGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 4363  
Db 4119 ATTGAGAGGATGAGGATGATGATGATGATGATGATGATGATGATGATGATGAT 4178  
QY 4364 TGTGCTATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4423  
Db 4179 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4238  
QY 4424 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4480  
Db 4239 TGTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4298  
QY 4481 CATACCAATGCAATGCTGCGAG-----AGCGAATCTACACGCTG 4522  
Db 4299 TGTCAACAAATTAACCGAGCTGAGAGCTGAGAGGCAACAGCAGAGATCCGATG 4358  
QY 4523 GGTGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4582  
Db 4359 GAAATATCTCAAGATCACTTGAATGTCGAGAGAGGATACCTGCGCTTCTTCAAGT 4418  
QY 4583 GGCACCTTCAAGAGCTGATATCAATATCAATATCAATATCAATATCAATATCAATAT 4642  
Db 4419 GGCACCTTCAAGAGCTGATATCAATATCAATATCAATATCAATATCAATATCAATAT 4478  
QY 4643 CAAGCAATCAATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4702  
Db 4479 CGAGCAGCTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4538

QY 4703 ATTGATCTCTTTTACACTCAATCTGTCATGTTGATGATGATGATGATGATGATGATGAT 4762  
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QY 4763 GCAAAAGAAAAAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4822  
Db 4599 GCAAGAGAAAA--GTTTGGAGGTCAGAGATCTTCAATGACAGAGAGAGAGAGAGAG 4655  
QY 4823 CTATATGCTATGAAAAAGATGAGGCTCTAAAAACATTAAGAGATTCAGAGCCAG 4882  
Db 4656 CTACATTCATGAAAAAGCTGAGGCTCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 4715  
QY 4883 GTGCGCAGCAGAGCAATGATCTTGAATATGATGATGATGATGATGATGATGATGATGAT 4942  
Db 4716 GAACAAAATCCAGAGAGATGATCTTGAATATGATGATGATGATGATGATGATGATGAT 4775  
QY 4943 TATGTTATCTATGCTGAAATGATGATGATGATGATGATGATGATGATGATGATGAT 5002  
Db 4776 CATGATGCTATCTGCTTAAATGATGATGATGATGATGATGATGATGATGATGATGAT 4835  
QY 5003 CACGTTAAGCGGCTCTGAGCTATCTGATGATGATGATGATGATGATGATGATGAT 5062  
Db 4836 GCAGATGAGAAATCTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4895  
QY 5063 AATGCTATTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5122  
Db 4896 GTGTGCTCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4955  
QY 5123 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5182  
Db 4956 TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5015  
QY 5183 GTAATGCTGTGCGGAGACCTGCTCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5242  
Db 5016 GTACTTGTCTTCCCAACCTTATCCGATGATGATGATGATGATGATGATGATGATGAT 5075  
QY 5243 TCGAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5302  
Db 5076 GCGTGTGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5135  
QY 5303 GCCGCGCTGTGTAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5362  
Db 5136 GCCGCGCTGTGTAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5195  
QY 5363 CGGATGTGCTTCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5422  
Db 5196 TGGCATGTCAATCTTCCATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5255  
QY 5423 CAAGACCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5482  
Db 5256 CGAGCATTGTGCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5315  
QY 5483 TGTGTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5533  
Db 5316 TGGCTGTGTGTCAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5375  
QY 5534 CGAAGAGCTATTCGGGCAATGTTGTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5593  
Db 5376 AGGAGAGGCTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5435  
QY 5594 ATACCTATGATTAAGCTTTTGAATGATTAATGATTAATGATTAATGATTAATGATTAAT 5653  
Db 5436 CTACATATCAATCTTCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 5495  
QY 5654 CTATAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5713  
Db 5496 CTTGAGGCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5555  
QY 5714 CTATGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5773  
Db 5556 CTATGAGATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5615  
QY 5774 GTCCGAATTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5833

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Db      5616 GCGAGACTTTGCGAGCCCTTGAGACACCGCTCCAGTACCCAGGCCCAACCACTCGA 5675
Qy      5834 GATCATATCATGATGAGACATACCATCTGTGCGGTGACCTTCATGTAATCTGCTGACATCCT 5693
Db      5676 GCTCATGCGCATGACCTGCTCCATGATGAGCGGAGATCCGATCCACTGCTTGAACATCCT 5735
Qy      5894 CAGCGCCCTTACGAAGAATCTTTTGGCGGAGAGGCAATCCGATAGAGAGACGGGTGA 5953
Db      5736 TTTGCGCTTACACAGCGAGTCTCTGGAGACACTGGGGAGTTGACATCTCTGCGGACGA 5795
Qy      5954 GATTGTGAG-----ATAGCGGCCGCCCGAGTACGAGGGCGTACGAGCCCTCTCATC 6007
Db      5796 GATGAGAGAGCGGTTGTGTGCAATCCTTCCAAAGTCTTTAGAGCTTATCAACAAC 5855
Qy      6008 AACGCTGTGCGGTGACGCGTGAAGATGTCGCCCGGCTTATTCAGACGCTTGGGAAA 6067
Db      5856 CACTTGGCGCGGAGAGAGAGAGAGGTGTCTGCAAGTGTCTTCAAGTGTCTTACAGGGG 5915
Qy      6068 GCACAGAGCGCGCGGCGG 6084
Db      5916 ACACTTGGCTTAGCGGG 5932

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## RESULT 5

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US-10-377-139-16
; Sequence 16, Application US/10377139
; Publication No. US20040175761A1
; GENERAL INFORMATION:
; APPLICANT: MacKinnon, Roderick
; APPLICANT: Jiang, Youxiong
; APPLICANT: Lee MacKinnon, Alice
; APPLICANT: Ruta, Vanessa
; TITLE OF INVENTION: Voltage Sensor Domains of Voltage-Dependent Ion Channel Proteins
; TITLE OF INVENTION: Uses Thereof
; FILE REFERENCE: Seq. Nos. 1-21 for 1119-9
; CURRENT APPLICATION NUMBER: US/10/377,139
; CURRENT FILING DATE: 2003-03-01
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 6503
; TYPE: DNA
; ORGANISM: Bos Taurus
US-10-377-139-16

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Query Match      15.0%; Score 974; DB 18; Length 6503;
Best Local Similarity 55.7%; Pred. No. 7e-260;
Matches 2068; Conservative 0; Mismatches 1570; Indels 72; Gaps 8;

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Qy      2413 TGTGGGACTGTGTGTGGGTTTGTGTAATTTCAAGAGGTGGTATGCTCATGCTCTTG 2472
Db      2175 TCTGGAGTGTCTGCTCCGCTGTGATGTCCATTAGCAGAAATGAGATTGATGTG 2234
Qy      2473 ATCCCTTGTGAGCTTTCATCAACGCTGTGATGTCATTCAGCAACAGATGTCATGCAA 2532
Db      2235 ACCATTGTGTAACCTCACCATCAACATGTCATGTCATGTCATGTCATGTCATGTCATG 2294
Qy      2533 TGGATCAACGATATGAACAGAGATGAGACCGCTGCTCAAGAGTGGCACTATTTCT 2592
Db      2295 TGAAGCACTACCAATGACACGAAATTTAGAGAGATGTCGAGGTTGAAACCTGTCT 2354
Qy      2593 TCAACCGCACTTTGGCATGAGCGCCACATGAACTAATGAGCATGAGCCCAAGTACT 2652
Db      2355 TCAAGAAATTTACAGCAGAGATGACCTTCAAGATCATTTGCTTGAACCTTACTACT 2414
Qy      2653 ATTTCCAGAGGGGTGAGACATTTTCATTCATTTATCTGTGCTTATTCCTATTGGAAC 2712
Db      2415 ACTTCCAGCAGGGGTGAGAACTTTGACAGCATCATCTGATCTCATGCTCATGAGC 2474
Qy      2713 TGGGACTCGAGGGGTTCAGGGTCTGTCCGTAATGCGTCTTTCGATTCGCTGCTGTAT 2772
Db      2475 TGGGCGCTGTCCCGCATGGCAATCTGTGGTGTCTGCTCTTCTGCTCTTCTGCGGTCT 2534

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Qy      2893 TGGGAATGCACTGTTGGAAAAAATTATCATGATATACAGAACCGCTTCCGGA---G 2949
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Qy      2950 GCGACCTGGCGCGCTGGAACCTTCAACGATTTATGACAGCTTATGATCTGTTCGGG 3009
Db      2715 GCTCTCTGCGCGCTGCGCTGACATGATGGAATTTCTTCAATGCTTCTTCATCTTCGGA 2774
Qy      3010 TGTCTGCGGAGAAATGATGAGTTCATGATGAGTGGAGCTGCATGTACGTG---GGCATGTCT 3066
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Qy      3367 ACAAGCACTGAGAGCTGGGCCACGACGAGATCTGCGGACGCGCTCATCAAGAGGGA 3426
Db      3120 GCGCCCGCACCCCAACAGAGAGAGAGAGAGCGCGCCCAAGCGGCAAGAGAGCGCGTTTG 3179
Qy      3427 TCAAGAGAGAGAGCAACTGAGGTGCGCATGCGGGATGAGATGAAATCAGATACAG 3486
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Qy      3487 GCGACATGAAGAACAAACAGCGGAGAAATCCAAATATCTAAATTAACGCAACGATATTG 3546
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Qy      3667 TCAAGACGAGAGCCCAAGGGGACGCGAGACATGAGAGGGCGAGAGAACCGGACG 3726
Db      3405 CTGGGGCCGAGGCAATGAGGTTCAAGGACATTTGGGAGCAGCGCGGAGCAGAGGCC 3464
Qy      3727 CCAAGAGAGATTAGGTTCTGACGAGAGAACTGACGAGAGGGCGAATGCGAGAGG 3786
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Qy      3787 GCGCGCTGACGAGTATCATATTAATTCATGACAGAGAGATATCTGATGATATTC 3846
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3847 CAGTGAATGCGCCCGGATTCGTACTATAAGAAATTCGATCTTAAGCCGGTGAAGATG 3906  
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3645 CACAGGCCCAAGGAGGCTGTGGAGGCTGCGAAGCTGTACCGCATCGTGAAGC 3704  
3967 ATTAATATTTTGAACAGCTGTATCACTATATTTTAATGATGCTTAAGTTGGCAT 4026  
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4027 TAGAAGATGATACATCTGCAACAAAGACCATCTGAGAGATTTTATATCTATGACA 4086  
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3885 AAGATGTCTTCAACCAAGCGGTGTGTGGCTGATTTGTGATTTGATGCTTCA 3944  
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4267 CGTTAAGACATGACCACTACGTCGATGTCCTGATGACGAGGCAATGAGGTGTGTG 4326  
4005 CTTTGCCTGCTGACGACCCCTGCGAGCGCTGTGACGATTTGAGGCAATGAGGTGTGTG 4064  
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4544 --GACATCTTATGACAGAGAGCAGAGAGATTAACAAGCATGAAAGAGTGGCT 4601  
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4602 CCAAGAAAGCCCAAGAGCCATCCACGCGCTGTGAACAGATACAGAGGCTTCAATTTG 4661  
4909 AATATGATACGATTAAGAAATTCGATATATATGATTTATGATGCTGTGAACATGT 4968

4662 ACATTTGACCAAGAGGCTTTCAGCTGACATCATCTTTCTATCTGCTTAACATG 4721  
4969 TCACCATGACCTTCGATGTTACGATGTGTGACACGATTAACGCGGTCTTACATATC 5028  
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5680 AAGAGGCTTACCGACGACGATCTACGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5739  
5442 CGAGAGCCCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5501  
5740 CGAGAGGCACTTACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5799  
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5882 GCGAATCTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5741  
5974 GCCCGATACGAGAGGCTTACGAGCCGCTTCAATGATGATGATGATGATGATGATGATGATGATGATGAT 6033

Db 5742 ACCGTCGAAGATCTCTTCTAGAGCCCATCATCACACGCTGCGCGGAAAGCAGAGAGG 5801  
QY 6034 ACTGCCCCCGGCTTAATCCAGCAGCCTGCGGAAAGCAGAGCGCGCGC 6083  
Db 5802 TGTGGCCACGATCATCAGCGGGGCTTCGCGCGGACCTCTGCGAGCGC 5851

## RESULT 6

US-10-202-824-5

; Sequence 5, Application US/10202824

; Publication No. US2003017648A1

; GENERAL INFORMATION:

; APPLICANT: Wood, John N.

; Akopian, Armen N.

; TITLE OF INVENTION: Ion Channel

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ZENECA Pharmaceuticals

; STREET: 1800 Concord Pike, P.O. Box 15437

; CITY: Wilmington

; STATE: Delaware

; COUNTRY: USA

; ZIP: 19850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/202,824

; FILING DATE: 26-Jul-2002

; CLASSIFICATION: &lt;Unknown&gt;

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/669,656

; FILING DATE: 24-Jun-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Hohenschutz, Liza D.

; REGISTRATION NUMBER: 33,712

; REFERENCE/DOCKET NUMBER: PHM.70086

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (302) 886-7466

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7052 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: cDNA

; FEATURE:

; NAME/KEY: CDS

; LOCATION: 204..6602

; SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-202-824-5

Query Match 14.5%; Score 944.8; DB 16; Length 7052;  
Best Local Similarity 50.9%; Freq. No. 1.1e-25;  
Matches 3060; Conservative 0; Mismatches 2667; Indels 285; Gaps 23;

QY 288 TTGAGGCGACCTTCCCGCGGAAATTGCGCTCACTCCTCTCGAGATATGATCCCTAC 347  
Db 399 TTCTATGCTGAGCTTCCGAGAACTGCTCGGGAGCGCCCTGAGGACCTAGACCTTTTC 458  
QY 348 TACAGCAATGTAAGTGTGATGTTTAAGCAAAAGAAAGATATTTTGGCTTTTCT 407  
Db 459 TACAGCACACCGGACATTCATGTGTGATTAAGCAAGACCAATTCAGATTCAGT 518  
QY 408 GCATCAAAAGCAATGTGATGCTCGATTCATTCGATACGTCGTGGCCATTTAC 467  
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QY 468 ATTCTAGTGCATTCATATTTTCCCTATTCATCATCACCAATTTCTGTAAGTCATC 527  
Db 579 GTGTGTGCATTCCTGTGTTCTCATATTCATCAACCATCATATTTTGTGTAAGTC--- 635

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Db 636 ---GTGTGCATGACCCGCAATCGATCTTCCAGAGAAAGTGATGATCGTCTCATTT 692  
QY 508 TACACATTTGAAATGACGCTGTTAAAGTATGACAGAGGTTTCATTTTATGCGCGTTTACG 647  
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QY 1068 CAATGCGACGACATTAAGTGTGCTGCGAGGGGTTTGTCCGAATCCGAATTAATGACTAC 1127  
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 Db 2049 ATCATGACTTCTGTATTTAGAGAGCTTGAAGAGTCTTAAGCTGAAGTCCACCTGCTTG 2108  
 QY 1917 TATGCGCATCTAGGCTCCGACACTCATCTGTATACCTGACATGCTCCGATATCTAT 1976  
 Db 2109 ATCAGCTTCGCTCAAGAGTATCTGATCTGGAGTGTCTCCCAAGTGAAGAGTTCAAG 2168  
 QY 1977 ACCTTCATGCGCGATCTACTGCGCGGATGCGCTCATGGGCTGACGACATATGACAG 2036  
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 QY 2823 GGAGGCACTAGGGCGCTTTGGTATCTGACATTTGTACTTTGATTTATCATCTTTCATC 2882  
 Db 3069 GGGAACTCAGTGGGGGCGCTGGGCAACCTGACCTTTATCTGGCCATCATGCTGTTCATC 3128  
 QY 2883 TTTCGGGATGGGATGCAATGTTGGAAGAAATATCATGATCAACAGGACCGCTTT 2942  
 Db 3129 TTGCGCTGGTGGAAAGCAAGCTTCTTCAGAGACATGCGGTGCCAGAGAGCGGCTTC 3188  
 QY 2943 CC-----GATGCGACCTGCGCGCTGGAATTTCAACCGACTTTATGACAGCTTCATG 2996  
 Db 3189 TCCGATGGAACCGCGAGAGCTCGGCTGGCAATGTGTACTTTCATTCCTTCCTG 3248  
 QY 2997 ATGCTTTCGGGCTGTCTGTGGAGATGATGATGATGATGATGATGATGATGATGATG 3056  
 Db 3249 GTGCTTTCGGAATCTCTGCGGAGATGATGATGATGATGATGATGATGATGATGATG 3308  
 QY 3057 GGCATGATGTC---GTGATTCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 3113  
 Db 3309 AGCCGAATATCATCTGCTCATCTCTTCTTCTGATGATGATGATGATGATGATGATG 3368  
 QY 3114 GTACTTAACTTTTCTTACCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTT 3173  
 Db 3369 GTGCTAACCTTTTCACTGCTTATCTGCTGATGATGATGATGATGATGATGATGATG 3428  
 QY 3174 CCGACTGCGATTAACATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3233  
 Db 3429 CCAAGATGACGCGGAGTGAACATGATGATGATGATGATGATGATGATGATGATG 3488  
 QY 3234 AAAAGTTGGGTTAAGCGTAATTTGCTGATTTGTTTCAAGTTAATTAATTAATTAATTA 3293  
 Db 3489 GGCATGCGGCGACAGAGGCGCTGCAATGATCA-----GCAGCCACTGCCGATT 3541  
 QY 3294 AATCAATTAAGTATCAACATCAAGTGAAGAGCAACAGATCAAGTGAATTTGAGC 3353  
 Db 3542 CCGTGGCCCAAGGTGAGACCCAGCTGGGATGAACCCCACTCAACAGCTCAGAGC 3601  
 QY 3354 GAAGAGATGATGAACAGATGAGAGCTGGGCAACAGATCTGCGCGAGCTC 3413  
 Db 3602 CAAAGAACCAATGCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 3661  
 QY 3414 ATCAAGAGGGGATCAAGAGGAGAGAGCACTGAGAGTGGCAATCGGAGATCGAGTGA 3473  
 Db 3662 TCTCAGTAG-----CCCAAGAGAAATCAAGGAGCTTCACTGATATCCCAAGCTGTG 3716  
 QY 3474 TTCAAGATACACGCGCATGATGAAGACAAAGCCGAAGAAATCAATATCTTAATTAAC 3533  
 Db 3717 GTCTCTGTGCCAATGTGTGAGGGGGAATCTGACTGACGAGCTGAGGAAGATATGAG 3776  
 QY 3534 GCAACGATGATTTGGCACTAATTAACCAACAGACATGATGAGAACAGAGCTTAAC 3593  
 Db 3777 CAGGCTTCGAGAGCTCTCGGAGAGAGAGACCCCAAGGACAGCAGAGCA----- 3829  
 QY 3594 CATAGAGTTTGTCTTACAGAGACGACAGCTGCCAGATTAATCATATGATGAGCAT 3653

Db 3830 -----GTGGCACAAGTCCAAAATGTAACCAACAGGACAGCAAGGCCA 3878  
 Qy 3654 AAGATTCACATCTTAAAGACCAAGACCCAAAGGAGGCGAGACATGAGGGGCGAG 3713  
 Db 3879 GCGCTCAGATGTCCTCTAGAGACCTGGCTCCATACCTGGTGAAGCTGGAAAGAGAG 3938  
 Qy 3714 GAGAACGCGACCGCAGCAAGAGATTTAGTCTCGACGAGAACTGACGAGAGGCG 3773  
 Db 3939 GATAGCCCTCAGTCCCTGCGCGAG-----GAGTGGATGACACGAGCTCTCTAGAGGCG 3992  
 Qy 3774 GAATGCGAGAGGGCCCGCTCGACGATGATATTTATTCATGCAACGACGAGATATA 3833  
 Db 3993 AGCAGCGTGAAGCTGCGCGAGCCCAAGAGAAATCCTAGAGAAATCCCGAGCTGCGAGAT 4052  
 Qy 3834 CTGAGTAATATCAGCTGATTTGGTCCCGCATTCGATCTAATAAGAAATTTCCGATCTTA 3893  
 Db 4053 GACCTGAGACGAGCCGATGATCTTTTCAAGAGGCTGACCTGCGCGCTGCTGCTGC 4112  
 Qy 3894 GCGGTGACGATGATCGCGCTCTGCAAGATGCGGCAATTTACGACTGAAGACTTTT 3953  
 Db 4113 AAGTGAAATCTAGCAAGTCTCCTTGGGCAAGGCTGGCAGGTCGCAAGACTGCTAC 4172  
 Qy 3954 CAATTAATGAAATTAATATTTTGAACAGCTGTTATCACTATGATTTTAATGATAGC 4013  
 Db 4173 CGCATCGTGAAGCAGCTGTTGAGATTTCAATCTTCATGATCTGCTCAGCAGT 4232  
 Qy 4014 TTAGCTTTGGCATTAGAAGATGATCTGCAAAAGACCCATCTGACAGATATTTTA 4073  
 Db 4233 GAGAGCGTGGCTTTGAGATTAATCTGGAAGAGAAACCCGAGTGAAGTCCGTCG 4292  
 Qy 4074 TACTATATGACAGAAATATTACGGTTAATCTCTTGGAAATGTTATCAAGTGTG 4133  
 Db 4293 GAGTACACTAGCAGAGTTCACCTTCATCTGCTTTGAGATGCTGCTCAAGTGGTA 4352  
 Qy 4134 GCGCTGGCTTAAAGTATCTTCAACGCGGTGTTGGCTCGATTTGCGATTTGTC 4193  
 Db 4353 GCGTATGCTTCAAAAGATTTTCAACAGATGCTGAGTGGTGGCTGAGACTTCTCATTTG 4412  
 Qy 4194 ATGGTATGCTTATCAACTTGTGCTTCACTTGTGAGCTGGTGTATTCAGGCTTC 4253  
 Db 4413 AAGATCTCCGTAAGACCTCATAGCGAAGATCTTGAATTCGACGTGGCGTCCATC 4472  
 Qy 4254 AAGATATGGAAGCTTAAGAGCACTGAGACCACTAGTCCATGTCGCGTGAAGGCG 4313  
 Db 4473 AAGGCTTGGAGCTCTCCGCTGCGCTCGACCGCTGGGGCTGTGTCAATTCGAAGGC 4532  
 Qy 4314 ATGAGGTCGTCGTTAATGAGCTGTGTAAGCTTATACGCTTCATCTTCAATGTGCTATTG 4373  
 Db 4533 ATGAGGATGATGATGATGCTCTGTGGGCGCATCCCTTCATCAATGAAGTCTCTC 4592  
 Qy 4374 GTGTGCTAATATTTTGGCTAATTTTTCGCAATTAAGGCTGTACAGCTTTTGTGGA 4433  
 Db 4593 GTCTGCTCATCTTGGCTCATCTTCAGCATTAAGGCGGTAACCTTCGCGGGA 4652  
 Qy 4434 TATTTTAAGTGGAGACATTAAGCAAGCTGACGACGAGATCATACAA----- 4488  
 Db 4653 TTTTTCGAAGTGGTCGACACCAAGATTAACCATTTTCAAGTGAATTCAGATGTCG 4712  
 Qy 4489 -----ATCGAATGCTCGAGAGCGGAGAACTACAGGTGGGTGAATTC 4532  
 Db 4713 AATTAACAGTCCGAGTGCACATCAAAACAGACCGGCGCATCTTCTGTGGTCAAGTC 4772  
 Qy 4533 GCAATGAATTTGATCATGATGATGACGCTATCTGTGCTTTTCAAGTGGCACTTC 4592  
 Db 4773 AAGTCAACTTCGACAAAGTGTATGGCTACCTCGCATCTTTCAGTGGCAACTTC 4832  
 Qy 4593 AAGAGCTGATACAAATGATGAAGATCTATCGATTCAGAGGAGGAGCAAGCAACA 4652  
 Db 4833 AAGAGCTGATGACATATGATGACAGCTGTGATTTTCGAGAGATCAACAGTCAAGCT 4892  
 Qy 4653 ATTCGTGAAGACGATCTACATGATTTATATTTGATTTCTTCAATATTTGATTC 4712  
 Db 4893 AACTGGAGAACAACTTGTACATGTAAGTCTGTAAGTCTGCTGCTTTCATCATTTTGGTGGC 4952

Qy 4713 TTTTCACTCATCTGTCTATGCTGTATCAATGATTAATTTTAATGACCAAGAA 4772  
 Db 4953 TTTTCACTCATCTGTCTATGCTGTATCAATGATTAATTTTAATGACCAAGAA 5012  
 Qy 4773 AAGAGCTGATCAATTTGAATGTTCAATGACAGAGATCGAAGAAATGATCTATATGCT 4832  
 Db 5013 AAGCTGAGAGG---CCAGACATCTTCAACAGAGAGAGAGAGAGATCTACATTC 5069  
 Qy 4833 ATGAAAAAGATGGGCTTAAAAACCATTAAGAGCATTCGACAGCAAGGTGGCAACA 4892  
 Db 5070 ATGAGAGAGTGGGCTCCAGAGAAACCCAGAGCCATCCAGCGCCCTGAATTAAGTAC 5129  
 Qy 4893 CAAGCAATGCTTTGAAATGATTAACCATTAAGAAATTCGATATTAATGATGATTC 4952  
 Db 5130 CAAGCTTCTGTGTTGAATGATGATGACAGGCAAGGCTTGAATCATCATATGATTC 5189  
 Qy 4953 ATTTGCTGAACATGTTCAATGACCTGATCGTACATGCTGACATGCTGACAGATTAAC 5012  
 Db 5190 ATCTGCTCAATATATCAATGATGATGATGATGATGATGATGATGATGATGATG 5249  
 Qy 5013 GCGTCTAGACTATCTCAATGATGATGATGATGATGATGATGATGATGATGATG 5072  
 Db 5250 AAGTTCGCGGAGATCAACAGATCTTGTGCGCTTTCACGCGGAGATGATGATG 5309  
 Qy 5073 AAAATATTCGCTTACGATATCAATTTTATGAGCATGAGATTTATTTGATGATGAT 5132  
 Db 5310 AAGATGTTGCGCTGAGATGATCAATTCACCAAGCGCTGAGAGATGTTGATTCATTA 5369  
 Qy 5133 GTTGTATTTATTCATCTTGAATGATGATGATGATGATGATGATGATGATGATGAT 5186  
 Db 5370 GTGTGATCTCTCATCTTGGAGTCTGCTGTTTTCGCAATCTTAAGTCACTGAGAAAC 5429  
 Qy 5187 TTGTGTGCGGACCTGCTCGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5246  
 Db 5430 TACTTCTCCCGACGCTCTCCGAGTCACTGCGGATGATGATGATGATGATGATGATG 5489  
 Qy 5247 CTGTGAAGGAGGCAAGGAGGATGAGACATGCTCTTGGCGTGGCATGTCGTCGCG 5306  
 Db 5490 CTGATCCGACGACCAAGGAGATGAGAGCTGCTCTTGGCGTGGCATGTCGTCGCG 5549  
 Qy 5307 GCGCTGTTCAACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5366  
 Db 5550 GCGCTTCAACATGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5609  
 Qy 5367 ATGTGCTTCTTCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5426  
 Db 5610 ATGGCAGCTTCTGCTAATGATGATGATGATGATGATGATGATGATGATGATGAT 5669  
 Qy 5427 ACCTTGGCGAGCATGATCTGCTCTTCAAGATGATGATGATGATGATGATGATGAT 5486  
 Db 5670 ACCTTGGCGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5729  
 Qy 5487 GTATGAGCGCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5537  
 Db 5730 CTCTCAGCGCCATCTCAACAGGGGCTCTCTCACTGAGACCCCAACCTGCGCAACG 5789  
 Qy 5538 AAGGCTATCCGCGCAATGCTGTTCAAGACCGTGAATTAAGTTCCTCTCATAC 5597  
 Db 5790 AAGGCTATCCGCGCAATGCTGTTCAAGACCGTGAATTAAGTTCCTCTCATAC 5849  
 Qy 5598 CTAGTTAATAGCTTTTGAATGATGATGATGATGATGATGATGATGATGATGATGAT 5657  
 Db 5850 ATATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 5909  
 Qy 5658 AGTCAGGCGACGAGAGCTGCAAGAGGCTTCAACGAGAGAGAGAGAGAGAGAGAGAG 5717  
 Db 5910 AAGTACGACCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5969  
 Qy 5718 GAGATCGAGAGAGATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 5777  
 Db 5970 GAGACCTGGAGAGAGTTCGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 6029

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Qy 5778 GAATTCCTGAGCTAGTGGAGCCCGCTGCAGATCCAAACGAGATGACAGATC 5837
Db 6030 GACTTCGGGACAGCCTCTCCGGCCCTTAGAATCCCAACCCAGCAATATATTA 6089
Qy 5838 ATATGATGACATATCCCATCTGTGCGGTGACCTCATGTATCGGCGACATCTCGAC 5897
Db 6090 ATCCAGATGACCTGCGGTGTGCTCCGGGGATAGATTCATCTGTGACATCTTTT 6149
Qy 5898 GCCCTTACGAAAGCTTTTGTGCGGGAAGGCAATCCGATGAGAGAGAGCGGTGAGATT 5957
Db 6150 GCCTTCACAAAGACGTCTTGGAGAAATCCGGGGAGTTGACTCCCTGAAAGCAATATG 6209
Qy 5958 GGTGAG-----ATAGGCGCCCGCCGAGTACGAGGGGCTAGAGCCGCTCATCAAG 6011
Db 6210 GAAGGAAGTTTATGGACCAATCTTCAAGAGATCTTAAAGCAATGCAACCAACC 6269
Qy 6012 CTGTGCGCTCAGCGTGAAGATGACTCGCCCGCTAATCAGACGCGTGGGAAAGCAC 6071
Db 6270 CTCGGGTGGAAGCAGGAAGACCTCTCAGCCACAGTCAATTCAAAGGCTTACCGAGCTAC 6329
Qy 6072 AAGCGCGCGCGC 6083
Db 6330 ATGCTGCACCGC 6341

RESULT 7
US-10-297-022-40
: Sequence 40, Application US/10297022
: Publication No. US20030216310A1
: GENERAL INFORMATION:
: APPLICANT: INCYTE GENOMICS, INC.
: APPLICANT: THORNTON, Michael
: APPLICANT: WALIA, Nalinder K.
: APPLICANT: YUE, Henry
: APPLICANT: NGUYEN, Daniel B.
: APPLICANT: LAL, Preci
: APPLICANT: GANDHI, Ameena R.
: APPLICANT: TRIBOULEY, Catherine M.
: APPLICANT: YAO, Monique G.
: APPLICANT: RAMKUMAR, Jayalaxmi
: APPLICANT: AU-YOUNG, Janice
: APPLICANT: LU, Yan
: APPLICANT: TANG, Y. Tom
: APPLICANT: AZIMZAI, Yalda
: APPLICANT: BRUNS, Christopher M.
: APPLICANT: GRIFIN, Jennifer A.
: APPLICANT: YANG, Junming
: APPLICANT: BAUGHN, Mariah R.
: APPLICANT: SANJANWALA, Madhu S.
: APPLICANT: RAUMANN, Brigitte E.
: APPLICANT: LEE, Ernestine A.
: APPLICANT: HAFALIA, April
: APPLICANT: GREENE, Barrie D.
: APPLICANT: KHAN, Farrah A.
: APPLICANT: KEARNEY, Liam
: APPLICANT: ELLIOTT, Vicky S.
: APPLICANT: SEILHAMER, Jeffrey J.
: APPLICANT: POLICKY, Jennifer L.
: APPLICANT: BOROWSKY, Mark L.
: APPLICANT: BURFORD, Neil
: APPLICANT: DING, Li
: APPLICANT: LU, Dyrng Aina M.
: APPLICANT: HILLMAN, Jennifer L.
: TITLE OF INVENTION: TRANSPORTERS AND ION CHANNELS
: FILE REFERENCE: PI-0109 PCT
: CURRENT APPLICATION NUMBER: US/10/297,022
: PRIOR APPLICATION NUMBER: 2002-11-25
: PRIOR FILING DATE: 2000-05-26; 2000-06-01; 2000-06-08; 2000-06-16; 2000-06-22; 2000-06-23
: NUMBER OF SEQ ID NOS: 54
: SOFTWARE: PERL Program
: SEQ ID NO 40
: LENGTH: 6027

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: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc feature
: OTHER INFORMATION: Incyte ID No. US20030216310A1 6355991CH1
US-10-297-022-40

Query Match      14.4%; Score 941; DB 17; Length 6027;
Best Local Similarity 51.6%; Pred. No. 1,16-250;
Matches 3003; Conservative 0; Mismatches 2425; Indels 387; Gaps 22;

Qy 190 AGAAAAACAAAGAAATCCGATATGATGACGAGACGAGATGAGATGACCAACCGG 249
Db 95 AAAGGCAAGAAATCCCAACCAAGAAAGATGACGAGAAATGAGCCCAAGCCAA 154
Qy 250 ATCTTACATTTGAACAGGCTGCAATCTGTTCATGATGAGGAGCTTCCGCGG 309
Db 155 ATAGTGAATGAGGAGGAAAGAACTTCATTT---ATTATGAGAGACATTCCTCAG 211
Qy 310 AATTGCGCTCAGCTCTCTGAGAGATATGATCCCTTACTACAGCAATGTACTGACATTG 369
Db 212 AGATGGTGTGAGAGCCCTGAGAGACCTGAGACCCCTTACTATATCAATAGAGACTTTTA 271
Qy 370 TAGTTGTAAGCAAGAAAGATATTTTGGCTTTTCTGATCAAAAGCAATGTGATGC 429
Db 272 TAGTATGATTAAGGAGAGGAGCCATCTTCGGTTCAATGACCACTTGCCTGTACATTT 331
Qy 430 TCGATTCATTCATCCGATACGATGATGAGGATTTACATTTAGTGATCATTAATTTT 489
Db 332 TAATCCCTTCAATCTCTTATGAAATAGCTATTAAGATTTTGTATTCATTCATTTTCA 391
Qy 490 CCTTATTCATATCAACCAATTTCTGCACTGATGATCTGATGATATGCGGCAAGC 549
Db 392 GCATGCTAATATATGATGATATTTTGAACAACTGTGTATATGACATGATGATACCTC 451
Qy 550 CCAC---GGTTAGTTCACAGAGTGAATTTACCGGATTTACATCAATTTGATCAGCTG 606
Db 452 CTGATGGAACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 511
Qy 607 TTAAGTATGAGCAAGAGTTTCAATTTATGCGGTTTACATTTAGATGATGATGATG 666
Db 512 TAAATATTTATGCAAGGAGATTTCTTTTAAAGATTTTACTTCTTGGATTCATGATG 571
Qy 667 ATTGCTGAGCTTGTGATATAGCTTATGATGATGATGATGATGATGATGATGATGATG 726
Db 572 ACTGCTGATTTACTGTCATTTACATTTGATGATGATGATGATGATGATGATGATGATG 631
Qy 727 ATCTAGAGCCCTGCAAGCTTTTGGGTCGAGAGGCTTAAACGATGATGATGATGATG 786
Db 632 ATGCTGCGCATTTAGAACATTTCAAGATTTCCAGACATTTGATGATGATGATGATG 691
Qy 787 CAGGCTTGAAGACCATGCTGCGCGCTCATGATGATGATGATGATGATGATGATGATG 846
Db 692 CAGGCTTGAAGACCATGCTGCGCGCTCATGATGATGATGATGATGATGATGATGATG 751
Qy 847 TTATCTGACATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 906
Db 752 TGATCTGACATTTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 811
Qy 907 GCGTCTCACCGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 966
Db 812 GCAACTGAGAGATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATG 871
Qy 967 CCGACGAGA----- 975
Db 872 GTATAGAAAGATATATATGATGATGATGATGATGATGATGATGATGATGATGATG 931
Qy 976 -----ACTGGACTATCAATGCAATGATGATGATGATGATGATGATGATGATGATG 1029
Db 932 AGTTGACTGGAATCAATATATCAATGATGATGATGATGATGATGATGATGATGATGATG 991
Qy 1030 TCTCATTTCCGATATGCGGCAATATATCCGATGCGGCGGATGATGATGATGATGATGATG 1089

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D	b	992	TAAATGCACTACATATGTGGAAATATAGCTCTGATGCAGGGCAATGTCCAGAGGGATATATGT	1051
Q	y	1090	GCCCTGACAGGGGTTTGGTCCGAATTCGGAATTTATGGCTTACACACACTTCGATTCGTTGGAN	1149
D	b	1052	GTGTGAAAG---CTGTGTGAAGAAATCCCAATTTATGGCTTACAAACCTTTGATACCTTCAAGT	1108
Q	y	1150	GGGCTTTCCTGTCCGCTTCCTGGCTGATGTGACAGAGCTTCTGGAGGATCTGTACACAG	1209
D	b	1109	GGGCTTTTGTGTCTTGTGTTCGACTATGATCAGAGCTTCTGGGAAATCTTTATCAAC	1168
Q	y	1210	TGGTGTGGCGCGCCCGGACCATGGCACTGCTGTCTTTATATGTCATCATCTTCTCAG	1269
D	b	1169	TGACATTACGTGCTGCTGGGAAACAGTACATGATATTTTGTATGTGTCATTTTCTTG	1228
Q	y	1270	GTTCATTCTTATCTGTGAATTTGATTTTGGCCATTTGTGCATGTGCTATGACGAATTCG	1329
D	b	1229	GCTCATTTCTACTTATATTAATTTGATCTGTGCTGTGTGGCCATGTGCTTACAGAGAACGA	1288
Q	y	1330	AAAGGAAGGCCGGAAGAAAGAGGGCTCCGAAAGAGAGGCGGATTCGTAAACCGAAGAG	1389
D	b	1289	ATCAGGCGACCTTGTGAAGAAAGCAGAAACGAAGAAGGCGG---AATTCAGCAGATGATTT	1344
Q	y	1390	CTGCGCGCCGCAAGCGGCCAAGCTGAGAGAGGGGCGCAATGGCAGAGCTCAGGACGAG	1449
D	b	1345	GAACAGCTTAAAAAGCAAC-----AGAGGCGAGCTCAGAGGAG	1384
Q	y	1450	CGGATGGCGGCTGCCGCGAAGAGGGCTGCATCTCCGAATATGGCCAAAGTCCGAGT	1509
D	b	1385	CAAGCGAACCTGCTCAGAACATTTCCAGAGAGCCCACTGCGACGAGGAGCTTCAGACA	1444
Q	y	1510	ATTCTTGCAATCAGCTATGAGCTATTTTGTGGCGCGAAGAGGCGACAGATGACAAACA	1569
D	b	1445	GCTCATCTGAAAGCCTCTAAG--TTGAGTTCMAAGGTCTAAGGAAAGAAAGAAATCGAG	1502
Q	y	1570	AAGGAAGATGTCATTCCGAGCCTCGAGGTGAGTGCAGTCCGATGAGGCTTTACAA	1629
D	b	1503	GAAAGAAAGAAACAGAAAGAGCAGTCTGTGGGGAAAGAAAGATATAGATGAAATTCGA	1562
Q	y	1630	GACAAACGACCTTACCAACAGACACACCAAGCTTACCAAGTTCTTAAATGTAGACGCAAT	1689
D	b	1563	AAATCTGAATCTGTAGAGCAGCATCAGAG-----GAAGATTTTCCTTCTC	1610
Q	y	1690	CCTTATCCTTACCTGGTTACCGTTTAACTATGCAAGGGGATCAGTATGTTCTCAAGT	1749
D	b	1611	CATTGAAGGGACCGATTTGACATATGAAAGAGTAC-----TCTCCTCCACACCC	1660
Q	y	1750	ACACGATACGGAACGGAAGCTGCGCTTGGTATACCCGGTAGCGATGTCATGCAATTGG	1809
D	b	1661	AGTCTTGTGTAGCATCCGTGGCTCCCTATTTTACCAAGGCGAAATAGCGAACAGCC	1720
Q	y	1810	TATGTGTCAACATTCAGGATGCCAGACGACCTTGCCCTATGCGCGACGACTCGAATGCG	1869
D	b	1721	TTTTTACGTTTGAAGGGGCGAAGAAAGATGTGGGATCTTGAGAACGACTTCCGAATGATG	1780
Q	y	1870	TCACCCCATGTCCGAGAGAGATGGGGCATATAGTCCCGTATCTAATGGCAATCTAG	1929
D	b	1781	AGCAGACGACCTTTGAGGATTAACGAGACCGGTAAGATTTCTTGTGTTGTGCCCGACAC	1840
Q	y	1930	GCTCCCGACATCTCATGTATACCTTGCACTCAGTCCCGAATATCGTATATCTCAATGGCG	1989
D	b	1841	ACGGAGAGAGCGCAACAGCAACTGAATCAGACCAATGATGTCAT-----	1885
Q	y	1990	ATCTACTGGCGGCGATGGCCGTCATGGCGTCCAGACATGACCAAGAGAGCAAAATTC	2049
D	b	1886	-----CCGGATGCTGGCAGTGT	1904
Q	y	2050	GCAACCGAACACACGCAATCATATGATGGCGGCCCAATATGGCGGCAACCTGTCTGG	2109
D	b	1905	TCCACCGAATGGGAATGACACAGCACTGTGGATGCAATGGTGTGTCTTGTGGTTGG	1964
Q	y	2110	ACACCAATACAAAGCTGCATATCGGCACTACGAATTTGGCTGGAGTGACACGACGAAG	2169
D	b	1965	TGAGCTTCAAGTTCTTACATGCGCTGTGTGGACAGCTTCTGCCAGAGGTGATATAT-----	2019

OY	2170	CTGGCAAGATTAAACATCATGACATACATCCTTTATTCGAGCCCGTCCAGACCAACGCTGG	2222
Db	2020	-----GATPAGCGAGCTCTGTATGACATATGAAACACACACTGGAA	2059
OY	2230	TTGATATGAAGAAGATGTGANTGTCCTGTAAATGACATCATTCGAAGCCCGCTGTGGCACA	2289
Db	2060	CTGAATATGAGAAAGAAAGGATCAAGTTCTTTCACGTTTCCATGAGCTTTCATGAAGATC	2119
OY	2290	GTCGGGCAAGCGATCGCGGTGTCTCCGTTTACATATTTCCCAACAGAGAGATGACGAGG	2349
Db	2120	CTTCCCAAGGCACGAGCATGTATGTACCGACATCTTCAACAATACATGTGAGAAC	2179
OY	2350	ATGGCGCAGCTTCAAGACAAAGGCACTCCGAAGTATCTCAAGGCAATCGATGTGTTTT	2409
Db	2180	TTGAAAGATCCAGGCAAAATGCCACCGTGTTGAT---AATTTTCCAAATATTTCT	2236
OY	2410	GTCGTGGGACTGTGCTGGGTTTGTGTAAATTTCAAGAGTGGGTATCCGTCATGCTCT	2469
Db	2237	TAACTCTGGACTGTCTCCATATTTGGTTTAAAGTAAACATGTTGTCAACCTGGTGTGA	2296
OY	2470	TCGATCCCTTGAGAGCTCTTCATCAAGCTGTGTCATTTGTGTCAACACGATGTTCATGG	2529
Db	2297	TGAACCAATTTGTGACTGTGGCATACACATCTGTATGTCTTAAATACCTTTTATATGG	2356
OY	2530	CAATGATTCACACAGATATGAACAAGAGATGGAACGCGTGTCTCAAGATGGCACTATT	2589
Db	2357	CCATGGAGCACTATCCATATGACGAGCACCATTTCAATATATGTGCTTACATGAGAAACTGG	2416
OY	2550	TCTTACCGCGCACTTTTGCCATCGAGGCGACACATGAAGCTAAATGGCCATGAGCCCAAGT	2649
Db	2417	TATTCACCTGGGATCTTTACACGACAAAATGTTTCTGAAAATTTATTTGCCATGATCTTACT	2476
OY	2650	ACATATTTCCAGAGAGGCTGGAACATCTTGCACATTCATTCGTGGCCCTATTCGTAATGG	2709
Db	2477	ATATATTTCCAGAAAGGCGTGGAAATCTTTGACGGTTTATATGTGACCTTAGCCTGGTAG	2536
OY	2710	AACTGGGACTCGAGGGTGTCCAGGGTGTCTCCGATATGCGTTCCCTTCGATGTGTGGTG	2769
Db	2537	AACTTGGACTCGCAATGTGGAAAGATTAATCTGTCTCCGTTCAATTCGATGTGTGGAG	2596
OY	2770	TATTCAACTGAGCAAGCTTGGGCGCCACACTTAATTTACTCATTTGCATTATGGAACGA	2829
Db	2597	TTTTCATGTGGCAAAATCTTGGCCACAGCTAAATATGTCTAATAAGTATCATCGCAATT	2656
OY	2830	CCATGGCGCTTTGGGTATCTGACATTTGTACTTTGATATATCTTCACTTTTCGGG	2889
Db	2657	CCGGGGGGGCTCTGTGGAAATTTAACCCCTGCTTGGCCATCATGTCTTCAATTTTTCGG	2716
OY	2850	TGATGGGAATGCACTGTTTCGGAAGAATTAATCATGA---TCACAAGGACCGCTTTCGG	2946
Db	2717	TGATCGCATGTCACTCTTTGTATTAAGCTACAAAGATGTGTGTGCAAGATGCCAGTG	2776
OY	2947	ATGGCACTGTGCGCGCTGGAACCTTCAACCGACTTATATGACACAGCTTCAATGATCGTTCC	3006
Db	2777	ATTGTCAACTCCACAGCTGTGACATGAATGATGACTTCTTCACTCCTTCTGTATGTGTCC	2836
OY	3007	GCGTCTCTGCGGAGAAATGATTCAGATCCATGTGGGACATGATGATGATGAT---GGGCGATG	3063
Db	2837	GCGTCTGTGTGGGAGTGGATGAGACACATGTGGGACTGTATGTAGAGTTCGTGTCAAG	2896
OY	3064	TCTGTGCAATTCCTTCTTCTTGTGGCACCGTGTTCATCGGCATCTTGTGTACTTAAC	3123
Db	2897	CCATGTGCTTACTGTCTTTCATGATGTGTCAATGTGATTTGGAACCTAGTGTACTGATTC	2956
OY	3124	TTTTCTTAGCTTGTCTTTTGTTCAAATTTGGCTCATCTAGCTTATCAGCGCCGACTGGCG	3183
Db	2957	TCTTCTGTGGCTTGTCTGTGAGCTCATTTATGTGACGACAACTTGGACCCCTGATGTAG	3016
OY	3184	ATAAGATATCAATAAATPAGCCGAGGCGCTTCAATCCAAATTCGCGCATTTAAAGTTAGG	3243
Db	3017	ATAATGAATGATATATCTCCAAATGTCTGTGATGATGATGACAAAGAGATGATATG	3076







Qy 3550 ACTCAATTAACCAACCAATAGACTGAAACAGAGCTAAACATAGAGTTGTCT 3609  
Db 3366 GTCCAGCAAGCAAGCAATCCACCTG--TGTCCGCTGGCCAGAGCCCTCCGAT 3423  
Qy 3610 TACAGACGACGACCTGCCAGATTTAATCATATGTAAGCCATAAGATGACCATTC 3669  
Db 3424 TCCAGGACCTGGA---GCCAGGTGTCAAGCACTGCTACTGTAGGCCAGAGCCAGTGC 3479  
Qy 3670 AGAGCAAGACCAAGGAGGAGCCGAGAGCATGAGAGGCGAGAGAGAGCCGACCA 3729  
Db 3480 ATCTAGGCCCACTGAGCGAGCAAGTGAAGAACCCAGGCCAGGGGTGGGTGA 3539  
Qy 3720 GCAAGAGGATTTAGTCTGCAAGAGACTGACGAGAGGGCCGATGCCAGAGGGCC 3789  
Db 3540 GA-----CCCCAGAGACAGTTGCTCCAGGGGCGACAGACAGACATGA 3583  
Qy 3790 CGCTGACGATGATATCATTTATTCATGACACAGAGAGATATATCTGATGATATTCAG 3849  
Db 3584 CCAACACCGCTGAGCTCTGAGAGCATCTGACCTGGCCAGATGTCAAGACCCAG 3643  
Qy 3850 CTGATGCTGCCCGCATTCGTAATAAGAAATTTCCATCTTACCGGTGACATGACT 3909  
Db 3644 AGGACTGCTTACATGAAAGCTGTGTCCGCGCTGCTGCTGCTGCGGTGACACACAC 3703  
Qy 3910 CGCCGCTTGGCAAGGATGGGCAATTTACGACTGAAACCTTTCAATTAATGAAATA 3969  
Db 3704 AGGCCCCAGGAGGCTGTGTGGCGGTGGCCAGAGCTGCTACCAATCTGTGGACCA 3763  
Qy 3970 AATATTTTGAACAGCTGTATCACTATGATTTTATGATAGCTTACCTTTGGCATTA 4029  
Db 3764 GCTGGTGGACATTCATCATCTTCAATGATCTCACTCAGAGGTGGAGCGGCTTGG 3823  
Qy 4030 AAGATGTACATGTGCAAAAGACCAATACGACAGATTTTATATCTATGACAGAA 4089  
Db 3824 AGGACATCTACCTAGAGAGCGGAAACATCAAGATTTCTGCTGATGATGCCAGAA 3883  
Qy 4090 TATTTACGTTAATTTCTTCTTGAATGTTATCAAGTGTGGCGCTTCAAG 4149  
Db 3884 TGTTCACATATGCTTCTGCTGAGATGCTGCTAAGTGGGTGCTTACCGCTTCAAGA 3943  
Qy 4150 TGTACTTACCAAGCGGTGTGTGTGCTGATTTGCTGATTTGCTATGCTTATCA 4209  
Db 3944 AGTACTTACCAAGTGTGTGTGCTGCTGATTTGCTATGATGATGCTTCTGCTGCA 4003  
Qy 4210 ACTGTGTGCTTCACTTGTGAGAGTGTGTGATTTCAAGCTTCAAGATATGCAAGT 4269  
Db 4004 GCTGTGTGGCAACCTGTGGCTTTGCGAGATGGGCCCATCAAGTCACTGCGGACGC 4063  
Qy 4270 TAAAGACATGAGCACTAGGTGCTATGCTCCGATGACAGGGGCAAGGGTCCGTTA 4329  
Db 4064 TGTGTGACCTGCTCTGAGAGCTTGTCAAGATTTGAGGGGCAAGGGGTGTGTCA 4123  
Qy 4330 ATGCGCTGTGTAAGAGTATACCTGCTCATTTCAATGCTATTTGCTATATTTT 4389  
Db 4124 ATGCGCTGTGGGGCCATCCGCTCATGAGAGTCTCTCTGCTGCTCATCTTCT 4183  
Qy 4390 GGTCTATTTTTCATTAATGGGTGTACAGCTTTTGTGTAATAATTTTAAAGTGGAG 4449  
Db 4184 GGTCTATCTTCAAGATCATGGGGCTGTAACCTTTTGGGGAAGTTTGGAGGTGCATCA 4243  
Qy 4450 ACATGA-----ATGGCAAGAGCTCAGGCCAGAGATATACAAATGCGAATGCTGGC 4503  
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Qy 4504 AGAGCGAAGACTACAC-----GTGGGTGAATTCAGCATGATTTTCATCATG 4551  
Db 4304 AGTCTTGAACCTTGACCGGAGAAATTTGATGACCAAGAGTGAAGTCAACTTTGACAG 4363  
Qy 4552 TAGTAAGCGGTATCTGTGCTTTTTCAGAGTGGCACTTCAAGAGCTGTGATCAAAATCA 4611  
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Qy 5032 ATGCGATATTTGTATTTTTCAGTTCCGATGCTATTAATAATATTCCTTTAGAT 5091  
Db 4841 ACCTGCTTTTGTGGCCATTTCAAGGCGAGTATGTCAAGCTGCTGCCCTGCC 4900  
Qy 5092 ATCACTATTTATGAGCAATGAAATTTATTTGATGATGATGTTGCTATTTTATCACT 5151  
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Qy 5152 TAGTCTTGTACTAGGATTTATGAGAGTACTTGTGCTGCCGACCTGCTCCAG 5211  
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Qy 5212 TGTGTGCTGTGGCAAAAGTGGGCGGTGTCTTGCATGTGTGAAGGAGCCAGGCAATTC 5271  
Db 5021 TCATCCGCTGTGCGGAAATAGGCGCATCTCAGATGATCCAGGGGCAAGGGGATCC 5080  
Qy 5272 GGAATCTCTTTTGTGCTGTGGCCATGTGCTGCGGCGCTTGAATCTGCTGCTGCTG 5331  
Db 5081 GCAGCTGCTCTTTGCTCCTCAATGATGCTGCTGCTGCTTCAAAATCGGCTGCTGCTG 5140  
Qy 5332 TGTCTGTGATGATGATCTTTGCAATTTTCCGATGCTGCTTCAATGACGGAAG 5391  
Db 5141 TCTTCTGTGATGATGATCTTTCACTCATCTTTGAGATGCGCAATCTGCTTATGATG 5200  
Qy 5392 AGAAGAGCGGATTAAGAGCTTCAACATTTCAAGACCTTTGGCAGAGCATGATCTGC 5451  
Db 5201 GGGAGGCTGGATGAGAGAGATTTCAACTTCCAGACTTGGCAGAGCATGTGTGCC 5260  
Qy 5452 TCTTTCAGATGTGACGCTCAGCCGTTGGAGTGTGATCTGAGAGCCATTAATGAGG 5511  
Db 5261 TCTTTCAGATGACACAGCTGCGGCTGGAGTGTGCTTCAAGCCCATCTTCAAACTG 5320  
Qy 5512 AAGATGGA-----TCACCGGACAGCGCAAGAGGTATCCGGGCAATTTGTGTT 5562  
Db 5321 GGGCTCTTACTGAGACCCCACTTGGCCCAAGCAATGGCTTCTGGGGGAGATGCGGGA 5380  
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Db 5441 TCAACATGTATCATTTGCTATCTTGAAGATTCAGCGTGGCCACAGAGAGAGCAAG 5500  
Qy 5683 AGGTCTAACCGACGACGACTACAGATGTATGATGATCTGGCAAAATTCGATCCGG 5742

Db 5501 AGCCCTGAGTGAAGACGACTTCATATGTTCTATGATCTGGGGAATTTGACCCAG 5560  
 QY 5743 AGGGCAACCAAGTATACGATATGATCAAGCTGTCCGAATTCCTGACGTAAGAGCCCC 5802  
 Db 5561 AGGCCATCACTTATTTAGTATGCTGCTGTCTGATCTTGGCAGCGCCCTGTGAGC 5620  
 QY 5803 CGCTGAGATCCCAAAACGAGACAGTACAGATCATATGATGAGCATATCCCATCTGTC 5862  
 Db 5621 CACTCCGATTCGCAAGCCCAACCAATAGAGCTCTCAACAGAGACTGCCCCATGATA 5680  
 QY 5863 GCGGATACCTCATGATCTGGGTCATCTCTGACATCTCTGACGCCCTTATGAAAGACTTTCGCG 5922  
 Db 5681 GTGGGATCCGATTCATTTGATGATGATCTTCTTTCCTTTCACCAAAAGGCTCTGGGG 5740  
 QY 5923 GGAAGGCAATCCGATAGAGAGACGCGGTGAGATTGATGAG-----ATAGCGCCGCC 5976  
 Db 5741 AGCTGGGGAGATGAGACGCCCTGATGATGAGATGAGAGATTCATGAGCAAGCAAC 5800  
 QY 5977 CGGATACGAGGCGTACGAGCCCTCTCATCAACGCTGTGGCGCTGACGCTGAGAGTACT 6036  
 Db 5801 CATCAAGATCTCTTACGAGCCCATCAACCACTCCGCGCAAGCAGAAAGAGTGT 5860  
 QY 6037 GCGCCCGGCTAATCCAGCAGCGCTGGCGAAGCAGAGCGCGCGC 6083  
 Db 5861 CGGCTATGTTATCCAGAGAGCCTTCGCGAGCACTGCTGCAACGC 5907

## RESULT 9

US-09-896-994-1  
 ; Sequence 1, Application US/0986994  
 ; Publication No. US20030074024A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ken Stokes  
 ; Jos e Morissette  
 ; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
 ; SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. US20030074024A1 is  
 ; STREET: One Liberty Place - 46th Floor  
 ; City: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WordPerfect 6.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/896,994  
 ; FILING DATE: 02-Jul-2001  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/514,907  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul K. Legaard  
 ; REGISTRATION NUMBER: 38,534  
 ; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (215) 568-3100  
 ; TELEFAX: (215) 568-3439  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 6048 bases  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: double  
 ; TOPOLOGY: linear  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
 US-09-896-994-1  
 Query Match 14.4%; Score 940.2; DB 10; Length 6048;

Best Local Similarity 55.4%; Pred. No. 1,8e-250;  
 Matches 2052; Conservative 0; Mismatches 1583; Indels 72; Gaps 9;

QY 2413 TGTGGAGCTGTGCTGGGTTTGTGTAATTTACAGAGTGGGTATGCTCATGCTTTCG 2472  
 Db 2087 TCTGGGAGTGTGCGCCGCTGTGATGTCCATCAACAGAGATGAATGGTGGTATGAG 2146  
 QY 2473 ATCCCTTCGTGAGCTCTTATCAAGCTGTGATGTTGGTCAACGATGTTCAATGCA 2532  
 Db 2147 ACCCGTTTACTACCTTACCAATCATATGTGATGCTACTCAACACCTCTTCAAGCC 2206  
 QY 2533 TGGATCACCAAGATATGAACAAGAGATGAACGCGTCTCAAGATGCAATATTTCT 2592  
 Db 2207 TGGAGACTACAAACATGACAAATGAAATGAGAGATGTGTGAGGTGGAAACCTGTCT 2266  
 QY 2593 TCAACGCACTTTTGGCATGAGGCGCACCATGAGTAAATGGCCATGAGCCCCAGTACT 2652  
 Db 2267 TCAAGAGGATTTTTCAGAGAGATGACCTTCMAAGATCAATGCCCCCTGACCCCTACT 2326  
 QY 2653 ATTTCCAGAGAGGCTGGAAACATCTTCGACTTCAATATGTCGCCCCATATGCTATTG 2712  
 Db 2327 ACTTCAACAGAGGCTGGAACATCTTGCACAGATCATGCTCATCTTACCTTCAATGAG 2386  
 QY 2713 TGGGACTCGAGGAGTGTCCAGGCTGTCCGTAATGCGTCTTTGATGTTGCTGCTGAT 2772  
 Db 2387 TGGGCTGTGCGCGATGAGCAACCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2446  
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 QY 3130 TAGCTTGTCTTGTGCAATTTTGGCTCATCTGATGATGATGATGATGATGATGATGAT 3189  
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 QY 3250 GTAAATGCTGATTTGTTTAAATTAATGATGATGATGATGATGATGATGATGATGAT 3309  
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 QY 3310 AACCATGAGTGAAGAGACCAACCAATGATGATGATGATGATGATGATGATGATGAT 3369  
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Qy 3850 CTGATTCCTCCCGGATTCGATATTAAGAAATTTCCGATCTTACCGGCTGACATGCT 3909  
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Qy 3970 AATATTTGAAACAGCTGTATCTATGATATTTATGATAGTACTTATGCGATTAG 4029  
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Qy 4090 TATTTAGGTTATTTCTTTGGAATGTTAATGAAGTGGCGCTCGGCTCAAG 4149  
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Db 4334 ACATGATCATCTATTTTGTATTTTCAATCTTATCATCTTTGAGTCTTCTTCACTCACTCT 4393  
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QY 5623 TTAATATGATTCGTCGTCATTCGAGAACTATATGTCAGCCACGAGAGACGTGCAAG 5682
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QY 5683 AGGGTCAACCGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 5742
Db 5351 AGCCCTGAGTAGAGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 5410
QY 5743 AGGGACCCAGTACATACGATGATCAGTCGTCGCAATTCCTGAGACGATGAGACCC 5802
Db 5411 AGCCCACTAGTTATGATGATTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 5470
QY 5803 CGCTGAGATTCACCAACCGACGACGACGACGACGACGACGACGACGACGACGACGACG 5862
Db 5471 CATTCGATTCGCAACCGACGACGACGACGACGACGACGACGACGACGACGACGACG 5530
QY 5863 GCGGTACCTCATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 5922
Db 5531 GTGGGAGCCGATTCATTCGATGACATTCCTTTGCTTCACCAAAAGGGTCTG936G 5590
QY 5923 GGAAGGCAATCCGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5976
Db 5591 AGCTGGGAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 5650
QY 5977 CGGATACGAGAGGCTACGAGCCGCTCATCAACGCTGCGTCAGCGTCAGAGAGTACT 6036
Db 5651 CATCAAGATCTCTACGAGCCATCAACGACGACGACGACGACGACGACGACGACGACG 5710
QY 6037 GCGCCCGGCTAATTCAGACGCGCTGGGAAAGCAAGGCGCGCGG 6083
Db 5711 CGGCATGTTATTCAGAGAGCCCTTCGCGAGGACGCTGCAACG 5757

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## RESULT 10

US-10-685-237-1  
 Sequence 1, Application US/10685237  
 Publication No. US20040236377A1

## GENERAL INFORMATION:

APPLICANT: Kenneth B. Stokes  
 Joseph Morissette

TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL  
 SENSING BY CARDIAC PACEMAKERS THROUGH  
 GENETIC TREATMENT

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris LLP  
 STREET: One Liberty Place - 46th Floor  
 CITY: Philadelphia  
 STATE: PA

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Wordperfect 6.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/685,237

FILING DATE: 14-Oct-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/514,907

FILING DATE: 08-Feb-2000

ATTORNEY/AGENT INFORMATION:

NAME: Paul K. Legard

REGISTRATION NUMBER: 38,534

REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 6048 bases

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-685-237-1

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Query Match 14.4%; Score 940.2; DB 18; Length 6048;  
 Best Local Similarity 55.4%; Pred. No. 1.8e-250;  
 Matches 2052; Conservative 0; Mismatches 1583; Indels 72; Gaps 9;

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QY 2413 TGTGGACGTCGTGCTGGGTTGGTGAATTCAGAGAGGGGATGCTCATGCTTTGG 2472
Db 2087 TGTGGAGAGCTGCGCCGCTGTGGATGTCATAGAGAGGAGAGAGAGTGGTGCATGG 2146
QY 2473 ATCCCTTGTCAGAGCTTCATCAGCGTGGATGTTGGTCAACAGACGTTTCATGGCAA 2532
Db 2147 ACCGTTTACTGACCTCACACATGCTATGATGATGCTACTCAACACACTTTCAATGGCCG 2206
QY 2533 TGGATCACCAAGATATGAAACAAGAGAGTGAACGCGTGTCAAGAGTGGCAATATTTCT 2592
Db 2207 TGGAGACATCAACATGACAGAGTGAATTCAGAGAGATGCTGAGAGTGGGAACTGGTCT 2266
QY 2593 TACCGCCACCTTTGCGATGAGGCCACATGAAGCTAATGGCCATGAGCCCAATGACT 2652
Db 2267 TCAAGAGGATTTTCAAGAGAGATGACCTTCAAGATCATTTGCCCTCGAACCCCTACTACT 2326
QY 2653 ATTTCAGAGAGGCTGGGAACATCTTCAGTTGATGATGAGGCGCTATGCTATTGGAAAC 2712
Db 2327 ACTTCAAGAGGCTGGGAACATCTTCAGTTGATGATGAGGCGCTATGCTATTGGAAAC 2386
QY 2713 TGGGACTCAGAGGTCGACAGGTCGTCGCTATGCGTTCTTTGATGCTGCTGAT 2772
Db 2387 TGGGCTGTGCGCGCATGAGCAACTGTGCGTGTGCGCTCTTCGCGCTGCGGCTG 2446
QY 2773 TCAACTGGCCAGTCTTGGCCCACTAATTTATCTCATTTGATTTGAGAGCAGCA 2832
Db 2447 TCAAGCTGGCCAAATATGAGCCCACTTGAACACATCTCAAGATCATCGGAACCTCAG 2506
QY 2833 TGGGCGCTTTGGGTATCTGACATTTGACTTTGATTCATTCATCTTCATCTTGGCGTGA 2892
Db 2507 TGGGGCACTGGGAACTGACACTGCTGTGACCATCATCTGTTCACTTTGCTGTGG 2566
QY 2893 TGGGAATGCACTGTTGGAAGAAATATCATGATCACAAGACGCTTTCGGATGGCG 2952
Db 2567 TGGGATGACAGCTTTTGGCAAGAACTACTCGAGGTGAGGAGCAGCACTCA---GGCC 2623
QY 2953 ACTGCGCGGCTGGAATCTCAACGACTTTATGACAGCTTCATGATGCTGCTCGGCTG 3012
Db 2624 TGCTGCTCGCTGGCAGATGATGAGACTTCTTCATGCTTCATATCATCTTCGCACTCC 2683
QY 3013 TCTGCGGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3069
Db 2684 TCTGTGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2743
QY 3070 GCATTCCTCTTCTTTGCGCACCGTTGATGCGCAATCTTGTGACTTAACTTTTCT 3129
Db 2744 GCTGCTGGGCTTCTTGTGTTGTTATGATGATGCGCAACTGTGTCGTAATCTTCTCC 2803
QY 3130 TACGCTTCTTTTGTGCAATTTTGGCTCATCTAGCTTTTCAAGGCGGACGCGCATGAAG 3189
Db 2804 TGGCCTTGTGCTGCACTGCTCTTCAAGGAGACAACTCAAGCCCTGTATGAGAGACAGAG 2863
QY 3190 ATACGATAATAATAGCGAGGCGCTTCAATGCAATGGCGGATTTAAAGTTGGTTAAGC 3249
Db 2864 AGATGACAACTCCAGCTGGCCCTGGCCGCAATCAGAGGGGCTGCGCTTTGTCAAGC 2923
QY 3250 GTAAATTCGTAATTTTCAAGTTAATGTAACAAATTTGACAAATTAAGTATC 3309
Db 2924 GAGACACTGAGATTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 2968
QY 3310 AACCATGAGTGAAGAGCAACCAAGATGATGATTTGAGAGGAGAGCATGTGACCA 3369
Db 2969 AGAAGCCCGAGCCCTTGGCCGCGCAGGGCCAGCTGCCAGCTGCAATGGCAACCCCTACT 3028

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QY 3370 ACGAAGCTGGAGCTGGCCACGAGAGTCTGCGGAGCGCTCATCGAAGAGGGATCA 3429  
Db 3029 CCCCACACCCCAAGAGAGGAGGAGGCTCCCAACCCGCAAGAAACAGATTGAGG 3088  
QY 3430 AGGAGCAGACGCACTGAGAGTGGCCATGCGGAGATCGATGGAATTCAGATACAGCGG 3489  
Db 3089 AAGCGAGCAACCAAGCCAGGGCACCCCGGGGATTC-----AGAGCGCG 3133  
QY 3490 ACATGAAGAACAAACAGCCGAAGAAATCCAAATATCTAAATACGACAGATGATTGCA 3549  
Db 3134 TGTGTGTCCCACTTCCTGTGGCCGAGTCAAGATGACCAAGAGAGATGAGAGAA 3193  
QY 3550 ACTCAATTAACCAACCAAGCAATTAAGCTGGAACAGAGTAAACATAGAGTTGTCT 3609  
Db 3194 ACAGCTGGGACGAGAGAGAGAGTCAAGACAGAGAAATCCAGCTGTGTCCGGCT 3253  
QY 3610 TACAGAGCAGACGACTGCGACATTAATCTATATGTAAGCCTAAGATGACCATTC 3669  
Db 3254 GGGCCAGAGGCTCTCGGATTCAGGACCTGGAAGCAGGTGTCAAGGACTGCTCTCTG 3313  
QY 3670 AGAGAGAGACCAAGGAGGAGCGCCGAGAGCATGAGGCGCAGAGAAAGCGCACGCC 3729  
Db 3314 AGGCGAGGCGCAGTCAATCTCAAGCCGACTGCGCAGCAGTGAAGCGGAACCCAG 3373  
QY 3730 GCAAGAGGATTTAGTCTCGACGAGGAAGTGAAGGAGGCGCAATGCCAGAGGGCC 3789  
Db 3374 CCCCAGGCTGGGTAGACCCAGAGAGAGCATGTTCTCGAGGGCAGCACAGACATGA 3433  
QY 3790 CGCTGACGCTGATATCATTTATTCATGACAGAGAGATATCTCATGATATTCAG 3849  
Db 3434 CCAACACGCTGAGTCTCTGAGAGAGATCCCTGACTGCGCCAGATGTCAAGAGCCAG 3493  
QY 3850 CTGATTCCTCCCGCATTCGTAATTAAGAAATTCCTGATCTTACCGGTGACATGACT 3909  
Db 3494 AGGATGCTTCACTGAAGGCTGTGTCCGCGCTGTCTGCTGTGCGGTGACACACAC 3553  
QY 3910 CGCGCTTGGCAAGATGGGCGCATTTACGATGAACCTTTCAATTAATGAATAA 3969  
Db 3554 AGGCGCCAGAGAGGCTGTGGGCGGTGGCAGAGCCTGTAACACATCGTGGAGCA 3613  
QY 3970 AATATTTGAAACAGCTGTATCACTATGATTTATGATGATGATGATGATGATG 4029  
Db 3614 GCTGTTGAGAGCATTCATCATCTTCATGATCTCAAGAGTGAAGCGCTGCGCTCG 3673  
QY 4030 AAGATGATCTGCGCAAAAGACCATATGCGAGATATTTATATATATGACAGAA 4089  
Db 3674 AGGATCTACCTAGAGAGCGGAGACCATCAAGGTTCTGCTGATGATGCCAGAA 3733  
QY 4090 TATTTAGGTTATATCTTCTTGGAAATGTTAAATGAATGTTGGCGCTCGCTCAAG 4149  
Db 3734 TGTTCATATATGCTTCTGCTGAGAGATGCTCAAGTGGGTGGCTTACGCTTCAAG 3793  
QY 4150 TGTATCTTACCAACGCTGTGTGGCTGATTTGATGATGATGATGATGATGATG 4209  
Db 3794 AGTACTTACCAAGTCTGTGTGGCTGATTTGATGATGATGATGATGATGATG 3853  
QY 4210 ACTTGTGCTTCACTTGTGAGCTGTGTGATTCAGACCTTCAAGATATGCAAGCT 4269  
Db 3854 GCTGTGTGGCCAAACCTGTGGCTTGTGCGAGATGGGCCCATCAAGTCACTGCGGAGC 3913  
QY 4270 TAAAGCACTGAGACCATAGTGTCCATGCTCCGATGCAAGGAGCAATGAGGCTGCTTA 4329  
Db 3914 TGTGTGCTTCCGCTCTGAGAGCTGTGTGACATTTGAAGGCAATGAGGCTGCTTA 3973  
QY 4330 ATGCGCTGTGTAAGAGTATACGCTCATCTTCAATGATGATGATGATGATGATG 4389  
Db 3974 ATGCGCTGTGTGGGCGCATCCGCTCATATGAAAGTCTCTCTCTGCTCATCTTCT 4033  
QY 4390 GGGCTAATTTTGGCATTAATGGGTGTAAGCTTTTGTCTGGAATAATATTTAAGTCGAGG 4449  
Db 4034 GGTCTATCTTCAGCATATGAGGCGTGAACCTTGTGCGGGAAGTTTGGAGGTGCATCA 4093

QY 4450 ACATGA-----ATGCGAAGAGCTCAGCGACAGATCATACCAATGCGATGCTGGC 4503  
Db 4094 ACCAGACAGAGGAGACTTTCCTTTGAATACCATGTGAAACAAGAGCCAGTGTG 4153  
QY 4504 AGAGCGAAGACTAC-----GTGGGTAAATTCAGCAATGAAATTTGATCATG 4551  
Db 4154 AGTCTTGAACCTGACCGGAGAAATTTGATGTGACCAAGGTGAAGTCAACTTGAACAG 4213  
QY 4552 TAGGTAAAGCGTATTTGTGCTTTCCTTTCAGATGAGCACTTCAAGGCTGATCAATCA 4611  
Db 4214 TGGGGCGGGTACCTGCGCTTCTGCAAGTGGCAACATTTAAGCTGATGACATTA 4273  
QY 4612 TGAAGATGTATGATTCAGAGAGTGGAGCAAGCAACCAATGTTGTAAGCAATCT 4671  
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QY 4672 ACATGATTTATATTTGATTTCTTCAATATTTGATTTGATTTTCACTCAATCTGT 4731  
Db 4334 ACATGATCATCTATTTTGTATTTTCAATTTTCACTTTTGGGCTTTTCAACCTGACTCT 4393  
QY 4732 TCATTGGTGTATCTTGTATATTTTATGACAAAGAAAGAAAGAGAGTGAATTAAG 4791  
Db 4394 TTATTTGGTGTATCTTGTACAACTTCAACCAAGAAAGAAAGTTAAGGCGCGCAG--G 4450  
QY 4792 AAATGTCATGACAGAGATCAGAAAGTAACTATTAAGTATGAAAAAGATGGGCTGA 4851  
Db 4451 ACATTTTATGACAGAGAGCAAGAAAGTAACTAATTAAGTATGAAAGAGTGGGCTCA 4510  
QY 4852 AAAAACAATTAAGGCAATTCACAGAGCCAGGTGGCAGCAACAGCAATAGCTTTGAAA 4911  
Db 4511 AGAAGCCCAAGAGCCATTCACAGGCGCCCTGGAACAAGATACAGGCTTCATATTCAGCA 4570  
QY 4912 TAGTAAAGGATTAAGAAATTCATATATATATATATATATATATATATATATAT 4971  
Db 4571 TTGTGACCAAGAGGCTTTTACAGTCAACATCATGTTCTGATCTGTTGAATATAGGGA 4630  
QY 4972 CCATGACCTGATGATTAAGATGATGAGTGGAGCAGTATTAAGCGGCTCTAGACTATCA 5031  
Db 4631 CCAATGATGTGAGACAGATBACCAAGTCTGAAAGAAATCAACATCTTGGCCAGATCA 4690  
QY 5032 ATGCAATATTCAGTATATTTTCAAGTCCGATGCTATTAATAATATTCGCTTACAT 5091  
Db 4691 AACTGCTTTTGTGGCCATCTTCAAGGCGAGTATGTCAAGTGGCTGCGCCGCC 4750  
QY 5092 ATCACTATTTATGAGCCATGAAATTTATGATGATGATGATGATGATGATGATG 5151  
Db 4751 ACTACTTCTTCAACAAGCTGGAATATCTTGAATGATGATGATGATGATGATG 4810  
QY 5152 TAGGCTGTATAGGATATTAATGAGAGTACTTGTGCGCGGCGCTGCGAG 5211  
Db 4811 TGGGACATGTCTCTCGGACATCAACAGAAATCTTCTCCCGAGCGCTTTCGAG 4870  
QY 5212 TGTGTGCTGTGGCAAGTGGGCGGTGTCTTCACTGATGTAAGGAGCAAGGCGCATTC 5271  
Db 4871 TCATCCGCTGGCCGAAATAGGCGGACATCTCAGACTATTCGAGGGGCAAGGAGATCC 4930  
QY 5272 GGAACATGCTTTTGGCGTGGCCATGTGCGTGGCGGCGCTTCAATCTGCTGCTGC 5331  
Db 4931 GCACGCTGCTTGTGCTTCAATGATGTCCCTGCTGCTTCAACATCGGCGTGCCTGC 4990  
QY 5332 TGTTCCTGTGATGATATCTTGGCAATTTGCGCATGTGCTTCAATGACGGAAG 5391  
Db 4991 TCTTCTGCTGATGATATCTTCACTCACTTGTGAGTGGCAACTTGCCTTATGCAAGT 5050  
QY 5392 AGAAGAGCGCATTAAGACGCTTCAACATTCAGAGCTTTGGCAGAGCATGATCTGCG 5451  
Db 5051 GGGAGGCGTGGATGAGAGACATGTTCAACTTCAGACCTTGGCAACAGCATGTGCTGCC 5110  
QY 5452 TCTTTCAATGTGACAGTCAAGCGGCTGGAGTGTGATCTGACGCCATTAATGAAG 5511  
Db 5111 TCTTTCAGATCAACAGTGGCGCGCTGGAGTGTGCTTCAAGGCCCATCTCTCAACACTG 5170  
QY 5512 AAGCATGGA-----TCACCCGACAGCGACCAAGAGTATCCGGGCAATGTGTGTT 5562

Db	5171	GGCGCCCTTACTGGAGACCCCACTTGGCCAAACAGAAATGGCTCTCGGGGGGACCTGGCGGGA	5230
QY	5563	CAGGCAACGTTGGAAATAACGTTTCTCCTCTCATACCTAGTAAAGCTTTTGTAGTTTA	5622
Db	5231	GCCGAGCCGCGGGGATCCTCTTCTTTCACACCTTCATCATCATATCTCTCTCTCATCGGG	5230
QY	5623	TTATATGTACATTGTGCTGCTCATTTCTCGAGACTATATGTCAGAGCCAGGAGACGTGCAAG	5682
Db	5291	TCAACATGTATATTGCCATCATCTCTGGAGAACTTCAGCGTGGCCACGAGAGAGACACCG	5350
QY	5683	AGGCTTACCCGACGACGACTACGACATGTACTATAGATCTGCGACATTCGATCCGG	5742
Db	5351	AGCCCTGAGAGGAGACGACTTCGATATGTTCTATAGATCTGGGAGAAATTTGACCCAG	5410
QY	5743	AGGCAACCCAGTACATACGCTATGATACAGCTGTCGGAATTCCTGGACGTATCGAGCCCC	5802
Db	5411	AGGCACTCACTTTATTGATGATTTCGCTCTGCTGACTTTGGCCAGCCCTCTGTCTAGC	5470
QY	5803	CGCTGCAGATCCACAAACCGAAACAGTACAAAGATCATATCGATGACATAACCATCTGTG	5862
Db	5471	CATCTCGATGCGCAAGCCCAACAGATAAAGCTCATCAACATGGACCTGGCCATGTGGA	5530
QY	5863	GCGGTACCTCATGTACTGCGGTGACATCTCTGACGCCCTTAACGAAAGACTTCTTTGGC	5922
Db	5531	GTTGGGAGCCGATCCATGTGATGACATCTCTCTTTCCTTCAACCAAAGGGTCTCGGGGG	5590
QY	5923	GGAAAGGCAATCCCAATAGAGAGACGGGTGAGATTGGAG-----ATAGCGGCCCCC	5976
Db	5591	AGTCTGGGGAATGAGACGCCCTCTGAAGATCCAGATGAGAGAAAGTTCATGGCAAGCAAC	5655
QY	5977	CGGATACGGAAGGCTACGAGGCCGCTCTCATCAACGCTGTGGCGCTGACGCTGAGAGTACT	6036
Db	5651	CATCCAAGATCTCTTAAGAGCCCAATCAACACCACTCTCGGCGCAAGACCAAGAGGTGT	5710
QY	6037	GCGCCCGGCTAATCCAGACAGCCCTGCGGAAGAAAGCAAGGCGCGGCGC	6083
Db	5711	CGGCATGTTATCCAGAGAGCTTCCGAGGCAACCTCTCTGCAACGC	5757

RESULT 11  
 US-10-852-840-1  
 ; Sequence 1, Application US/10852840  
 ; Publication No. US2004024257A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ken Stokes  
 ; Jos e Morissette  
 ; TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC  
 ; SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATY  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Woodcock Washburn Kurtz Mackiewicz and Norris  
 ; STREET: One Liberty Place - 46th Floor  
 ; CITY: Philadelphia  
 ; STATE: PA  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19103  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Wordperfect 6.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/852,840  
 ; FILING DATE: 26-May-2004  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/682,433  
 ; FILING DATE: 17-JUL-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Paul K. Legaard  
 ; REGISTRATION NUMBER: 38,534  
 ; REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586

Query	Match	14.4%	Score 940.2	DB 18	Length 6048
Best Local Similarity	55.4%	Pred. No. 1.0e-250			
Matches 2052	Conservative	0	Mismatches 1583	Indels 72	Gaps 9
TELECOMMUNICATION INFORMATION: TELEPHONE: (215) 568-3100 TELEFAX: (215) 568-3439 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 6048 bases type: nucleic acid STRANDEDNESS: double TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-852-840-1					
QY	2413	TTGTGGGACCTGTGTGGGTTTGGTTTGAATTTTCAGAGTGGAGTATCGCTCATGCTCTTCG	2472		
DB	2087	TTCTGGAGGTGTGCTCCGCTGTGATGTTCATCAAGCAGGAGTGAAGTTGGTGTATGG	2146		
QY	2473	ATCCCTTCGTGAGCTCTTCATCAACGCTGTGCATTTGTGTCAACACGATGTTCCAGCA	2532		
DB	2147	ACCGTTTACCTGACCTCACCATCACTATGTGCATCTGACTCAACACACTCTTCATGGCGC	2206		
QY	2533	TGATTCACCAAGATATGAACAAGAGATGGAACCGCGCTCAAGAGTGGACAACTTCT	2592		
DB	2207	TGAGGACCTACAAATGAAAGTAAATTCAGAGAGATGTGCAAGTGGAAACTGTCT	2266		
QY	2593	TCACCGCACCTTGGCCATGAGGCGCACATGAGCTAATGGCCATGAGCCCAAGTACT	2652		
DB	2267	TCACAGGAGTTTTCACAGCAGAGATGACTTCAAGATCATGGCCCTGACCCCTACTACT	2326		
QY	2653	ATTTCAGAGAGGCTGGAAACATCTTGCATCTTATTCGTGCGCTTATCGTATTTGAGAC	2712		
DB	2327	ACTTCACCAAGGGCTGGAAACATCTTGCACAGCAATCTGCATCTTACCTCAATGAGAC	2386		
QY	2713	TGGACATCGAGGGGTGTCCAGGGGTGTCTCCGATATGCGTCTCTTTCGATTTGCTGCGTAT	2772		
DB	2387	TGGGCTGTCCCCGATGAGCACTTGTGTGGTGTGCGCTCTTTCGCGTGTGGGGTCT	2446		
QY	2773	TCAAATGGGCCAAGTCTTGGGCCACACTTAACTTACTCATTTGCATTTGGAATGGGACGCCA	2832		
DB	2447	TCAGCTGGCCAAATCAATGGGCCACCTGGAACAACATCAATCAATGAGTGGGAACTCAG	2506		
QY	2833	TGGGCGCTTTGGGTAATCTGACATTTGTAACCTTGACATATCATCTTTCGCGGGA	2892		
DB	2507	TGGGGGCACTGGGGAACCTGACACTGTGTCTAGCCATCATCTGTCTTCTTGTCTGTGG	2566		
QY	2893	TGGGATGCAACTGTTCGGAAGAATTAATCAATGATCAAGAGACCGCTTTCGGATGGCG	2952		
DB	2567	TGGGCAATGACCTCTTGGCAAGAACTACCTGGAGCTGAGGAGCAGCAGACTCA--GGCC	2622		
QY	2953	ACCTGGCGCGTGGAACTTACCGACATTTAGCAAGCTTCATGATGTGTTCGGGGTGC	3012		
DB	2624	TGCTGCTCTGCTGACATGATGACATCTTTCATGCTTCTTAATCATCTTCCGATCC	2688		
QY	3013	TCTCGGAGATGATCGAGTCAATGTGGGACTGATGAT--GGGCGATGTCTGT	3068		
DB	2684	TTCTGTGAGAGATGTGATGAGACATGTGGGACTGATGAGAGTGTGGGGGACATCATAT	2743		
QY	3070	GCATTCCTTTCTTCTGGCCACCGTTGTCAATGGGCAATCTTGTGTACTTAACTTTTCT	3129		
DB	2744	GCTGCTGTGTCTTCTGTGTGTATGTGCATTTGGCAACTGTGTGTGTCTGTGATCTCTTCC	2803		
QY	3130	TAGCTTGCTTTTGCCAAATTTTGGCTCATCTAGCTTATCAGCGCCGACTCCGATTAAG	3188		
DB	2804	TGGCTTGTCTCTAGCTCTTTCAGTGTGAGCAACCTTCACGCCCTGTATGAGGACAG	2866		
QY	3190	ATACGAATAAATAGCCGAGGCTTCAATGCAATTTGGCCGATTTAAAGTTGGGTTAAGC	3248		
DB	2864	AGATGAACAACTCCAGCTGGCCCTGGGCCCATTCAGAGGGGCGCTGGCTTTGTCAAGC	2922		
QY	3250	GTAATATTGCTGATTTGTTCAAGTTAATAGCTAACAAATTGACAAATTAAGTATGATC	3308		



Db 2924 GGACCACTGGGATTTCTGTGTGTCCTCGGCGCACCGGCC-----TC 2968  
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Db 2969 AGAAGCCCGCAGCCCTTCCCGCCCGCAGGCGCAGCTCCAGCTGCAATCCACCCCTTACT 3028  
Qy 3370 AGCAATGAGATGGGCGCAGACGAGATCTCGCGAGCGCTCATCAAGAAAGGGGATCA 3429  
Db 3029 CCCCCCAACCCCGAGAGGAGGAGGCTCCACCCCGAGAGAAACACAGTTTGAAG 3088  
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Db 3134 TGTGTGTCCATCGCTGTGGCCGAGTCAGACACAGATGACCAAGAAAGGATGAGAGA 3193  
Qy 3550 ACTCAATTAACCAACCAACATAGACTGGAACAGACTAAACATAGAGTTTGTCT 3609  
Db 3194 ACAGCTGGGACGAGAGAGAGTCACAGACAGACAGAAATCCAGCTGTGTCCGCT 3253  
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Qy 3670 AGACGAGAGCCACAAAGGCGACCGCGAGAGTGAAGGCGGAGAAAGCGCGCA 3729  
Db 3314 AGGCGGAGGCGAGTGCATCTCAGGCGGACTGCGCGGACAGATGAAACCGGACCCGAG 3373  
Qy 3730 GCAAGAGGATTTAGTCTCGACAGAGAACTGACAGAGAGGCGAAATGCGAGAGGGCC 3789  
Db 3374 CCCCAGGTGCGGTGAGACCCGAGAGGACAGTTGTCTCGAGGCGACGACACAGCATGA 3433  
Qy 3790 CGCTGACGAGTATATCTTATTCATGACACAGAGATATCTCGATATATTCAG 3849  
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Qy 4330 ATGGCTGTGTCAAGCTATACGTCATCTTCAATGTGCTATGTGTGTATATTTT 4389

Db 3974 ATGCCCTGTGTGGGCGCATCCCTGTCAATGAAAGTCTCTCTGCTGCTCATCTTCT 4033  
Qy 4390 GCGTAAATTTTGGCAATATGGGTGTACAGCTTTTGTGTGAAAAATTTTAAGTCGAG 4449  
Db 4034 GGTCTACTTTCAGATCATGGGCGTGAACCTTTTGGGGGAAATTTTGGGAGTGCATCA 4093  
Qy 4450 ACATGA-----ATGGACGAAAGCTCAGCCAGAGATCATCAAAATGCAATGCTGCG 4503  
Db 4094 ACCAGACAGAGGAGACTTGTCTTTGAATCAACATGTGTAAACAAAGACAGCTGTG 4153  
Qy 4504 AGACGAGAACTAC-----GTGGTGAATTCAGCAATGAATTTGCATCATG 4551  
Db 4154 AGTCTTGAATTTACCGGAGAAATTTGATGACCAAGGTGAAGTCAACTTTGACAAAG 4213  
Qy 4552 TAGGTAAAGGTATGTGCTTTTCCAGAGTGGCACTTCAAGGCTGTGATCAATCA 4611  
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Qy 4612 TGAAGATGTATGATTTCAAGAGGTGACAGCAACCAATTCGTGAAGCAACATCT 4671  
Db 4274 TGTATGAGCTGTGACTCAGGGGATGTGAAGAGAGCTCAGTGGAAATACACTCT 4333  
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Qy 4732 TCATTGTGTATATGATTAATTTTAATGACAAAAAGCAAGGTGATCATTAAG 4791  
Db 4394 TTATGTGTGTATGATGACAACTTCAACCAAGAAAGAAATTTAGGGGCGCAG--G 4450  
Qy 4792 AATGTGTGACGAAAGATGAGAAAGTACTTAATGTGATGAAAGATGGGCTCTA 4851  
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Qy 4852 AAAACCATTTAAAGCATTCAGAACCAAGGTGCGCACCAAGCAATAGCTTTGAAA 4911  
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Qy 4912 TAGTAAACGATTAAGAAATTTGATTAATCATATGTTATTTGATGTGAAATGTTCA 4971  
Db 4571 TTGTGACCAAGAGGCTTTGACCTCACATCATGTTTGTGATCTGCTGAAATGTGGA 4630  
Qy 4972 CCATGACCTCGATCTGATGAGTGTGAGCGTGCAGACGTATTAAGCGGCTCTAGACTATCA 5031  
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Db 4751 ACTACTTCTTCAACCAAGCGTGAATTTCTTGAATTTGATGATGATGATGATGATGATG 4810  
Qy 5152 TAGGTCTTGTACTTGAAGATTTATGAGAAAGTACTTGTGTGCGCGACCTGTCCGAG 5211  
Db 4811 TGGGCACTGTGCTCTCGACATCAATCCAGAAAGTACTTCTTCCCGACGCTTCCGAG 4870  
Qy 5212 TGTGTGCGTGTGCGAAAGTGGGCGGTGTCTTGTGAGTGTGAGAGGACCAAGGCAATTC 5271  
Db 4871 TCAATCCGCTGTGCGCAATGAGCGCATCTTCAAGCTGATTCAGAGGCGCCAGAGGATCC 4930  
Qy 5272 GGAACGTCTTGTGCGTGTGCGCAATGCTGTGCGGCGCTGTGCAACATCTGCTGTGC 5331  
Db 4931 GCAAGCTGTCTTGTGCGCTGTGATGATGCTGTGCGCTGTGCTGTGCAACATGCGGCTGTGC 4990  
Qy 5332 TGTGTGCGTGTGATGATCTTGTGCGATTTTGTGCGAGTGTGCTTGTGATGACGTGAAG 5391  
Db 4991 TCTTCTGTGATGATGATGATCTTGTGCGATTTTGTGCGAGTGTGCTTGTGATGATGAT 5050  
Qy 5392 AGAAGCGGCAATTAAGAGCTTCAACATTTCAAGACTTTGCGACAGAGATGCTGCG 5451  
Db 5051 GGAAGGCTGTGCGATGAGACATGTTCACTTCCAGACCTTGTGCGCAAGACATGCTGTGCC 5110

Qy	5452	TCCTTTCAGATCTCAGACGTCACCCGGTGGAGTGGTACTGAGCGCCATTATTCATATGAG	5511
Db	5111	TCCTTCAGATCAACACGTCGGCCGGCTGGATGGCTCCTCAAGCCCACTCTCAACACTG	5170
Qy	5512	AAGCATGCGA-----TCACCCGACAGCGCAAAAGGCTATTCGGGGCAATTGTGGT	5562
Db	5171	GAGCGCCCTTACTGGGACCCCACTCGCCCAACAGCAATGGCTCTCGGGGGGACCTGCGGGGA	5230
Qy	5563	CAGGACCGGTGGAAATAAGTTTCTCCCTCATACCTAGTAACTATTAAGCTTTTGGATGTTA	5622
Db	5231	GCCACGCGTGGGCACTCTCTTCTTCACCACTCATATCATCATCTCTCTCTCATCGTGG	5290
Qy	5623	TTAATATGTACATTGCTGTGCTCATCTTCGAGAACTATAGTCAGAGCCACCGAGACGTCGAA	5682
Db	5291	TCACATGTATCATTTGCCATCATCTCGAGAACTTCAGCGTGGCCACGAGGAGACACCG	5356
Qy	5683	AGGGCTTACCGACGACGACTACGACATGTACTATGAGATCTGGCAGCAATTTCGATCCGG	5742
Db	5351	AGCCCTGAGTGAAGAGACGACTTCGATATGTTCTATGAAATCTGGGAGAAATTTGACCCAG	5410
Qy	5743	AGGGACCCAGTATACATACGCTATATATGAGCTGTCCGAAATCTTGAGCGTATCGAGCCCC	5802
Db	5411	AGGCACTCAAGTTTATTTAGTATTTCCGATTCGTCTGTCTGACTTTGGCCGACGCCCTGTCTAGC	5470
Qy	5803	CGCTGCAGATCCACAAACCGAACAAAGTACAAAGATCATATCGATGACATTCGATCTGTG	5862
Db	5471	CATCTCGTATCGCCAAAGCCCAACGAGTAAGCTCATCAACATGGACTTGGCCCATGTGGA	5530
Qy	5863	GGCGTACCTCATGTACTGCTGGCTGCACATCTCTGACGCCCTTACGAAACACTTCTTGGGC	5922
Db	5531	GTGGGGACCGCATCCATTGCATGTAGCACTTCTTTGGCTTTACCCAAAGGGTCTGGGGGG	5590
Qy	5923	GGAAGGCAATCCCATATAGAGAGACGGGTGAGATTGTGAG-----ATAGCGGCCCC	5976
Db	5591	AGCTCGGGGAATGGAACGCCCTCTGAAGATCTCAGATGAGAGAGAAAGTCAATGGCAGCAACC	5656
Qy	5977	CGGATACGGAAGGCTACGAGCCCGCTTCATCAACGCTGTGGCGTCAAGCGTGAAGTACT	6038
Db	5651	CATCCAAAGATCTCTTACGAGCCCACTCACCACTCCGGCGCAAGACAAAGAGGTGT	5710
Qy	6037	GGCGCCGGCTAATCCAGACCGCTTGGGCAAAAGCAAAAGCCCGCGCGC	6083
Db	5711	CGGCGATGTTATCCAGAGCGCTTCCGACAGCACTCTCTGCAACGC	5757

Query Match	Similarity	14.4%	Score 939.4	DB 9	Length 6048
Best Local	Similarity	5.7%	Pred. No. 3,1e-250		
Matches 2064	Conservative	0	Mismatches 1571	Indels 72	Gaps 11
Qy	2413	TGNGGACGTGTGTGGGTTTGGTTGAATTCAGAGTGGGTATCGCTACGTCTTTCG	24772		
Db	2087	TCTGGAGATGTGTCCCTGTGTGATGTCCATTCAGACGAGGAGTGAATGTGTGTATCG	2146		
Qy	2473	ATCCCTTGTGTGAGCTCTTATCACGCTGTGTGATGTGTGTACACAGATTTTACATGGCA	2532		
Db	2147	ACCGTTTACTGACCTTACCATCACTATGTGTGATGTGTATCAACACTCTTACATGGCGC	2206		
Qy	2533	TGATTCACACAGATATGACAGAGGATGTGAGACGCGTCTCAAGATGGCAACTATTTCT	2592		
Db	2207	TGAGGACTACACATATGACAGTGAATTCAGAGAGATGTGTGAGTGTGAAACCTGGTCT	2286		
Qy	2593	TCACCGCACCTTTGCCATCGAGGCCACATGAAAGTAAATGGCCATGAGCCCAAGTACT	2652		
Db	2267	TCAACAGGGAATTTTACAGACAGATGTACTTAAAGATCATTTGCCCTCGACCCCTTACT	2326		
Qy	2653	ATTTCACAGAGGCTGTGAACATCTTGCATTTCAATTATGTGTGCTTATCGTATTTGAAC	2712		
Db	2327	ACTTTCACACAGGCTGTGAACATCTTTCACACAGCATCATCGTATCTTAAAGCTCATGAGC	2386		
Qy	2713	TGGGACTCAGAGGTGTCCAGGCTGTGTCCGATATGCTCTTTCGATGTGTGTGTAT	2772		
Db	2387	TGGGCTGTGTCCCGATGACGACATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2446		
Qy	2773	TCAAACTGTCCCAATCTTGTGGCCCACTTAAATTTACTCATTTGCATTTAGGAGCGACA	2832		
Db	2447	TCAAGCTGTCCCAATCATGTGGCCCACTTGAACACACTCATTCAGATCATCGGGAATCTAG	2506		
Qy	2833	TGGGCGCTTGGGTATCTGACATTTGTACTTTGCATTTATCATCTTATCTTTGGGTGA	2892		
Db	2507	TGGGGGACCTGGGGAACTGTGACCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2566		
Qy	2893	TGGGAATGTCACTGTGTGGAAAGAAATATATATATATATCAAGAACCGTTTCCGATGGCG	2952		
Db	2567	TGGGACATGACCTTTTGGCAAGACTATCTGGAGCTGTAGGAGACGAGACTCA---GGCC	2623		
Qy	2953	ACCTGCGCGCTGTGAACCTTCAACCACTTATATGACACAGCTTCATGATCGTGTCCGGTGC	3012		
Db	2624	TGCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2683		
Qy	3013	TCTGCGGAGAAATGATGTGATGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3069		
Db	2684	TCTGTGTGAGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGATGTGAT	2743		
Qy	3070	GCATTTCCCTTCTTTTGTGCCACCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3129		
Db	2744	GCCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2803		
Qy	3130	TAGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3189		
Db	2804	TGGCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2863		
Qy	3190	ATAAGAAATAAATATGACGAGCGCTTCAATGTGAATGTGCGCATTTAAAGTTGGTTAAG	3249		
Db	2864	AGATGAACACCTCCAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2923		
Qy	3250	GTAAATATTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3309		
Db	2924	GGACCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	2978		
Qy	3310	AACCATCAGGTGAAGAGACCAACCATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3369		
Db	2979	AGCCCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3038		
Qy	3370	ACGAATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3429		
Db	3039	CCGAGAGACGAGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3098		
Qy	3430	AGGAGCAGACGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	3489		

Db 3099 ACCAGGCGAGGCGACCCCCGGGG---ATCCAGAGCCCGTGTGTGGCCATGCTGTGGC 3155  
 Qy 3490 ACATTAAGAAACAACAAGCCGGAAGAAATTCAAATATCTAAATAACGAACGATGATTGGCA 3549  
 Db 3156 CGAGTCAGACACAGATGACCAAGAAAGAGATGAGAGAACAGCTGGGACCGAGAGAGGA 3215  
 Qy 3550 ACTCAATTAACCAACAAGACATATAGCTGGAAACAGAGCTAAACCATAGAGTTGTCT 3609  
 Db 3216 GTCCAGCAAGCAGAGAAATCCAGCCTG--TGTCCGCTGGCCAGAGGCCCTCCGAT 3273  
 Qy 3610 TACAGACGACGACACTGCGACATTAATCATATGTAGCCATTAAGATCAGCAATTC 3669  
 Db 3274 TCCAGACCTGAGGCGAGGTGCA-----GCGACTGCTCTCTCG 3313  
 Qy 3670 AGGACGAGAGCCACAAGGCGACGCCGAGACGATGAGGGCGAGAGAAAGCCGACGCCA 3729  
 Db 3314 AGGCGGAGGCGCAGTCATCTCAGGCCGACTGGCGGACGATGGAAGCGGAACCCCAAG 3373  
 Qy 3730 GCAAGAGATTTAGTCTCGACGAGAACTGGAACGAGAGGGCGAATCCGAGAGGGCC 3789  
 Db 3374 CCCAGGGTGGCGGTAGACCCCAAGAGACATTTGCTCCGAGGGCAGCACAGACATGA 3433  
 Qy 3790 CGCTGACGATGATATTCATTATTATGACACAGACGAGATATATCTGATGATATTCAG 3849  
 Db 3434 CCAACAACGCTAGCTCTCGAGACAGATCCCTGACCTGGCCAGATGTCAGAGACCCAG 3493  
 Qy 3850 CTGATTTGTCGCCCGCATTCGTAATAAGAAATTTCCGATCTTAGCCGATGACATGACT 3909  
 Db 3494 AGGATGCTTCACTGAAGGCTGTGTCCGCGCTGTCCCTGTGTGGGAGCACACAC 3553  
 Qy 3910 CGCCGTTCTGGCAGAGATGGGGCAATTTACACTGAAATCTTTCAATTAATTGAAATA 3969  
 Db 3554 AGGCCCCAGGGAAGGTCTGGTGGCGGTGGCCGACACCTGTCACACATCTGGAGCA 3613  
 Qy 3970 AATATTTGAAACACCTGTTATCACTATGATTTATGATAGTAGCTTAGCTTTGGCATTAG 4029  
 Db 3614 GCTGTTGAGACATTCATCATCTTCAATCTACTCAGACGTGAGAGCGCTGGCTTCG 3673  
 Qy 4030 AAGATGACATCTGGCACAAAGACCATATGACAGATATTTTATATAATATGACAGAA 4089  
 Db 3674 AGGACATCTACTAGAGAGGAGGAGACATCATAGTTCTGTGTAGATATGCCAGAA 3733  
 Qy 4090 TATTTACGATATATTTCTTTGGAATGTTATCAAGTGTGTGGCGCTCGCTTCAAG 4149  
 Db 3734 TGTTCACATATGTCCTTGTGTGAGATGCTGCTCAAGTGGTGGCTTACAGCTTCAAG 3793  
 Qy 4150 TGTACTTACCAACGCGTGTGTGCTGATTTGCTGATTTGTCATGATGCTTATCA 4209  
 Db 3794 AGTACTTACCAATGCTGTGTGTGCTGCTGCTCTCATGCTGATGCTTCTTGTGCTA 3853  
 Qy 4210 ACTTGTGCTTCACTTGTGTGAGCTGTGTGATTAAGCTTCAAGCTTACAGTACGAACT 4269  
 Db 3854 GCTGTGTGGCAACACCTGGGCTTTGGCGAGATGGGCCCATCAAGTCACTGGGAGCG 3913  
 Qy 4270 TAAAGCACTGAGACCTAGCTGTGCTGCTGCTGATGAGGGCATGAGGCTGCTGTTA 4329  
 Db 3914 TGCCTGCACTGCTGCTCTGAGAGCTGTGCTGCTGCTGCTGAGGGCATGAGGGTGGTCA 3973  
 Qy 4330 ATGGCTGTGTCAGAGCTATACCGTCTCATCTTCAATGCTGATTTGGTGTGCTCAATATTT 4389  
 Db 3974 ATGGCTGTGTCAGAGCTATACCGTCTCATCTTCAATGCTGATTTGGTGTGCTCAATATTT 4033  
 Qy 4390 GGTCAATTTTGGCAATATGAGTGTGACGCTTTTGTGCGAAATATTTTAAAGTCCGAG 4449  
 Db 4034 GGTCTATCTTCAAGATCATGAGCGTGAACCTCTTTGGCGGAGAGTTTGGAGGTGCATCA 4093  
 Qy 4450 ACATCA-----ATGGACGAACTCAGACGAGATCATACCAATGCGAATGCTGCG 4503  
 Db 4094 ACCGACGAGGAGGAGACTTGTCTTGAACCTACCATGCTGACAAAGAGCCAGTGTG 4153  
 Qy 4504 AGAGGAGAACTACAC-----GTGGGTGAATTCAGCATGGAATTTGATCATG 4551

Db 4154 AGTCTTGAACCTTACCGGAGAAATTTGATCGGACCAAGGTGAAGTCACTTGAACAAG 4213  
 Qy 4552 TAGGTAAAGCGTATTTGTGCTTTTTCAGATGGCCACTTCAAGGCTGATGACAAATCA 4611  
 Db 4214 TGGGGCGGGGATCTTGCCCTTCTGCAAGTGGCAACATTTAAAGCTGATGACATTA 4273  
 Qy 4612 TGAACGATGATGATTCAGAGAGGTGGAACAAGCAACAAATTTGTAAGCAATCT 4671  
 Db 4274 TGTATGACGCTGTGACTCAGGGGGTATGAAGACAGCTTCAAGTGGAAATCAACCTCT 4333  
 Qy 4672 ACATGATTTATTTATTCGATTTCTCATCATATTTGATGATCTTTTCACTCACTGT 4731  
 Db 4334 ACATGATCATGATTTTGTATTTTTCATCATCTTTGGTCTTTTCAACCTGAACTCT 4393  
 Qy 4732 TCATTGTGTATTCATTTGATATTTTAAATGACAAAGAAAGCAAGGTGATCATAG 4791  
 Db 4394 TTATTGTGTATCATTTGACAACTTCAACCAAGAAAGAAAGTTAGGGGGCCAG---G 4450  
 Qy 4792 AAATGTCATGACGAAATGACAAAGTAATACTAATGCTATGAAAAAGATGGGCTGTA 4851  
 Db 4451 ACATCTTATGACAGAGAGGAGAAAGTACTAATGCAATGCAATGAAAGAGCTGGCTCA 4510  
 Qy 4852 AAAAACCAATTAAGCCATTTCCAGACCAAGGTGGCGACCAAGCAATAGCTTTGAAA 4911  
 Db 4511 AGAAAGCCGAGAGGCCATCCAGCGCCCTGAAACAATACAGGGCTTCATATTGACA 4570  
 Qy 4912 TAGTAAAGGATTAAGAAATTTGATATATATATATATATATGATGCTGAAATGTTCA 4971  
 Db 4571 TTGTGACCAACAGGCTTTGACGTCACATCATATGTTCTGATCTGTTGAATATGTTGA 4630  
 Qy 4972 CCATGACCTCGATGCTTGAATGCTGTGGACACTGATTAAGCGGCTCTTACATATCA 5031  
 Db 4631 CCATGATGTGAGAGACAGATGACCAAGTCTGAGAAATCAACATCTTGGCCAGATCA 4690  
 Qy 5032 ATGCAATTTGATGATTTTTCAGTTCCGATGCTATTAATAATATTCGCTTACAT 5091  
 Db 4631 ACCTGCTTTGTGGCATCTTTCACAGGCGAGTGTATGTCAAGTGGCTGCTGCCGCC 4750  
 Qy 5092 ATCACTATTTATGAGCGATGAAATTTATTTGATGATGATGATGATGATGATGATGAT 5151  
 Db 4751 ACTACTACTTCAACCAACGCTGAAATATCTTCACTGCTGTGTGATCTCTCCATCG 4810  
 Qy 5152 TAGCTCTTGTATTAAGCATTTATTCGAAAGTACTGTGTGCGGACCCCTGCTCGAG 5211  
 Db 4811 TGGGACCTGTCTCGGACATCATCGAAAGTCTTCTCCCGACGCTCTTCAG 4870  
 Qy 5212 TGTGCGGTGTCGCAAAAGTGGCGGTGTCTTCACTGTGAAGGAGCCCAAGGCAATTC 5271  
 Db 4871 TCATCCGCTGCGCGAATGAGCCGATCTTCAAGCTGATCCGAGGGGCAAGGGGATCC 4930  
 Qy 5272 GGAACCTGCTTGGCGTGGCCATGTGCTGCGGCGCTGTCAACATCTGCTGCTGC 5331  
 Db 4931 GACGCTGCTCTTGGCCCTTCAATGATGCTGCTGCTGCTCTTCAACATCGGGCTGCTGC 4990  
 Qy 5332 TGTTCCTGTATGATTCATCTTTGCAATTTTGGCATGTGCTTCTTCAATGACAGGAG 5391  
 Db 4991 TCTTCTGCTGATGATTCATCTTCACTTGTGATGAGCACTTCTGCTTATGCAAGT 5050  
 Qy 5392 AGAAGAGCGGATTAAGAGCTTACAACTTCAAGACTTGTGGCGAGAGCATGATCTGC 5451  
 Db 5051 GGGAGGCTGGATGAGACAGATGTTCAATCTTCAAGCTTGTGGCAAGCATGCTGTGCTGC 5110  
 Qy 5452 TCTTTCAGATGACAGCTCAGCGGTGGAGTGTGTAAGTGAAGCCATTAATGAAGG 5511  
 Db 5111 TCTTCAGATCACCAGCTGCGCGGTGGAGTGTGCTCCTCAGCCCATCTCAACACG 5170  
 Qy 5512 AAGATGGA-----TCACCCGACAGGCAAGAAAGCTATTCGGGCAATTTGTGTT 5562  
 Db 5171 GGGCGGCTTACTGGAACCCCACTGTGCCCAACAGCAATGCTCTCGGGGGAGCTGGGGA 5230  
 Qy 5563 CAGGACGCTGGAATAAGTTTCTCCTCATACCTAGTATTAAGCTTTTGAATGTTA 5622  
 Db 5231 GCCAGCGGTGGGATCTCTTCTTCAACCACTACATCATATCTCTCTCATGCTGG 5290

QY	5623	TTAATATGATCAATTGCGTGTATCTTCCGGAACCTATAGCAGGCCACCGAGGACGTCGAA	5682
Db	5291	TCAACATGTACATTGTCCATCATCTCTGGAACTTCAGGTGGCCACGAGAGAGACACCG	5350
QY	5683	AGGGTCTAACCGACGACGACTACGACATGTACTATGAATCTGGCAGCAATTCGATCCGG	5742
Db	5351	AGCCCTGTAGAGGAGCAGCTTCGATATGTTCTATGAAATCTGGGAGAAATTGACCCAG	5410
QY	5743	AGGGCACCBAATACATAGCTATATGATGACGTCCGAAATTCCTGTAAGTATGGAGCCCC	5802
Db	5411	AGGCACTCAATTTATGTAGATTTGCGTCTGTCTGACTTTTGGCCAGCCCTGTCTTGAGC	5470
QY	5803	CGCTGCAGATCCACAACCCGAACAAGTACAAGATCATATATGATGACATACCACTCTGTG	5862
Db	5471	CACCTCGATGCGCAGAGCCCAACCAAGATTAACGCTTCATCAATGGACCTGGCCATGTGGA	5530
QY	5863	GCGGTACCTCATGTACTGCGTCCGACATCTCTGAGCCCTTAACGAAAGACTTCTTTGCGC	5922
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QY	5923	GGAAAGGCAATCCGATAGAGGAGACGGGTGAGATTGGTGA-----ATAGCGGGCCGC	5976
Db	5591	AGTCTGGGAGATGAGACGCCCTTGAAAGATCCAGATGAGAGAAAGTTCATGCGACCCAAC	5656
QY	5977	CGGATACGAGAGGCTACGAGGCCGCTTCATCAACGCTGTGGCGTTCAGCGTGAAGAGTACT	6036
Db	5651	CATCCAAAGATCTCTTACGAGCCCATACACACCACTCCGGCGCAAGACAGAAAGGTGT	5710
QY	6037	GCGGCCGGCTAATCCAGACGCGCTGCGGAAAGCACAABGGCCGCGGC	6083
Db	5711	CGGCAATGTTATCCAGAGAGCTTTCGACAGCACCTGTCTCAACGC	5757

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RESULT 13
US-10-914-133-3
; Sequence 3, Application US/10914133
; Publication No. US20050003445A1
; GENERAL INFORMATION:
; APPLICANT: Splawski, Igor
; APPLICANT: Keating, Mark T.
; TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
; TITLE OF INVENTION: SCNSA AND METHODS FOR DETECTING SAME
; FILE REFERENCE: 2323-168
; CURRENT APPLICATION NUMBER: US/10/914,133
; CURRENT FILING DATE: 2004-08-10
; PRIOR APPLICATION NUMBER: US 09/840,125
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/634,920
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 60/190,057
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: US 60/147,488
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 6048
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(6048)
; US-10-914-133-3

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	Query Match	Score	DB	Length
Best Local Similarity	55.7%	Pred. No. 3,1e-250		
Matches	2064	Conservative	0	Mismatches 1571; Indels 72; Gaps 11;
Oy	2413	TCGTGGACATGTTCTGCGGTTTGGTTGAAATTTCAGAGTGGGTATCGCTACTCGTTCTCG	2472	
Db	2087	TCGTGGAGATGCTGCCCCGCTGTGGAGATGTCATCAACAGAGAGTGAAGTTGGTGGTCATCG	2148	

QY	2473	ATCCCTTCGTCGAGCTCTTCATCAACGCTGGTCGATTGGTGTCACACCATGTTCCGCA	2532
Db	2147	ACCCGTTTACTGACCTCAACATCACTATGTGCACTGTACTCAACACACTCTCAATGGCGC	2206
QY	2533	TGATCAACCAAGATATGAACAAGAGATGGAAACCGGTCTCAAGATGGCACTATTCT	2592
Db	2207	TGGGCACTCAACATATACAGTAATTCAGAGAGATGTGCAAGGTGGAAACCTGTGCT	2266
QY	2593	TCACCGCAACCTTTGGCATGAGGCGCACCAATGAAGTAAATGGCCATGAGCCCAAGTACT	2652
Db	2267	TCACAGGGAATTTTCACAGCAGAGATGACTTTCAGATCATTTGCCCTCGAACCCTCACT	2326
QY	2653	ATTTCAGAGAGGCTGGAAACATCTTGACCTTCATTATCGTGCCCTATCGCTATTTGAAC	2712
Db	2327	ACTTCCAAAGGGGTGGAAACATCTTGACAGACATCATGTCATCTTAAGCTTACATGAGC	2386
QY	2713	TGGGACTCGAGGGTCCAGAGTCTGTCGCTATTTGGCGTTCCTTTCGATTTGGCTGTAT	2772
Db	2387	TGGGCTGTCCCGATAGCACTTTGTGCGGTGCGCTCTTTCGCGCTGTGCGGTCT	2446
QY	2773	TCAAACTGGCCAACTCTTGGCCGACACTTAATTACTCATTTGCATTATTTGGAGCGACA	2832
Db	2447	TCAAGTGGCCAAATCATATGGCCACCTTGAAACACTCATCAAGATCATCGGAACTCAG	2506
QY	2833	TGGGCGCTTTGGGTAATCTGACATTTGTACTTTGCATTATCATCTTTCCTTTGGCGTGA	2892
Db	2507	TGGGGGCACTGGGGAACTGACACTGTGTGTAGCAATCATCTGTTCATCTTTGCTGTGG	2566
QY	2893	TGGGAATGCAACTTTTCGGAAGAATATATCATGATCAACAAGACGCTTTCCGANTGGCG	2952
Db	2567	TGGGCAATGCACTTTTGGCAAGACTACCTCGAGCTGAGGAGCAGAGACTCA---GGCC	2623
QY	2953	ACCTGCGCGCTGGAACTTCAACGACTTTATGCAAGACTTTCATGATCTGTGTTCCGGGTGC	3012
Db	2624	TGCTGCTCTCGCTGGCAATATGGAATCTTTCATGCTTCTCTCATATCTTCCGCAATCC	2683
QY	3013	TCTGCGGAGATGGATGGAATGCAATGCGGACATGCGGACATGTAAGT---GGGCGATGTCTCGT	3069
Db	2684	TCTGTGAGATGATGAGATCGAAGCAATGTGGGACTGTGATGAGAGTGTCCGGGCACTCATAT	2743
QY	3070	GCATTTCCTTTCTTTGGCAACCGTTTGCATTCGGCAATCTTGTGTACTTAACCTTTTCT	3129
Db	2744	GCTGTGTCGTCCTTCTTCTTGTATGTGTCATTTGGCACTTTGTGTCTGTGATCTTCTTCC	2803
QY	3130	TAGCTTGTCTTTTCCAAATTTTGGCTCATCTGACTTATACAGCGCGCACTGCGGATAAG	3189
Db	2804	TGGCTTGTCTGCTAGCTCTTCTTCACTGCAACAACCTCAACGCCCTGTGATGAGACAGAG	2863
QY	3190	ATAAGAAATTAATATGCGAGGCGCTTCATCGAATTTGGCGCATTTTAAAGTTGGGTTAAG	3249
Db	2864	AGATGAACAACCTCCACTGCTGCGCCCTGCGCAATCCAGAAGGGCGCTGCGCTTGTCAAGC	2923
QY	3250	GTAATATTGCTGATTGTTTCAAGTTAATAGTAAACAATTTGACAAATTCAAATTAAGTATC	3309
Db	2924	GGACCAACTGGGATTTTTCG-----TGTGTCTTCCTCGGCAACGGGCTCAAGAACCCGC	2978
QY	3310	AACCATCAGGTGAGAGGACCAACCAAGATCAATTGATTTTGGAGCGAAGACATGTGACA	3369
Db	2979	AGCCCTTTCGCGCCAGAGGCAAGCTGTCCAGCTGATTTGCCAACCCTCACTCCCGCAAC	3038
QY	3370	ACGAATCGAGCTGGGCAACGACGAGATCTTCGCGCAACGGCTTCATCAAGAAGGGATCA	3429
Db	3039	CCGAGAGCGGAGAAAGTGTCTCCACCCGCAAGAAACACAGTTTGAAGAAAGCGAGACA	3098
QY	3430	AGAGGCAAGCGCACTGAGGTGCCATTCGGGATTCGGAATGGAATTCACGATACACGGCG	3489
Db	3099	ACCAAGGCGAGGACCCCGGG---ATCCAGAGCCGTGTGTGTGCCATTCGCTGTGGC	3155
QY	3490	ACATGAGAAACAACAACCGCAAAATTCAAATATCTTAAATTAACGCAACGATGATTTGGCA	3549
Db	3156	CGAGTCAACACAGATACCAAGAAGAGATGAGGAGAACAGCCTGGGCAACGAGAGAGA	3215
QY	3550	ACTCAATTAACCAACCAAGACATATGACTGGAAACGAGCTAAACCATATAGAGTTTGTCT	3609

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Qy 3610 TACAGCAGCAGACCTGCCAGCATTTAATCATATGTAGCCATTAAGATGACCATTTCA 3669  
Db 3274 TCCAGCCTGGAGCAGAGTGTCA-----GCCAGCTCCTCTCTG 3313  
Qy 3670 AGGACGAGAGCAGCAGAGGAGCCGCCAGATGAGAGGCGAGAGAAAGGCCACGCCA 3729  
Db 3314 AGGCGCAGAGCCAGTGCATCTCAGGCCGAGCCGAGCAGAGTGAGAACGCCAACCCACG 3373  
Qy 3730 GCAAGAGATTTAGTCTCCAGCAGAACTGACAGAGAGGCGAGATGCCAGAGAGGCC 3789  
Db 3374 CCCAGAGGTGGGGTGAAGACCCAGAGAGCAGTTGCTCCGAGGGCAGCAGACAGACAGA 3433  
Qy 3790 CGCTGACGCGTATATCTATTATTCAGCAGCAGAGATATCTCGATGAATATCCAG 3849  
Db 3434 CCAACACCGCTGAGCTCTGAGCAGATCCCTGACCTCGCCAGGATGTCAAGACCCAG 3493  
Qy 3850 CTGATGCTGCCCGATTCGATCTAATAAGAAATTTCCATGCGCGTGAACCATGACT 3909  
Db 3494 AGGACTGCTTACAGAGAGCTGTGTCCGCGCTGTCCCTGCTGTGCGGTGACACACAC 3553  
Qy 3910 CGCCGTTCTGCGCAAGAGATGGGCAATTTACGACTGAAACTTTTCAATTAATTGAATA 3969  
Db 3554 AGGCCCCAGGAGAGGTCTGTGGGGGTGGCCAGACCTGCTACCAATCGTGAGACACA 3613  
Qy 3970 AATATTTGAAACAGCTGTATCACTATGATTTTAATGATGAGTACCTTTAGCATTTAG 4029  
Db 3614 GCTGGTTCGAGACATTCATCATCTTCATGATCTCAAGAGTGAACGCTGGCCTTCG 3673  
Qy 4030 AAGATGTACATCTGCGCAAAAGACCAATCTGAGAGATTTTATATCTATATGACAGAA 4089  
Db 3674 AGGACATCTTACCTGAGAGAGCGAGAACCATCAAGTTCCTTGAAGATCCGACAGAA 3733  
Qy 4090 TATTTACGTTATATTTCTTTGAAATGTTAATCAAGTGTGGCGCTCGGCTTCAAG 4149  
Db 3734 TGTTCACATATGTCTTGCTGTGAGATGCTGCTCAATGAGGTGGCTTACGCTTCAAGA 3793  
Qy 4150 TGTATCTTCAACCAAGCGGTGTGTGTGGCTGATTTGCTGATTTGATGCTTATCA 4209  
Db 3794 AGTACTTCAACCAAGCGGTGTGTGTGGCTGATTTGCTGATTTGATGCTTATCA 3853  
Qy 4210 ACTTCGTTGCTTCACTTGTGAGAGTGTGTATTCAGCTTCAAGCTTCAAGCTATGGAAGT 4269  
Db 3854 GCCGTGTGGCCAAACCTGTGGCTTTGCGAGATGGGCCCATCAAGTCACTGGGAGGC 3913  
Qy 4270 TAAAGCACTGAGACCACTAGTGCATGCTCCGATTCAGAGGCGTGAAGGTCGTGTTA 4329  
Db 3914 TGGGTGACCTCCGTCCTCTGAGAGCTGTGTACATTTGAGGGCATGAGGGTGTGTCA 3973  
Qy 4330 ATGCGCTGTGTAACAGTATACCTTCATCTTCAATGTGCTATGTTGTCTAATATTT 4389  
Db 3974 ATGCGCTGTGAGGCGCATCCGTCATCATGAAGTCTCTCTGCTGCTCATCTTCT 4033  
Qy 4390 GGTCTAATTTTGGCATATGAGGTGTACAGCTTTTGTCTGAGAAATATTTTAAAGTCCAGG 4449  
Db 4034 GGTCTATCTTCAAGATATGAGGCGTGAACCTTTTGGCGGAAAGTTTGGAGGTGCATCA 4093  
Qy 4450 ACATGAG-----ATGGCAGAAAGCTCAGCAGAGATCATACCAATGCGAATGCGTSCG 4503  
Db 4094 ACCAGACAGAGGAGAGCTTGGCTTTGAACATACATGTGACACAGAGCCAGTGTG 4153  
Qy 4504 AGAGCGAAGACTTACAC-----GTGGGTGAATTCAGCAATGAATTTGATCATG 4551  
Db 4154 AGTCTTGAACCTTGAACCGAGAAATTTGACTGAGCCAGAGTGAAGTCACTTTGACAG 4213  
Qy 4552 TAGGTAAAGCTATCTGTGCTTTTCCAAAGTGCACCTTCAAGGCTGTGATACAAATCA 4611  
Db 4214 TGGGGGCGGGTACCTGGCTTTCTGAGGTGGCAATTTAAAGGCTGATGACATTA 4273  
Qy 4612 TGAAGATGTATGATTCAGAGAGGTGACAAGCAACCAATTCGTGAAGCAATCT 4671

Db 4274 TGTATGACGCTGTGGACTCCAGGGGATATGAAGACAGCCTCAGTGGGATACACCTCT 4333  
Qy 4672 ACATGTATTAATTTGGTATTTCTTCATCATATTTGATCTTTTTCACACTCAATCTGT 4731  
Db 4334 ACATGTATCTATTTGTCACTTTTTCATCATCTTTGGGTCTTTTTCACCTGAACTCT 4393  
Qy 4732 TCAATGGTATCATTTGATTAATTTTATGCAAAAGAAAGAGAGGATCATTTAG 4791  
Db 4394 TTAATGGTATCATTTGATTAATTTTATGCAAAAGAAAGAGGATCATTTAG 4450  
Qy 4792 AATGTTCATGACAGAAATCAGAAAAATCTAATAATGCTATGAAAAAGATGGCTCTA 4851  
Db 4451 ACATCTTCATGACAGAGAGAGAAAGATCTCAATGATCATGAAGAGCTGGCTCCA 4510  
Qy 4852 AAAAACCTTAATAAGCCTTCCAGACCAAGGTGGCCAGCAGCAATATCTTTGAAA 4911  
Db 4511 AGAAGCCCGAGAACCCATCCAGGCGCCCTGAACAGTACAGGGCTTCATATTCGCA 4570  
Qy 4912 TAGTAAACGATTAATAATGATTAATCATTTATGTTATTCATTTGCTGAACTGTCA 4971  
Db 4571 TTGTGACAGAGAGCCCTTGAAGCTCAGCATATGTTTGTATCTGCTGAATATGTGA 4630  
Qy 4972 CCATGACCTTCGATCGTTACAGATCGTCGACAGCTATTAACGCGGTCTAGACTATCA 5031  
Db 4631 CCATGATGTGAGACAGATGACCAAGTCCCTGAAGAAATCAACATCTTGGCCAAAGTCA 4690  
Qy 5032 ATGCGATTTGCTATTTTCACTTCGATTCGAATGTCTATTAATAATATTCCTTTAGAT 5091  
Db 4691 ACCGTCTTGTGGCCATCTTCAAGCGAGTCTATTTGTCACAGCTGCTCCGCGCC 4750  
Qy 5092 ATCACTATTTATGAGCAATGSAATTTATTTGATGATGATGCTATTTATTCATCT 5151  
Db 4751 ACTACTCTTCAACCAAGCTGGAATATCTTGACTTGTGATGTATCTTCTTCATCG 4810  
Qy 5152 TAGCTCTGTACTTGAAGATTTATGAGAAGTACTTGTGTCGCCAGCCTGTCCAG 5211  
Db 4811 TGGGCACTGTGCTCTCGAGACATATCCAGAAATCTTCTCCCGAGCGCTTCCGAG 4870  
Qy 5212 TGTGTGCTGTGCGAAAGTGGGCGGTGCTTTCGACTGTGTGAAGAGAGCCAGGGCATTC 5271  
Db 4871 TCATCCGCTGGCCGGAATAGGCGCATCTCAGACATGATCCAGGGGCGCAAGGGAGATCC 4930  
Qy 5272 GGAACGCTCTTGTGGCGTGGCCATGTGCGTGGCGGCGCTGTAAATCGCGCTGCG 5331  
Db 4931 GCACGCTGCTTGTGCTCCTCATGATGTCCTGCTGCTCTTCAACATCGGCGCTGCTGC 4990  
Qy 5332 TGTTCGTGTCATGTTGATCTTTGCAATTTTGGCATGTGCTTTCATGACGTGAAG 5391  
Db 4991 TCTTCTGTGATGTTTATCTATCTATCTTATGAGGCAATTTGGCTTATGCAAGT 5050  
Qy 5392 AGAAGAGGCGATTAAGAGCTTCAACTTCAAGACCTTTGGCGAGCATGATCTGCG 5451  
Db 5051 GGGAGGCTGGCATGAGACATGTTCAACTTCAGACCTTGCAGCAAGCATGTGTCGCC 5110  
Qy 5452 TCTTCAGATGTGACGTCGAGCGGTTGGATGAGTGAACGGAAGCCATTAATGAAG 5511  
Db 5111 TCTTCAGATGACCAAGTGGCGGCTGGAGTGGCTCTTCAGCCCAATCTTCAACATG 5170  
Qy 5512 AAGCATGCGA-----TCACCCGACAGCGCAAAAGGCTATCCGCGCAATTTGTT 5562  
Db 5171 GGGCGGCTTACTGAGACCCCACTGTGCCAAACAGCAATGTGCTCGGGGGAGCTGGGGA 5230  
Qy 5563 CAGGACCGTTGAAATACGTTTCTCTCTCATACCTAATTAAGCTTTTGAATGTTA 5622  
Db 5231 GCCCAGCGGTGGGATCTCTCTTTCACACCTTACATCATCTCTCTCTCATGCGG 5290  
Qy 5623 TTAATATGTCATGCTGTGATCTGAGAACTATATAGCAGGACCGAGAGAGTGAAG 5682  
Db 5291 TCAACATGTATATGTCATATCTGAGAACTTCAAGCTTCAAGGAGAGAGACCG 5350  
Qy 5683 AGGCTTAACGAGCAGACCTACAGATGATGATGATGATGATGATGATGATGATGATGAT 5742  
Db 5351 AGCCCTGAGTGAAGAGAGCTTGTGATGTTTATGATGATGATGATGATGATGATGATGAT 5410





QY	3370	ACGAATCTGAGTGTGGCCACGACGAGATCTCTGCCGACGGCTCATCAAGAGGGGATCA	3422
Db	3189	CCGAGACGAGGAAGTGCTCTCCACCCTCGAAGAAACAAGTTGAGGAAGCGAGCA	3244
QY	3430	AGAGACGACGCACTGGAGGTGGCCATCGGGGATCGATGGAATTCAAGATPACCGCG	3485
Db	3249	ACCAAGCCAGGGCACCCCGGGG---ATCCAGAGCCCGTGTGTGCCCATCGCTGTGGC	3305
QY	3490	ACATGAACAAACAAGCCGAAAGAAATCCAAATATCTAAATPACGCAACGATGATTGGCA	3544
Db	3306	CGAGTCAGACAAGATGACCAAGAAAGAGATGAGAAACAGCTGGGCAACGAGAAAGA	3365
QY	3550	ACTCAATTAAACCAACCAACAATAGACTGSAACAGACTTAAACATATAGAGGTTGTCTT	3605
Db	3386	GTCCAGCAAGACGACGAGAAATCCAGCCTG--TGTCGGCTGGCCCAAGGCCCTCCGAT	3422
QY	3610	TACAGGACGACGACACTGCCAGCAATTAATCTATATGTATGACCAATGAATCGACCATCA	3665
Db	3424	TCGAGGACCTGGAGCCAGGTGTCA-----GCGACTGCTCTCTCTG	3463
QY	3670	AGGACGAGACGCAACAAGGGCAGCGCCGAGACGATGAGGGCGAGGAAGCGCGACCGCA	3722
Db	3464	AGGCGGAGGCCAGTGCATCTCAGGCCCACTGGCCGACAGTGGAAAGCGAACCCACAG	3522
QY	3730	GCAAGAGAGATTTAGTGTCTCGACGAGAACTGGACGAGAGGGCGAATGCGAGAGGGCC	3785
Db	3524	CCCCAGGGTGGGTGAGACCCACGAGGACAATGTCTCGAGGGCGACAGACGACATGA	3583
QY	3790	CGCTCGAGGGGTATTCATTTATTCACACAGACGAGAGATTACTCATGAAATTTCCAG	3844
Db	3584	CGAACACCGCTGAGCTCTCGAGACAGATCCCTGACCTGGCCGAGATGCAAGGCCAG	3643
QY	3850	CTGATGTGCCCCCGATTCGTACTATTAAGAAATTTCCGATCTTAGCCGTCAGATGACT	3905
Db	3644	AGGACTGCTTACTGTAAGGCTGTGTGCGGCGGTGTCTCTGCTGTGGGTGACACCAAC	3703
QY	3910	CGCGTCTGCGAAGGATGGGGCAATTTACGACTGAAAACTTTCAATTAATGAAAAA	3965
Db	3704	AGGCCCCAGGAAAGGTCTGTGGCGGTGTGCGAACAACCTGCTACACATCGTGGAGCAC	3763
QY	3970	AATATTTGAAGACGTGTATCACTAGATTTTAAAGATGACTTACTTTGGCATAG	4022
Db	3764	GCTGGTTCGAGCATTAATCAATCTTCAATGATCTTACTAGACGATGAGACGCTGGCTTG	3823
QY	4030	AAGATGTACATCTGCGCAAGAACCCCATACTGCAAGATATTTTAACTATATGACAGAA	4085
Db	3824	AGGACATCTACTAGAGAGGGGAAGACATCAAGAGTTCTGTGTAAGTATCCGACAGAA	3883
QY	4090	TATTTACGTTATATTTCTTTTGGAAATGTTAATCAAGTGTGGCGCTCGGCTTCAAG	4149
Db	3884	TGTTTCACATATGTCTTGTGTGCGAGAGTGTCTCAAGTGGGTGGCTTACGCTTCAAGA	3943
QY	4150	TGTACTTCAACAACGCGTGTGTGGCTCGAATTTGATTTGTCAATGTTATCGCTTATCA	4209
Db	3944	AGTACTTCAACAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	4003
QY	4210	ACTTGTTGCTTCACTTGTGTGAGCTGTGTGTATTAAGCCTTCAAGCTATGCGAAGCT	4265
Db	4004	GCTGTGTGGCCAAACCTGTGGCTTTTGGCGAGATGGGCCCATCAAGTCACTGGCGAGC	4063
QY	4270	TAAAGACACTGAGACACTAGGTGCATGTCCCGATGACAGGGGATGAGGGTCCGTGTTA	4329
Db	4064	TGCTGTCACTCCGTCTCTGTAGAGTCTGTCAAGATTTGAGGGGATGAGGGTGGTGTCA	4123
QY	4330	ATGCGCTGTGTCAAGCTATACCGTTCATCTTCAATGTGTCTATTTGTGTGTATATTTT	4389
Db	4124	ATGCCCCGTGTGGCGCCATCCCGTTCATCAAGAGTCTCTCGTGTGCTCATCTTCT	4183
QY	4390	GGCTAATTTTTCGCAATAATGGGTGTACAGCTTTTGTCTGTGAAATATTTTAATGTCCAG	4449
Db	4184	GGCTATCTTCAAGATCAATGGCGTGAACCTCTTTGCGGGGAAGTTTGGAGGTGCATCA	4243

QY	4450	ACATGA-----ATGGCAGGAGCTGACGCAAGAGATCATGCAAAATGCGATGCTGG	4500
Db	4244	ACACAGCAGAGGGAGACTTGGCTTTGAATCAACCATGTGTGAACAACAAGCCAGTGTG	4300
QY	4504	AGAGCGAGACTTACAC-----GTGGGTGAATTCAGCAATGAATTTGCATCATG	4550
Db	4304	AGTCTTGAACCTTGACCGGAGAAATTGTACTGGACCAAGGTGAAGTCAACTTGAACAAG	4360
QY	4552	TAGGTAACGCGATATCTGTGCTTTTCCAAATGGCCACTTCAAAGGCTGTGATCAAAATCA	4610
Db	4364	TGGGGGGCGGGTACTGTGGCCCTTCCTGCAAGTGGCAACATTTAAAGGCTGATGTGCATTAA	4420
QY	4612	TGAAAGATGCTATGCGATTCAAGAGAGGTGGCAAGCAACCAATTCGTAAACGAATCT	4670
Db	4424	TGTATGACGCTGTGACCTCCAGAGGGGTATGAAAGAGACACTTCAGTGGAAATACACTCT	4480
QY	4672	ACATGTATTTAATTTGATTTCTTCATCATATTTGATTCCTTTTTCACATCATCTGT	4730
Db	4484	ACATGTACATCTATTTTGTATTTTCATTCATCTTTGGGTCTTTCTTCAACCTGAACCTCT	4540
QY	4732	TCATTTGTATTATCATGTATAATTTTAATGACAAAGAAAAAAGCAGGTGATCAATTAG	4790
Db	4544	TTATTTGGTGTATCATGTATGACAACTTCAACCAACGAAGAAAAAGTTAAGGGGGCAG---G	4600
QY	4792	AAATGTTATATACAGAAAGATACAGAAAAAGTACTATAAGCTATGAAAAAAGATGGCTCTA	4850
Db	4601	ACATCTTCATATACAGAGAGAGAGAAAGATCTCAAAAGCCATGAAAGAGCTGGGCTCCA	4660
QY	4852	AAAAACCATTTAAAGCCATTTCCAGAACCAAGAGTGGCGACCAACAGCAATAGCTTTTGAAA	4910
Db	4661	AGAGCCCCCAAGAGCCCATCCACAGGCCCTTGAAACAAAGTACCAGGGCTTCATATTCCACA	4720
QY	4912	TAGTAACCGATAAAGAAATTGCATATAATCATTAATGTTATTCATTTGCTGCAACATGTTCA	4970
Db	4721	TTTGACCAACAGAGGCTTTGATGACGTACCATCATCATGTTTCTGTATCTGTAATATGTGA	4780
QY	4972	CCATGACCCCTGATCTGTTACGATGCGTGGACAAGTATAACGGGCTCTAAGCTATCTCA	5030
Db	4781	CCATGATGCTGAGACACAGATGACCAAAAGTCTCTGAAATCAACATCTTGACCAAGATCA	4840
QY	5032	ATGGGATTTGTGTGTTATTTTTCAGTTCCGAATGTCATTATAAAATATTGGCTTTAGCAT	5090
Db	4841	ACGTGCTTTTGTGGCCATCTTCAAGCGAGTATATGTCAAGCTGGCTGCCCGCC	4900
QY	5092	ATCATATTTTATTGAGCCATGAGAAATTAATTGAATGATAGTGTCAATTTTATCACT	5150
Db	4901	ACTACTACTTACCAACAGCTGGAATATCTTCCACTCTGTGTTGTACTCTCTCCATCG	4960
QY	5152	TAGGTCTTTGACTTAGCGATATTTATCGAAGAAAGTACTGTGTCGCCACCTGTCTCGAG	5210
Db	4961	TGGGCACTGTGCTCTCGGACATCATCCAGAAAGTACTTCTTCCGCCAGCGCTTCCGAG	5020
QY	5212	TGTGTCCGTGTGGCAAAAGTGGGCCGTGTCTTCCACTGTGTGAAGAGAGCCCAAGGCCATTTC	5270
Db	5021	TCATTCGCGTGGCCCGGAATAGGCGCATCTTCAACATGTATCCAGAGGGGCCAAGGGGAACTC	5080
QY	5272	GGAACACTGCTTTGCGGTTGGCCAAATGTGCGCTGCGGCCCTGTTCAAACATCTGCGCTGCG	5330
Db	5081	GCAAGCTGTCTTTTGGCCTCATATATGTCCGTGCTGCCCTTTTCAACATCGGGGTGCTGCG	5140
QY	5332	TGTTCTGTGTGATGTTCAATCTTGGCCATTTTCGGCATGTGCTGTTCTTACATGACGTGAAG	5390
Db	5141	TCTTCTCTGTATGTTCAATCTTCAATCTTTGGCATGTGCCAACTTGCTTATGTCAAGT	5200
QY	5392	AGAAAGCGGATTAAGAGCTCTACAACTTCAAGAACTTTGGCCAGAGCATGATCTGCG	5450
Db	5201	GGAGGCGTGGATGAGACGATGTTCAACTTCCAGACCTTTCGCAACAGCATGTGCTGTGCC	5260
QY	5452	TCTTTCAAGATGTGACGCTCAGCCGGTTTGGGATGTGTACTGACGCACTTATCATATGAG	5510
Db	5261	TCTTCCAGATACCACTGTGGCGGGCTGTGGATGTGCTCTCAGCCCATCTCTCAACACTG	5320
QY	5512	AAGCATGCGA-----TCCACCCGACAGCGCAAAAGGCTATCTCGGGCAATTTGTGGTT	5562

DB 5321 GGGCCGCTTACTGCGACCCCACTCTGCCCAAGCAATGGCTTCGGGGGAGATCGCGGA 5380  
QY 5563 CAGCGACCGTTGGAAATACGTTTCTCTCATACCTAGTTATAGCTTTTGTATAGTAA 5622  
DB 5381 GCCCACCCTGGGCGATCTCTCTCTTCAACCACTACATCATCTCTCTTCATCGTG 5440  
QY 5623 TTTAATATGATCTGCTGCTATCTCGAAGAACTATAGTACGGCCAGGAGAGTGCAG 5682  
DB 5441 TCAACATGATCATCTGCTATCTCTGAGAACTTCGACGCGCCAGGAGAGACCG 5500  
QY 5683 AGGGTTAAACCGACGACGACTACGATCTGATGATCTGGACGAATTCGATCCGG 5742  
DB 5501 AGCCCTGATGAGAGAGGACTTGTATATGATCTGGAGAAATTTGACCCAG 5560  
QY 5743 AGGGCAACCAAGTACATACGCTATGATGATGCTGCAATTCGAGAGTACGAGCC 5802  
DB 5561 AGGCCACTGAGTTATTTAGTATTCGGTCTGCTGACCTTGGCCGACGCTGCTGAGC 5620  
QY 5803 CGCTGAGATTCACCAACCGAAGATGACATGATGATGAGCATACCATCTGTC 5862  
DB 5621 CACTTCGATATCGCAAGCCCAACCAAGTAAAGCTCATCAACATGAGACTGCGCATG 5680  
QY 5863 GCGGTACCTCATGATCTGCTGAGATCTGACGCTGACGCTTACGAAAGACTTTGGCG 5922  
DB 5681 GTGGGAGACCGCATTCATGATGATGATCTCTTTGCTTCAACAAAGGCTCTGGGG 5740  
QY 5923 GGAAGGCAATCCGATGAGAGAGACGCGTGAATGAGTGTGAG-----ATAGCGCCCGC 5976  
DB 5741 AGCTGGGGGAGATGAGACGCTTGAAGATCCAGATGAGAGAAATTCATGAGCCCAACC 5800  
QY 5977 CGGATCGAGAGGCTTCGAGCGCTGCTCATCAAGCTGAGCGCTGAGGAGATGACT 6036  
DB 5801 CATCAAGATCTCTTACGAGCCCATCAACACACATCTCGGCGCAAGCAAGAGAGGTGT 5860  
QY 6037 GCGCCCGGCTTAATCAGACGCTGCGAAGCAAGGCGCGCGC 6083  
DB 5861 CGGCCATGTTATCCAGAGAGCCTTCGCGAGGACCTGCTGCAACG 5907

RESULT 15  
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; Sequence 1, Application US/10333191  
; Publication No. US2003023583BA1

; GENERAL INFORMATION:  
; APPLICANT: Keating, Mark T.  
; APPLICANT: Splawski, Igor  
; TITLE OF INVENTION: Common Polymorphism in SCNSA Implicated in Drug-Induced Cardiac  
; FILE REFERENCE: 2323-154-11  
; CURRENT APPLICATION NUMBER: US/10/333,191  
; CURRENT FILING DATE: 2003-01-17  
; PRIOR APPLICATION NUMBER: PCT/US01/22639  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: US 60/219,738  
; PRIOR FILING DATE: 2000-07-20  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 8491  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (151)..(6198)  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)..(8491)  
; OTHER INFORMATION: n may be any base  
US-10-333-191-1

Query Match 14.4%; Score 939.4; DB 17; Length 8491;  
Best Local Similarity 55.7%; Pred. No. 3,9e-250;

Matches 2064; Conservative 0; Mismatches 1571; Indels 72; Gaps 11;  
QY 2413 TGTGGAGCTGTGTGGGTTTGGTTGAATTTACAGAGTGGGTATGCTATCGTTGG 2472  
DB 2237 TCTGGAGAGCTGCGCCGCTGTGATGTCCATCAAGAGGAGAGTGAAGTTGGTCATGG 2296  
QY 2473 ATCCCTTGCTGAGCTCTTCATCAAGCTGTGATTTGGTCAACAGATGTTCAATGGCAA 2532  
DB 2297 ACCCGTTACTGACCTCACCAATCATATGTGATGCTACTCAACACACTTTCAATGGCC 2356  
QY 2533 TGGATCACCAGATATGAACAAGAGATGAAACGCTGCTCAAGAGTGCACATATTTCT 2592  
DB 2357 TGGAGCATCAACAATGACAGAGATTCAGAGAGATGCTGAGAGGTCGGAACCTGGCT 2416  
QY 2593 TCAACGCCACTTTGGCATTCGAGGCCACATGAGGTATGGCCATGAGCCCCAAGTACT 2652  
DB 2417 TCAAGAGATTTTCAAGAGAGATGACCTTCAAGATCATGCTTCGACCCCTTACTACT 2476  
QY 2653 ATTTCCAGAGAGGCTGGAACATCTTGAATTCATATTCGTGAGCCCTATGCTATTTGAAC 2712  
DB 2477 ACTTCCAGAGGCTGGAACATCTTGAATTCATATTCGTGAGCCCTATGCTATTTGAAC 2536  
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DB 2537 TGGGCTGTCCGCGATGAGCAACTTGTGCTGCTGCGCTCTTCCGCTGCTGCGGCTCT 2596  
QY 2773 TCAAACTGCGCAAGTCTTGGCCCACTTAATTTATCTCATTTTCGATTTATGGAACGACCA 2832  
DB 2597 TCAAGTGGCCAAATATATGAGCCCACTTAACACATCTCAAGATCATGCGGAATCAG 2656  
QY 2833 TGGGCGCTTTGGGTAATCGACATTTGATTTGATTTATCAATCTTCACTTTTGGCGTGA 2892  
DB 2657 TGGGGGCACTGGGGAACCTGACACTGTGTGATGATTCATGCTGTTCACTTTTGGCTGG 2716  
QY 2893 TGGGAATGCACTGTTGGGAAGAATTAATGATGATCAAGAAGCGCTTTCCGAGTGGCG 2952  
DB 2717 TGGGCAATGACGCTTTTGGCAAGAACTACTCGAGGTGAGGAGACGCGACTCA---GGCGC 2773  
QY 2953 ACTGCGCGGCTGGAACTTCAACGACTTTATGACAGCTTCAAGATCGTGTCCGGGTGC 3012  
DB 2774 TGTGCTGCTGCGGACATGATGAGACTTCTTTCATGCTCTTCAATCATCTTCCGATCC 2833  
QY 3013 TCTGCGAAGATGAGATCGAGTCCATGTGGAGCTGACATGACG---GGCGATGCTCGT 3069  
DB 2834 TCTGTGAGAGTGTGATCGAGACCATGTGGGACTGACATGAGAGTGTGGGGGAGTATAT 2893  
QY 3070 GCATTCCTTTCTTTTGGCCACCGTTGTGATCGGCAATCTTGTGATTAACCTTTTCT 3129  
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DB 2954 TGGCTTGTGCTGACGCTCTTCAAGGACAACTCAAGCCCTGTATGAGAGACAGAG 3013  
QY 3190 ATACGAATAAATAGCGGAGGCTTCAATGAAATGAAATTTGAAATTTGAGGTTTAAAG 3249  
DB 3014 AGATGAACAACCTCCAGCTGGCCCTGCGCCGATCAAGAGGGGCGCTTGTCAAG 3073  
QY 3250 GTAATATGCTGATGTTTCAAGTTAATGATTAACGTAACAATTAACAATTAATGATC 3309  
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QY 3310 AACCATCAGTGAAGAGACCAACAGATGATGATTTGAGAGCGAAGCATGCTGAC 3369  
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QY 3430 AGAGAGAGACGCACTGAGGTGGCCATGCGGGGATGATGAAATTCAGATTAACGCGG 3489  
DB 3249 ACCAGGCGAGGGGACCCCGGGG---ATCAGAGCGCTGTGTGTGCCATGCTGTGTGC 3305

QY 3490 ACATGAAGACACAAAGCCGAGAAATCCAAATATCTAATTAAGCAAGATGATTGGCA 3549  
DB 3306 CGAGTCACACACAGATGACACAGAAAGAGATGAGAGACAGCTGGGCAAGAGAGAGA 3365  
QY 3350 ACTCAATTAAACACCAAGACATATAGATGAAACAGACTTAAACCATAGAGTTTGTCT 3609  
DB 3366 GTCCAGCAAGACAGAGAAATCCAGCTG--TGTCGGGTGGCCAGAGCCCTCCGAT 3423  
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DB 3424 TCCAGAGACTGAGCCAGGTGTCA-----GCGACTGCTCTCTG 3463  
QY 3670 AGAGAGAGACCAAGGAGACCGCCGAGATGAGAGGGGAGAGAAAGCCGACCA 3729  
DB 3464 AGGCGGAGCCAGTGATCTCAGGCCGAGCTGGCGGACAGTGAAGCCGAAACCCGAG 3523  
QY 3730 GCAAGAGAGATTTAGGTCTGACAGAGAACTGSAAGAGAGGGCGAATGCGAGAGGAGC 3789  
DB 3524 CCCCAGGTGGGGTGAAGACCCAGAGAGACAGTTGCTCCGAGGGCAGCACAGACATGA 3583  
QY 3790 CGCTGACGTGATATCATTAATGACACAGAGAGATTAATCTGATGAATATCCAG 3849  
DB 3584 CCAACACCGCTGAGCTCTGAGAGAGATCCCTGACTCGCCAGAGATGTCAGAGACCAG 3643  
QY 3850 CTGATGCTGCCCGGATTCGACTAATAAGAAATTTCCGATCTTAGCCGATGACATGACT 3909  
DB 3644 AGGACTGCTTACGTAAAGGCTGTGTCCGGCGCTGCTGCTGTGCGGTGAACACAC 3703  
QY 3910 CGCGCTTCTGCAAGAGATGAGGCAATTTACGACTGAATACTTTCAATTAATGAAATA 3969  
DB 3704 AGGCCCCAGGAGAGGTCTGTGGGGGTGGCCAGACCTGCTACACATCTGTGAAGCA 3763  
QY 3970 AATAATTTGAAACAGCTGTATCACTATGATTTTAATGAGTAGCTTAGCTTTGGCATTA 4029  
DB 3764 GCTGGTTCGAGACATTCATCATCTTCATGATCTCACTCAGCAGTGGAGCGCTGGCTTCG 3823  
QY 4030 AAGATGACATCTGCGACAAAGACCCATCTCAGAGATTTTATCTATATGACAGAA 4089  
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QY 4090 TATTAAGGTATATTTCTTTGGAATGTTAATCAAGTGGTGGCGCTGGCTTCAAG 4149  
DB 3884 TGTTCACATATGTCTTGTGCTGAGATGCTGCTCAAGTGGGTGCTTACGACTTCAAGA 3943  
QY 4150 TGTACTTCAACCAAGCGGTGTGTGGCTGATTTGATTTGATGTATGCTTATCA 4209  
DB 3944 AGTACTTCAACCAAGTGTGTGGTGTGCTGATCTTCTCATGTAGACGTCTCTGTGCA 4003  
QY 4210 ACTTGTGCTTCACTGTGTGAGCTGTGTGATTTCAAGCTTCAAGATGCGAAGCT 4269  
DB 4004 GCGGTGTGGCCAAACCTGGGCTTTGCGAGATGGGCCCATCAAGTCACTGGCGAGC 4063  
QY 4270 TAAGAGACTGAGACCACTAGTGCAGATGCCGATGAGGAGGATAGGGTGTCTGTA 4329  
DB 4064 TGCCTGACCTCGCTCTGAGACTGTGTACATTTGAGGAGCATGAGGATGTGGTCA 4123  
QY 4330 ATGCGCTGTACAAAGCTATACCTGTCAATTTGATGATTTGATGATTTT 4389  
DB 4124 ATGCGCTGTGGGGCCATCCGTCATGAAAGTCTCTGCTGTGCTCATCTTCT 4183  
QY 4390 GGTCAATTTTGGCAATATGGGTGTACAGCTTTTGTGCAAAATATTTAAGTGGAG 4449  
DB 4184 GGTCAATCTTCAAGATATAGGCGTGAACCTTTTGGCGGAAAGTTTGGAGGTGCATCA 4243  
QY 4450 ACATGA-----ATGGACGAAGCTCAGCCAGATCATCAAAATGCAATGCGTGG 4503  
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QY 4504 AGAGCGAAGACTAC-----GTGGGTGAATTCAGCAATGATTTGCATATG 4551  
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QY      5923 GGAAGGCAATCCGATAGAGAGACCGGTGAGATTGTGAG-----ATAGCGGCCCGCC 5976
Db      5741 AGTCTGGGAGATGACGCCCTGAAGATCCAGATGAGAGAAATTCAATGGCAGCCACC 5800
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-08-554-424-7  
Perfect score: 6513  
Sequence: 1 TCTAGAGCTGGCGCATAG.....ACGGAGTATTAGCTAGA 6513

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues  
Total number of hits satisfying chosen parameters: 66479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	787.6	12.1	4675	3 AK083220	Mus muscu
2	776.6	11.9	5943	9 AY416499	Hom sapi
3	696.8	10.7	5666	9 AY416501	Mus muscu
4	677.8	10.4	5710	9 AY416500	Par trogl
5	406.8	6.2	673	4 BM632901	Bj729409
6	334.6	5.1	866	4 BJ729409	Bj729409
7	327	5.0	537	4 BJ509823	BB170021A
8	321.4	4.9	829	7 CN527280	UI-M-HB0-
9	312	4.8	2802	3 AK032187	Mus muscu
10	310.4	4.8	928	5 BQ715936	AGENCOURT
11	302	4.6	502	4 BM633126	BM633126
12	301.2	4.6	771	9 CNS01235	AL101052
13	292.2	4.5	1777	3 BC029489	Hom sapi
14	288	4.4	768	6 CB520657	Hom sapi
15	281.6	4.3	688	6 BM650999	170006873
16	280.4	4.3	866	9 CG766052	TCB48.2 D
17	280.4	4.3	908	5 BQ946179	AGENCOURT
18	279.6	4.3	911	6 CD327202	AGENCOURT
19	271.6	4.2	760	5 BX876821	BX876821
20	271	4.2	718	6 CD804204	UI-M-GV0-
21	263	4.0	816	5 BQ444145	UI-M-EX0-
22	262.4	4.0	694	7 CN457096	UI-M-HN0-
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24	254.8	3.9	665	2 BB653350	BB653350

25	254.2	3.9	778	1 AU035605	AU035605
26	250.4	3.8	674	4 BG342331	BG342331
27	245.4	3.8	751	5 BU226444	BU226444
28	244.2	3.7	561	2 BF076296	BF076296
29	242	3.7	618	2 BB622500	BB622500
30	241.8	3.7	582	5 BP202326	BP202326
31	240.6	3.7	568	6 CB616190	CB616190
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33	239.2	3.7	819	7 CR847292	CR847292
34	238.4	3.7	544	2 BF323267	BF323267
35	238.4	3.7	639	9 CR189953	CR189953
36	238.4	3.7	1237	9 CL650204	CL650204
37	235	3.6	610	1 AL588672	AL588672
38	234.2	3.6	821	7 CO425057	CO425057
39	232.8	3.6	763	6 CA358980	CA358980
40	232	3.6	583	5 BP202296	BP202296
41	230.8	3.5	547	2 BF470392	BF470392
42	230.6	3.5	537	7 CR537070	CR537070
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44	225.2	3.5	881	9 CC542775	CC542775
45	225	3.5	606	6 CB581383	CB581383

## ALIGNMENTS

RESULT 1	AK083220	LOCUS	DEFINITION	AK083220	4675 bp mRNA linear HTC 03-APR-2004
ACCESSION	AK083220	VERSION	KEYWORDS	AK083220.1	GI:26101130
SOURCE	ORGANISM	REFERENCE	AUTHORS	REFERENCE	AUTHORS
Mus musculus (house mouse)	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning	Carninci, P. and Hayashizaki, Y.	High-efficiency full-length cDNA cloning
99279253	10349636	2	Normalization and subtractions of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	2	Normalization and subtractions of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
11042159	3	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Komuro, H., Akiyama, J., Nishi, K., Kiteunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kaishogi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, B., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	RIKEN integrated sequence analysis (RISA) system--384-format	RIKEN integrated sequence analysis (RISA) system--384-format	RIKEN integrated sequence analysis (RISA) system--384-format
20530913	11076861	4	Genome Res. 10 (11), 1757-1771 (2000)	4	Genome Res. 10 (11), 1757-1771 (2000)
11076861	4	THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	Functional annotation of a full-length mouse cDNA collection	THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.	Functional annotation of a full-length mouse cDNA collection
5	5	Nature 409, 685-690 (2001)	THE PANTOM Consortium and the RIKEN Genome Exploration Research	5	THE PANTOM Consortium and the RIKEN Genome Exploration Research

TITLE Group Phase I & II Team.  
 ANALYSIS of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 4675)  
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Konda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohse, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.jp/  
 URL: http://fanom.gsc.riken.jp/  
 Location/Qualifiers

FEATURES  
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 Best Local Similarity 55.2%; Pred. No. 6,4e-193;  
 Matches 1962; Conservative 0; Mismatches 1369; Indels 223; Gaps 13;

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2640 AGCCCAAGTACTATTCCAGAGAGGGCTGGAACATCTTGCATTTATCGTGGCCCTTA 2699  
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2700 TCGCTATTGGAAGTGGGACTCGAGGTGTCCAGGGTCTGTCCGTTATGCGTCTTTCGA 2759  
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2820 ATGGAGCGACATGGGCGCTTGGGTATCTGACATTTGACTTTCATTCATTCATCTTC 2879

Db 247 ATTTGAACTCCGTTGGGCGCTTGGGACCTGAGCTGGTGTGGCATCTGTTCTTC 306

Qy 2880 ATCTTGGCGGTATGGAATGCAATCTGTCGGAAGAAATTAATGATGA--TCACAGAGAC 2936

Db 307 ATCTTGGCGGTATGGAATGCAATCTGTCGGAAGAAATTAATGATGA--TCACAGAGAC 366

Qy 2937 CGCTTTCGAGATGCGAAGCTGCGGCTGGAACTTCAACGATTTATGACAGCTTCATG 2996

Db 367 ATCAGCCAGAGATGCAAGCTCCGCGCTGGCAATGAACGATTTTCCACCTCCCTC 426

Qy 2997 ATCGTGTCCGCGCTCTCGGAGAAATGATGATGATGATGATGATGATGATGATGATG 3056

Db 427 ATCGTGTCCGCGCTCTCGGAGAAATGATGATGATGATGATGATGATGATGATGATG 486

Qy 3057 GCGC--ATGCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 3113

Db 487 GCGGCGAGGCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 546

Qy 3114 GTACTTAACCTTTCTTACGCTTGTGCTTTGTCATTTTGGTCAATGATGATGATGATG 3173

Db 547 GTGCTGAATCTTATTTCTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTG 606

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Db 633 -- 632

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Db 633 --CTGCAATATTCGTTATCCGATC 657

Qy 3354 GAAGAGCATGTGACACGAACTGAGTGGGCGACGAGATCTGCGACGCGCTC 3413

Db 658 AAGAGGGGTGGCTGCGGCGCAATGATGATGATGATGATGATGATGATGATGATGATG 717

Qy 3414 ATCAAGAGGGATCAAGAGCAGACGCACTGAGAGTGGCCATGGGATGATGATGAA 3473

Db 718 CAACGGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 777

Qy 3474 TTACGATTCAGCGGACATGAAAGCAACAGCGGAAATTCAAATATTAATATAC 3533

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Qy 3594 CATGAGGTTGTCTTACAGACGACACCTGCGAGATTAATGATGATGATGATGATG 3653

Db 896 --TGTCTTCTTAATTAAC--CCAACTGACCTGGGCTGCCAT 938

Qy 3654 AAGATGCACTTCAAGAGCAGAGCGAGGCGCGAGCGAGCGAGCGAGCGAGCGAGCGAG 3713

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Dp	2173	CAAAATCCAAAGGATTTGCTTTGATTTGTCACAGCAACAGCCTTCGACATCGTATCAT	2232
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Dd	2473	CTTGTGCTCCCCGACCCTTATTCGCGGTATTCGAAATTTGGCCCGCATCGGGGCGCATCTTGGC	2532
OY	5246	ACTGTGAGAGGGAGCCAAAGGAGCATTTGGGACAATGCTCTTGCGGTTGGCCATGTGCTGCC	5305
Dd	2533	TCTGATCAAAGGGCGCCCAAAAGGAAATCCGCAACCTGTGCTTTGGCTTAATGATGTGCTGCC	2592
OY	5306	GGCCCTGTTCAAACATCTGCGCTGCTGCTGCTTCCTGGTCAATTTATCTTTGCCATTTTCGG	5365
Dd	2593	CGCCCTGTTCAAACATGCGCCCTCTGCTCTTCTCTGGTATGTCAATCTTCCCATCTTTGG	2652
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Dd	2653	GATGTCCAACCTTGCGGTACGTGAAGACAGAGGCGGCAATTGATGACATGTTTCAACATTTCSA	2712
OY	5426	GACCTTTGGCCAGACATGATCTGCTCTTTCAGATGTCAACGTCAACGCTGACGCGTTGGATGG	5485
Dd	2713	GACCTTTGGCCAAACGCAATGATCTGCTCTTTCAGATATCAACACCTGTGCTGGTGGGATGG	2772
OY	5486	TGTACTGAGACGCCATTTATCA-----TGAAGAACATGGGATCACCCGACAGCGA	5536
Dd	2773	CTTACTGTGCAATCTTGAAACGCCCCCTGACTGACGCTTGGACAGAGACATCCAGG	2832
OY	5537	CAAAAGCTATTCGGGCAATTTGTGGTTACAGGACCGTTGGAATAACGTTTCTCCTTCATA	5596
Dd	2833	AAGTGGCTTCAAAAGGGAGCTGCGGGAACCCCTCGTGGGATCTTCTTTCTGCAAGCTA	2892
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OY	5717	TGAGATCTGGACGAATTCGATTCGGAGGGACCCAGTACATACGCTATGATCAAGCTGTC	5776
Dd	3013	TGAGATCTGGAGAAAGTTTGTATCTGTATGTCACCCAGTTTCATGAGTACGTAAAGCTGTC	3072
OY	5777	CGAATTCCTGAGGATCTGAGGCCCGCGTGCAGATTCACAAACCGAAACAAAGTACAAAGAT	5836
Dd	3073	CGAATTTGCCGAGCGCTTGAGAGATCTCGCTCCAGATACCCAAAGCCAAACCAATCGAGCT	3132
OY	5837	CATATCGATGAGACATACCATCTGTGCGGCTGAACCTATGATCTGGCTGACATCTCTCGA	5896
Dd	3133	CATGCGCATGGAACCTGCCCATTGGTAGCGGAGATCGAATCCATCTGCTTGGACATCTTTT	3192
OY	5897	CGCCCTTACGAAAACCTTCTTTGCGGGGAAGGGCAATCCGATAGAGAGACGGGTGAGAT	5956
Dd	3193	CGCCCTTACCAAGCGAGTCTTGAGAGACATGTGGAGATTTGGAATCTCTGCGGAGCAGAT	3252
OY	5957	TGTGTAG-----ATAGCGGCCCGCCCGGATATGAGAGGGCTACGAGCCGCTCATCAAC	6010
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OY	6011	GCTGTGGCGTACGCTGAGAGATCTGCGCCGCGCTTAATTCAGACAGCTGCGGAAAAGCA	6070
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 VERSION AY416499.1 GI:39772459  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 5943)  
 Authors Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smutsky,J.J., Adams,M.D. and Cargill,M.  
 Title Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 Journal Science 302 (5652), 1960-1963 (2003)  
 PubMed 14671302  
 2 (bases 1 to 5943)  
 Authors Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Smutsky,J.J., Adams,M.D. and Cargill,M.  
 Title Direct Submission  
 Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 Comment This sequence was made by sequencing genomic exons and ordering them based on alignment.

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 Location/Qualifiers  
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 Best Local Similarity 45.4%; Pred. No. 5e-190;  
 Matches 2704; Conservative 0; Mismatches 2882; Indels 368; Gaps 21;

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 Db 160 AAGCCAAACAGCAGCTGGAAGCAGGAGAGTTTCCCTTTCATCTACGGGACATCCC 219  
 QY 306 CCGAATTGGCTCTCTCTCTCGAGATATGATCCCTTCAACAGCAATGTATGACA 365  
 Db 220 CAAGGCGGTGTGACAGTTCCCTCGAGAGCTTTGACCACTACTATTGACAGCAAAACC 279  
 QY 366 TTCTGATTTGAAGCAAGAAAGATTTTTCGCTTTTCTGCATCAAAAGCAATGG 425  
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 QY 426 ATGCTGCATTCATTCATCCGATAGTGTGAGCATTTTCTAGTGCATTCATTA 485  
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 Db 1177 TTGATCATCTTTGATGTTCTTTCTTATCTGTGTAATTGATCTTGTGCTGTGGTGGCATG 1236  
 QY 1314 TCGATATGCAATTTGAAAGAGAGGCGGAAGAAAGAGAGGCTGCGAAGAGAGGAGTA 1373  
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 Db 1350 GATGGCACTTACAGCAGAACTGTCTCAGAAAGATGCATGAGAGAAAGATGAAAGAG 1409  
 QY 1493 GCGCAAGAGTCCGACATATTCTTGCACTAGCTATAGCTATTTTGTGGCGCGAAGAGG 1552  
 Db 1410 AGGGGGCTCCCTCGAGGCTTTCTGAATCTTAACTCAAGTCAAGAGTCAAGAGGA 1469  
 QY 1553 CAAGATGACAAACAAAGAGAAAGATGTCATTGCGAGGCTGAGGTGAGTCCGAGTCC 1612  
 Db 1470 AAGACGTAACAGAGAGAAAGAGAGAGAAAGAAAGAACTCTCTGAGAGAGAGAGAAAG 1529

OY		1613	GGTGAGCGTTATACAAAGAACAACGAACACTTACCAGCAACCAAAGCTAACAAAATTGC	16712
Dd		1530	GGATCCCGAAGAAGTGTTTTTAAGTCAGAGTCAGAAAGATGGCATGAGAAAGAAAGCCTTTG	15898
OY		1673	TAAATGAGCACGACATCCTTATCCTTACCTGTTCAACGTTTAACTAACATAACGAGGGATC	17323
Dd		1550	GCTGCCAGACAAACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNTCACTGCTCAGAT	16494
OY		1733	ACGTAGTTCTCAACAATACAGATACGGAACGGAAGTGGCGCTTTGGTATACCGGTAG	17922
Dd		1650	CCCAGGCTGCCTCTCTCTCCCCGACAAAGCAAGCAGACATCTTCAgTTTAGGG	17098
OY		1793	CGATCGTAA GCCATTGTTATGTGTCAACATATCAGGATGCCAGCAGACTTGCCTTATGC	18524
Dd		1710	ACCTGG-----GCGGTTCCGAGACC	17308
OY		1853	CAGACACTCGAATGCCCTCACCCGATGTCCGAAGAATAAGGGCATCATATGTGCCGT	19122
Dd		1721	GGGCTCCAGAAATG-----AGTTGGCGGATACAGACACAGCAGGTGAGGA	17787
OY		1913	GTA CTATGGCAATCYAGGCTCCCGACACTCATCTGATACCTCGCATAGTCCCAATATC	19727
Dd		1779	GAGCAGAGGGCGCGCGGACCTCCCTTTATCCCATCCGGGCGCGGAGCCCGAGCAG	18388
OY		1973	GTA TACTCA CATGGCGATCTACTCGGCGGCA TGCGCGTCA TGGCGGT CAGCA CAATAC	20322
Dd		1839	CTACAGCGGCTPACAGCGGCTACAGCCAGGCGAGCGGCTCTCGSCATCTTCCCA GCGCT	18988
OY		2033	CAGA GAAGCAAATTTGGCGCAACCGCAACACAGCAATCATACGTGGGCGCCA CCAATGG	20922
Dd		1899	GCGGCGCAGCGTGAAGCGCAACAGACGCTGACATGCAACGCGGTGATCTCCATCTGG	19588
OY		2093	CGGCACCACTGTCTGGA CACCAATCA AAGCTCGATCGGCACTACGAATTTGGCCT	21522
Dd		1959	CGGCGCGGGCT-----	19699
OY		2153	GGA GTGCA CGAGCGAAGCTGGCAAGATTAA ACATGACAACTCTTTATCGAGCCGT	22122
Dd		1970	-----CCCATCGGCGGCGCTCCTCGCAGAAGCTACAACTGAGTGGAAT	2018
OY		2213	CCA GAACA AAAGGTGTTGATATGAAGAATGTATGTCCTGAATGACATATCGAACA	22722
Dd		2019	TAA GAAGAA AGCCCTGAGTCTCTTTAGTTTCATGACCAATTAGCCTCTACGGGCG	20787
OY		2273	GGCGCTGTCGGGCAAGTCGGGCAAGGATCGCGGTCTCCGTTTACTTTCCCAAC	23322
Dd		2079	GAA GACA GAATCAACAGTATATATGATG-----TTGTTAC	2114
OY		2333	AAGA GCATGACGAGATGGGCGGCACTTCAAAAGCAAGGCACTCGAATGATCTCAA	23922
Dd		2115	AAA TACA CTATAGAAAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	2174
OY		2393	AAGCATCGATGTTTGTGTGTGGGACTGTTGCTGGGTTTGTGAAATTCAGAGTG	24522
Dd		2175	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	2234
OY		2453	GGA TCGTACTCGTCTTCGATCCCTGTGTGAGCTCTTCA TCA CGCTGTGCA TTGTGT	2512
Dd		2225	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	2294
OY		2513	CAACA CGATGTTCA TGCAATGATCA CACGATATGA ACAAGAGATGAA CCGTGCT	25722
Dd		2225	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	2354
OY		2573	CAAGA GTGCA ACTATTTCTTCA CCGCACTTTGCA TCAGAGCCACATGAAGCTPAT	26322
Dd		2355	NNNNNNNNNNNNNNNGTTTTTCACTGGAATTTTCA CAGCGGAAATGTTCTCGAAGCTCAT	2414
OY		2633	GGCCA TGACCCCAAGTACTATTTTCA GAGAGGCGGAACATCTTCACTTCA TTA TCGT	2692
Dd		2415	AAGCATGGATCTCTATTA TTTTCAAGAAAGGTGGAACATTTTGA CCGATTTATGT	2474
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QY 5487 CATGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5546  
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QY	6011	GCTGTGCGGTAGCGCTGACAGTACTGCGCCCGGCTAATTCAGACAGCGCTGGCGAAACGA	6070	7-DEC-2003
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Db	5727	TTTGGCAAGCGGG	5740	
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ACCESSION	AY14501			
VERSION	AY14501.1	GI:39772461		
KEYWORDS	GSS.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 5666) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.			
TITLE	Interferring nonneutral evolution from human-chimp-mouse orthologous gene trios			
JOURNAL	Science 302 (5652), 1960-1963 (2003)			
PUBMED	14671302			
REFERENCE	2 (bases 1 to 5666) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A., Todd,M.A., Tenenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.			
AUTHORS	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
TITLE	Direct Submission			
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA			
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.			
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Best Local Similarity	56.1%;	Pred. No. 3e-169;		
Matches 1278;	Conservative 0;	Mismatches 960;	Indels 39;	Gaps 4;
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Db	3190	ATCCAGAGCGCTGCTTACCGAGAGGGTGTGTCAGAGGTTCAAGTGTCCGACAGTCAACA	3249	
QY	3904	ATGATCGCGCGTTCGCGCAGAGATGGGGCAATTTACGACGTGAAACTTTCAATTAATG	3963	
Db	3250	TCGAGGAAGACTAGGCAAGTCGTGTGATCTTCGCGAAACCTGCTTCTCAATTGTGG	3309	
QY	3964	AAAAATAATATTTTGAACAGCTGTATCACTATGATTTTAAATAGTAGTACCTTTGG	4023	
Db	3310	AGCACAATGTGTTGAGACTTTCATCATTTTCAATGATTCCTCCTCAGAGGTGAGACCCCTGG	3369	
QY	4024	CATTGAAGATGTACATCTGCCACAAAGACCCATACATGCGAGAGATTTTATACATATGG	4083	
Db	3370	CCTTCGAGGACATCTTACATTGAGCAGAGAAAGACCATCCGTACCATCCTGAGATATGCGG	3429	

QY	4084	CCAGAAATTTAAGGTTATATCTCTTGGAAAGTTAAATCAAGTGTGGCGCTCGCT	4143
Db	3430	ACAGGCTTCACTCACTCACTTCACTCCGGAGATGTTGCTCAAAATGGACACCTTAGGCT	3489
QY	4144	TCAAGTGTACTCGACCAACGCGTGTGGTGGCTCGATTTGCGATGTCATGATATCGC	4203
Db	3490	TGTCAGGTTCTTACCAAGATGCGTGTCGTGGTGGACCTTCTCATTTGTGCTNNNNNN	3549
QY	4204	TTATCACTTGTGTCCTTCACTTGTGGAGCTGTGTGATTCAGACCTTCAAGACTATGC	4263
Db	3550	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	3609
QY	4264	GAAAGTTAAGAGCACTGAGACCACTACGTGCATGTCCCGTATCAGAGGCACTGAGGGCT	4323
Db	3610	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	3668
QY	4324	TGCTTAATGCGCTGTGACCAAGCTATACGTCATCTTCAATGTGCTATTGTGTGCTAA	4383
Db	3670	TGGTGAAGCGCTTGTTGGTGGCGCATCCCTTCATCATGAAGTGTGCTGTGTGCTCA	3729
QY	4384	TATTTGGCTAAATTTTGGCCATAATGGGTGACAGCTTTTGTCTGGAAATATTTTAGT	4443
Db	3730	TCTTCTGCTGATTTTACAGATCAATGAGCGTTAACTGTGTTGCTGGGAAATACACT	3789
QY	4444	GCGAGGACATGAAT-----GGCAGCAAGCTCAGCCACAGATCA	4482
Db	3790	GCTTCAACGAGACTTCAGAAATCCGGTTCCAAATTCAGAGGTGAACATPAAACGACT	3849
QY	4483	TACCAATTCGCAATGCTCGAGAGCGAGAACTACAGTGGTGAATTCAGCAATGAAT	4542
Db	3850	GTCAGAGCTCATGAGAGGCAACAAACAGAGATCCGATGGAAAGCGTCAAGATCACT	3909
QY	4543	TGATTCATGTAGTGAACGCGTATCTGTGCTTTTCCAAGTGGCCACCTTCAAGGCTGGA	4602
Db	3910	TGCAACAGCTGGGGCAGGCTACCTGGCCCTTTCAGTGGCAACTTCAAAGGCTGGA	3968
QY	4603	TACAAATCATGAACGATGCTATTCGATTCAAGAGGTGACCAAGCAACCAATTCGTGAA	4662
Db	3970	TGCACTCATCTTAGCAGCTGTAGATTTCCGAAAGCGGACGACAGCTGATATGAGG	4029
QY	4663	GGAACATCTCAATGTAATTTATTTGTAATCTTCATCATATTTGGATTCCTTTTCCAC	4722
Db	4030	GCAACATCTACATGACATCTACTCTTGTCATCTTCATCATCTTGGCTCTTCCACC	4089
QY	4723	TCAATCTGTCATTTGTGTTATCTATTGATAATTTAATGACAAAGAAAAGCAGGTG	4782
Db	4090	TCAACCTGTCATGGGTGTCATCTGACAAATTCATTCACAGAAAGAAA---GTTTG	4146
QY	4783	GATCATTTGAAATGTTTATGACAGAAATTCAGAAAAGTACTAATATGCTATGAAAAGA	4842
Db	4147	GAGGTCAAGCATCTTATGACAGAGAAACAGAAAGTACTCAAGCCATGAAAGAGC	4206
QY	4843	TGGGCTCTAAAAAAACATTTAAAGCCATTCMAAGCAAGGTGGCGACCAACCAATPAG	4902
Db	4207	TAGGCTCCAGAGCCACAGAGGCCATTCGCCGACCTTTGAACAAAATTCAGAGGATTG	4266
QY	4903	TCCTTGAATAGTAAACCGATTAAGAAATTCGATATTAATCATTAATGTTATTCATTTGCTGA	4962
Db	4267	TCTTTGATTTGTCACCAACCAACCTTCGACATCGTATCATATGATCTCATTCGCTTA	4326
QY	4963	ACATGTTCAACATACCTCGATGCTGTTACGATGCTGGGACAGCTAATACGCGTCTTAG	5022
Db	4327	ACATGGGACCATATGCTGTGAGACAGACACACAGACCAAGCAGATGAGAACTTCTCT	4386
QY	5023	ACTATCTCAATGCGATATTTGTAATTTTTCAGTTCCGATGCTATTTAAATAATATTCG	5082
Db	4387	ACTGATTAATTCGTGCTTGTGTATCTTTCACCTGGAGTGTGTCTCAAAATGTTTG	4446
QY	5083	CTTTACGATATCACTATTTTATGAGCACTGAATTTATTTGATGATGATGTTGCTATTT	5142
Db	4447	CTTTGAACACTACTATTTTACCACTTGGCTGGAAACATTTTGAATTTGTGTGTGCTATTC	4506

QY	5143	TATCCACTTAAGCTCTTGTACTTAAGGATATATATCCAGAGTACTTCGTGTGGCCAGCC	5202
Db	4507	TCCTCATTGGGGAAATCTTCTGTGGATATCATTTGAAAGTACTTCGTCTCCCGACCC	4566
QY	5203	TGCTCCGAGTGGATGCGGTGTGGCCGAAAGTGGGCGGTGTCTTCGACTGTGTGAAGGGAGCA	5262
Db	4567	TATTCGCGCTCATTCCGATTGTGGCCGCAATCGGGCGCATCTTGCGCTGATCAAGGGCGCCA	4626
QY	5263	AGGGCAATTCGGACACTGTCTTGTGGCGTTGGCCATGTGTGCGCGCGCCCTTTCACATCT	5322
Db	4627	AAGGATCCGACACCTGTGCTCTTGTGCTTAAATGAATGTGCTGCCCGCCCTGTTCACACATCG	4686
QY	5323	GCCGTGCTGCTTCTGTGCTGTCAATGTTCATCTTGTGCAATTTTCGATGTGCTTCTTCATGC	5382
Db	4687	GCTTCCTGCTCTTCTGTGTATGTATGTTATCTTCTTCATCTTTGGGATGTCCAACTTGCGGT	4746
QY	5383	ACGTGAAGAGAGAGCGCGCATTAACGACTTACAACTTCAGACCTTTGGCCAGAGCA	5442
Db	4747	ACGTGAAGAGAGAGCGCGCATTAATGATGATCATGTTCAACTTCGACCTTTGGCAACGCA	4806
QY	5443	TGATCCGCTCTTTCAGATGTGACGCTGACGCGTGGAGATGGTGTACTGAGCGCCATTA	5502
Db	4807	TGATCTGCTGTCTTCAAGTACAGACCTCTGTGTGTGGATGGCTTACTGTGCTGCAATCC	4866
QY	5503	TCGA-----TGAGAAAGCATGCGATTCACCCGACAGCGCAAAAGGCTATCCGGGCA	5553
Db	4867	TGAACCGCCCCCTGACTGACGCTTGGACAAGAGGACCCAGAAAGTGCGCTTCAAAAGGG	4926
QY	5554	ATTGTGTGTACGCAACGCTTGGAAATTAAGTTTCTCCTCACTACCTGTATTAAGCTTTT	5613
Db	4927	ACTCGGGAAACCCCTCGTGGGCAATCTTCTTCTGTGAGTACATATCATCTCTCTTC	4986
QY	5614	TGATAGTTATTAATATGTACATTTCTGTCAATTCGAGAACTATATGTACAGCCACGAG	5673
Db	4987	TGATCGTGTAAACATGATCATGTCCATCATCTTGAGAACTTCAGCGTACCCACAGAG	5046
QY	5674	ACGTGCAAGAGGGTCTAACGACGACATTCGACATGTACTATGATCTGGAGCAAT	5733
Db	5047	AAAGCGCCGATCTCTGAGCGAGAGACGATTCGAGACTTTTATATGAGTCTGGAGAAAGT	5106
QY	5734	TCGATCCGAGAGGAGACCAGTACATATAGCTATGTGACTGTCCGAATTCCTGACGTAAC	5793
Db	5107	TTGATCTCGATGCCACACAGTTCAATCGAGTACTGTAAAGCTGTGGCCGACTTGGCCAGCGCC	5166
QY	5794	TGAGAGCCCGCGCTGAGATTCACAAACCGAAACAAAGTACAAATCATATCGATGACATAC	5853
Db	5167	TGGAGCAATCCCTCTCGAGTACCCAAAGCCCAACACATGAACTCATCCCAATGAGACTGTGC	5226
QY	5854	CCATCTGTGCGGCGTGAACCTCATGTACTGCTGCGCATCTCGAGCGCCCTTACGAAAGACT	5913
Db	5227	CCATGTGTAGCGGAGATGAAATTCACACTGTGTGACATCTTTTTCGCCCTTACCAAGCGAG	5286
QY	5914	TCCTTTGCGGAGAGGCGCAATCCGATGAGAGAGACGCGTGAATTTGTGAG-----ATAG	5967
Db	5287	TCCTGGAGAGACAGTGGGAGTGTGACATCTGCGGCAACAGATGAGAGGCGTTCGTGG	5346
QY	5968	CGGCGCGCGCCGGAATACGAGAGGCTTACGAGCCCGTCTATCAACGCTGTGAGCGTACGCTG	6027
Db	5347	CGTCCAAATCTTCCAAATGTCTTACGAGCCCTATACACACATCTTGGCGGCGCAAGCAGG	5406
QY	6028	AGAGACTATGCGCCCGGCTTAATTCACGACGCGCTTGCGAAAGCACAAAGCGCGCGCG	6084
Db	5407	AAAGAGTGTCTGCAAGTGTCTTGGACGTGTCTTACAGGGGACACTGTGCTAGGCGGG	5463

RESULT 4

AY416500

LOCUS AY416500

DEFINITION Pan troglodytes SCNA9 gene, VIRUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY416500

VERSION AY416500.1

KEYWORDS GSS.

5710 bp DNA linear GSS 17-DEC-2003

GI:39772460

SOURCE	ORGANISM
REFERENCE	Pan troglodytes (chimpanzee)
REFERENCE	Euarchyotiles
REFERENCE	Eukaryota; Metazoa; Chordata; Cetartata; Vertebrata; Euteleostomi;
REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE	1 (bases 1 to 5710)
REFERENCE	2 (bases 1 to 5710)
REFERENCE	Clark,A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
REFERENCE	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
REFERENCE	Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
REFERENCE	Adams, M.D. and Cargill, M.
REFERENCE	Interfering nonneutral evolution from human-chimp-mouse orthologous
REFERENCE	gene trices
REFERENCE	Science 302 (5652), 1960-1963 (2003)
REFERENCE	14671302
REFERENCE	2 (bases 1 to 5710)
REFERENCE	Clark,A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
REFERENCE	Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
REFERENCE	Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
REFERENCE	Adams, M.D. and Cargill, M.
REFERENCE	Direct Submission
REFERENCE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
REFERENCE	Rockville, MD 20850, USA
REFERENCE	This sequence was made by sequencing genomic exons and ordering
REFERENCE	them based on alignment.
REFERENCE	location/Qualifiers
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REFERENCE	/mol_type="genomic DNA"
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REFERENCE	<1..>5710
REFERENCE	/gene="SCN8A"
REFERENCE	/locus_tag="HCMS911"
ORIGIN	
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Best Local Similarity	42.4%; Pred. No. 2.7e-164;
Matches 2513; Conservative	0; Mismatches 3043; Indels 368; Gaps 26;
186	CGCAAGAAAAAACAAGAAATCCGATATGATGACGACGACGAGATGAAGTCCACAA 245
100	CTCAAGAACCAACCAAGGCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 159
246	CCGATCTCTACCTTGAACAGGGGTGCGCAATACCTGTTGCATTGACGAGCCTCCG 305
160	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 219
306	CCGAAATGGGCTCCACTCTCTGAGAGATATCATCTCCATCAGCAATGTACTGACA 365
220	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 279
366	TTCTAGTTGTAAGCAAGAAAGATATTTTTCGCTTTTCTGCATCAAAAGCAATGTGG 425
280	TTTGTAGATTAAACAGAGGAAACCTCTCTTCAAGATTAGGCAAGCGCTGCTGTAC 339
426	ATGCTCATTCATTCAATCCGATAGCTGTGTGGCATTTACATCTAGTGCATCATTTA 485
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486	TTTTCCTATTCATCATCAACAATTCCTGCTCACTCATCTGATGATATGCGGACA 545
400	TTTACATGATCATTTATGTGCACTATTTTGAACAACTGTGATTCATGACTTTAGTAC 459
546	ACGCCACGGTTGAGTCCACTGAGGTG--ATATTACCGGAATTTACACATTTAAATCA 602
460	CTCTCTGACTGGTCGAAGAGATGTGAGATACAGTTTCAAGGATTTTAACATTTAAATCA 519
603	GCTGTAAAGATGAGCAAGAGGTTTCAATTTATGACCGGCTTTTACATCTTGAAGATCA 662
520	CTAGGAANAATATTGCAAGAGGTTTCTGCATAGATGCTTACTTTTACGGATCA 579
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 Qy 1553 CAACGATGACAAACAAGAGAGATGTCCATTTCCGAGGCTCAGAGTGGAGTGGAGTC 1612  
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 Db 1530 GGATCCCGAAGAGGTGTTAAGTCAAGTC-----AGAAAG 1565  
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 Qy 1913 GTACTATGGCAATTAAGGCTCCCGACACTCATCTGATATCTCTGCACTGTCGCCAAATATC 1972  
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 5607 GGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5666  
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 LOCUS  
 DEFINITION 1700067505389 A.Gam.ad.cdNA1 Anopheles gambiae cdNA clone

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 BM632901  
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 SOURCE  
 ORGANISM  
 Anopheles gambiae (African malaria mosquito)  
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 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 1 (bases 1 to 673)  
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,  
 Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished (2002)  
 CONTACT: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltR@celera.com  
 Plate: NUD1004ABY row: C column: 18  
 Seq primer: M13 Reverse.  
 Location/Qualifiers  
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## ORIGIN

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 3668 CAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 3727  
 92 TAAAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 151  
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 152 CAGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 211  
 3788 CCGGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 3847  
 212 TCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 271  
 3848 AGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 3907  
 272 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 331  
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 3968 TAAATATTTGAAAACAGCTGTATCATGATTTTAAATGAGTGTGTGTGTGTGTGTGTGT 4027  
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Db	452	CGAAGATGTGATCTTCACAGCGCCCAATCTTCAGATATTTCTTATACAGATCG	511
Qy	4088	AAATATTAAGGTATATTTCTTCTTGGAATGTATATCAAGTGTGGCGCTCGGCTCAA	4147
Db	512	AAATTTACAGATGATCTTTTTTTTAAAGATGTATCAAAAGTGTAGCTTAGGTTTTAA	571
Qy	4148	AGTGACTTCACCAAGCGGTGTGTGGCTGATTCGTGATGTGCAAGTATCGCTAT	4207
Db	572	AGATATTTTACAAATGCTTGAGTGTGGCTTGATTTCAATACGAGATGATCTTGAT	631
Qy	4208	CAACTCGTCTCTCACTTGTGTGAGAGCTGTGTATTCAAAC	4249
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DEFINITION	Bj729409	MF015DA	cDNA Oryzias latipes cDNA clone MF015DA005d18 5',
ACCESSION	Bj729409		mRNA sequence.
VERSION	Bj729409.1	GI:45296721	
KEYWORDS	EST.		
SOURCE	Oryzias latipes (Japanese medaka)		
ORGANISM	Oryzias latipes		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Acuñapleuryll; Neopleuryll; Telosteil; Euteleostei; Neoteleostei;		
TITLE	Acuñapleuryll; Acanthopleuryll; Percomorpha; Atherinomorpha;		
JOURNAL	Belontiiformes; Adrianchthyidae; Oryziinae; Oryzias.		
COMMENT	1 (bases 1 to 866)		
	Kohara,Y., Shin-1,T., Kimura,T., Narita,T., Jindo,T. and Takeda,H.		
	Medaka EST Project in Takeda's lab		
	Unpublished (2001)		
	Contact: Tadasu Shin-i		
	Center For Genetic Resource Information		
	National Institute of Genetics		
	1111 Yata, Mishima, Shizuoka 411-8540, Japan		
	Tel: 81-559-81-6856		
	Fax: 81-559-81-6855		
	Email: tshini@genes.nig.ac.jp.		
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Best Local Similarity	63.0%;	Pred. No. 3.6e-75;	
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Qy	5011	ACGCGGTCTAGACTATCTCAATGATATTCGTAGTATTTTCAAGTCCGAATGCTAT	5070
Db	10	ACAAGATCTCTACTGATCAACCTGGTTTTCATTTGCTCTTTTACATGGGAAATGTCTC	69
Qy	5071	TAAAAATATTCGCTTTCAGATACATATTTTATTTAGGACATGGAATTTATGATAG	5130
Db	70	TCAAAATATCTCTCTGGGCACTATTTACCTTACCATTTGCGTGGAAATCTTTATTTTG	129
Qy	5131	TAGTTGATTTTATTCATCTTAGGTCTTGTACTTAGAGCATATTTACGAGAAGTACTCG	5190
Db	130	TGGTGGGATTTCTTTCATTTGATGATATGTTTATTCGAGATCATCGAGAAGTACTTG	189
Qy	5191	TGTGGCCGACCTGTCCGAGTGTGCTGTGGGAAATGGGCGGTGTCTTGTGACTGG	5256

Db	190	TGTCGCCAACCCCTGTTTCGAGTGAATCCGACATGACACGGATGTGGATGATCTCCGCTTGA	249
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Db	250	TTAAAGGCGCCAAAGGGGCAATTCGACGCGCTTCCTTTGCGCTTGATGATGTCCTTCCTGCCC	309
Qy	5311	TGTTCAACATCTGCGCTGCTGCTGTTCTCGTGATGTCATCTTTGCCATTTTCCGACATG	53707
Db	310	TGTTTACATAGGCGCTTCCTCTTTTCTCGTGCATGTTTCACTATGATCCATCTTTGGATGT	369
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Qy	5839	TATGATGGAATATAC	5854
Db	850	TTTCAATGATCTGCC	865
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B1509823			
LOCUS			
DEFINITION			
B170021A10B09.5 Bee Brain Normalized/Subtracted Library, B17 Apis			
DEFINITION			
B1509823			
VERSION			
B1509823			
KEYWORDS			
B1509823.1 GI:15360197			
SOURCE			
ORGANISM			
Apis mellifera (honey bee)			
Apis mellifera			
Bukaryote, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,			
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,			
Apoidea, Apis.			
1 (bases 1 to 537)			
Whitefield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L.,			
Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.B.			
Annotated expressed sequence tags and cDNA microarrays for studies			
of brain and behavior in the honey bee			
Genome Res. 12 (4), 555-566 (2002)			
JOURNAL			
MEDLINE			
PUBMED			
COMMENT			
Contact: Gene E. Robinson			
Department of Entomology			
University of Illinois			
505 S. Goodwin Ave., Urbana, IL 61801, USA			
Tel: 217 265 0309			

Fax: 217 244 3499

Email: [genetobi@life.uiuc.edu](mailto:genetobi@life.uiuc.edu)

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PCR Primers

FORWARD: TAATACGACTCATATAGGG

BACKWARD: ATTAACCCCTCCTAAG

Plate: BB170021A10 row: B column: 09

Seq primer: AGCGATACCAATTCACACAGA

High quality sequence stop: 537.

Location/Qualifiers

1. 537

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/db\_xref="taxon:7460"

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/sex="female"

/tissue\_type="brain"

/dev\_stage="adult worker honey bee"

/lab\_host="DH10B"

/clone\_lib="Bee Brain Normalized/Subtracted Library, BB17"

/note="Organ: brain; Vector: pT773-Pac; Site\_1: EcorI;

Site\_2: NotI; This BB17 cDNA library was generated by

subtraction of the BB16 library with 4000 previously

sequenced clones. The BB16 library was contributed by the

Soares laboratory and it was constructed and normalized

as described by Bonaldo, M.F., Lennon, G. and Soares,

M.B. (1996), Genome Research 6(9): 791-806. RNA was

prepared from dissected brains of adult worker bees of

various ages and various behavioral groups."

# ORIGIN

Query Match 5.0%; Score 327; DB 4; Length 537;

Best Local Similarity 75.7%; Pred. No. 2.9e-73;

Matches 405; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

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DB 303 GACAGTGCATGATATTTGCTATTTCAAGATGTAAGCTCGGTGGTGGAGCGTGTCTTG 362
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QY 5554 ATTGTGTTTCAAGCAAGCTTGAATTAACGTTTCTCTCTCAATACCTAGTTAAAGCTTT 5613
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483 TAATCGATTAATAATGATGATCCCGGATCTTGGAGATTAATTCACAGCAC 537

RESULT 8

CNS27280

LOCUS

DEFINITION

IMAGE:30653177 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS27280 829 bp mRNA linear EST 29-APR-2004  
 UI-M-HB0-cpc-d-18-0-UI.r1 NIH\_BMAP\_HB0 Mus musculus cDNA clone  
 IMAGE:30653177 5', mRNA sequence.  
 CNS27280.1 GI:46855436  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
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 Mammalia; Euteleia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 829)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Dr. James Lin University of Iowa  
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mouse1.html>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 The following repetitive elements were found in this cDNA  
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 Site\_2: Not I; The library was constructed according  
 Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with Ecor I adaptor, digested with NotI and then cloned  
 directionally into pYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is TTAATGAGT. This library was created for the University  
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH)."

# FEATURES

source

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QY 5086 TACGATATCAATTTTATGAGCCATGGAATTTATGATGATGATGATGATTTAT 5145
DB 3 TGGCCACTATTAATCAACAAGCTGGAACATCTTCATTTGCTGTGTATCTCT 62
QY 5146 CCATCTTAGTCTTGAATTAAGGATTAATGAGAGTACTTGTGCGGACCTGC 5205
DB 63 CCATCTTAGTCTTGTCTCTCGACATCAAGAGTACTTCTTCCCAACGCTCT 122
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# ORIGIN

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Best Local Similarity 63.5%; Pred. No. 9.6e-72;

Matches 526; Conservative 0; Mismatches 292; Indels 10; Gaps 2;

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Db      183 GGATTCGACAGTTCCTTCCTTCGCGCTCATATATGTCCTGCGCGCCCTTCAACATCTGCC 242
Qy      5326 TGTCTGTCCTTCGTCATGTCATCTTTGCCATTTTGGCATGTCGTCCTTCATGCAAG 5385
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Qy      5386 TGAAGAGAGAGCGCCATTAAGAGAGTCAACCTTAAGAGCTTTGGCGAGAGATGA 5445
Db      303 TCAAGTGGAGAGCGTCGATCGAGAGATGTTCACTTCAGACTTTGGCGAGAGATGC 362
Qy      5446 TCTGTCCTTTTCAGATGTCAGCTTCAGCGCGTGGAGTGGTACTGAGAGCCATTATCA 5505
Db      363 TGTGCTTTTTCAGATTCACCACTGCGCTGGCTGGAGTGGCTCTCAGCGCCATCTCA 422
Qy      5506 ATGAGAGAGAGTCCGATCCACCCGACGCA-----CAAGGCTATCCGGCAATT 5556
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Qy      5617 TAGTTATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5676
Db      543 TCTGTGTCACATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 602
Qy      5677 TCGAAGAGGCTTACACCGAGAGAGAGTACAGATGATGATGATGATGATGATGATGATGAT 5736
Db      603 GCACAGAGCCCTCGAGAGAGAGTACCTCAACATGTTCTATGAGATCTGGAGAAATGTCG 662
Qy      5737 ATCCGAGAGGAGCCAGTACATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5796
Db      663 ACCCGAGAGGAGCCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 721
Qy      5797 AGCCCGCTGAGATTCACAAACCGAAGATGATGATGATGATGATGATGATGATGATGAT 5856
Db      722 TCTGAGAGACTCCGATGCGCAAGCCCAACAGATGATGATGATGATGATGATGATGAT 781
Qy      5857 TCTGTGCGGTGACCTTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCATGTCAT 5904
Db      782 TGGTGAAGCGGAGAGCGATCCTGATGATGATGATGATGATGATGATGATGATGAT 829

```

RESULT 9  
AK032187 2802 bp mRNA linear HTC 03-APR-2004  
LOCUS  
DEFINITION Mus musculus adult male olfactory brain cDNA, RIKEN full-length  
enriched library, clone:6430408L10 product:sodium channel protein  
II homolog [Rattus norvegicus], full insert sequence.  
AK032187  
ACCESSION AK032187.1 GI:26328014  
VERSION  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

```

MEDLINE 20499374
PUBMED 11042159
REFERENCE
AUTHORS
3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Kono, H., Akiyama, J., Nishi, K., Katsunaka, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multichannel sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE
AUTHORS
4 The RIKEN Genome Exploration Research Group Phase II Team and the
PANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
5 The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
6 (bases 1 to 2802)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoaka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasuoka, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Kono, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohse, N.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T.,
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp,
URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in Riken
Division of Experimental Animal Research in Riken contributed to
prepare mouse cDNAs.
Please visit our web site for further details.
URL: http://genome.gsc.riken.jp/
URL: http://fantom.gsc.riken.jp/
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/sex="male"
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/clone_id="RIKEN full-length enriched mouse cDNA library"
/dev stage="adult"
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match=759)"
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 DPAALDPLPLIAKPNKQVLIAMDLPMSGDRILVDLIFATKRVLOESGEMALRI  
 OMERFMAINSKSVSEPIITTLKROKBEVAIVORARYRLKOKVKVKSISTYKRD  
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## ORIGIN

Query Match 4.8%; Score 312; DB 3; Length 2802;  
 Best Local Similarity 60.6%; Pred. No. 3.9e-69;  
 Matches 576; Conservative 0; Mismatches 350; Indels 24; Gaps 3;

QY 5137 TCATTTATCCATCTTAGGCTCTTGTACTTACGATATTTATCGAAGAGTACTTGTGCGC 5196  
 DB 2 TCATCTCTCCATGTAGGAGTGTCTTCGCGAGACTGATAGAGATTTTCGTGCTCC 61  
 QY 5197 CGACCTCTCCGAGTGTGCGTGTGGGAAAGTGGCCGTCTCTTGCAGCTGTGAAG 5256  
 DB 62 CTACCTCTGTCGAGTCACTCCGCTGCGCAGGATTGACGATCTTACGCTGATCAAG 121  
 QY 5257 GAGCCAAAGGAGTTCGACACTGCTCTCGCGTTGGCCATGCGTGGCCGCTGTTCA 5316  
 DB 122 GCGCCAAAGGAGTTCGACACTGCTCTCTGCTGTATGATGTCTCTGCGCTGTTA 181  
 QY 5317 ACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5376  
 DB 182 ACATCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 241  
 QY 5377 TCATGACAGTGAAGAAGAGCCGATTTAAGAGCTCTCAACTTCAAGCTTTGGCC 5436  
 DB 242 TTGCTTACGTTAAGAGGAGATTTGATGATGATTTCAACTTCAAGCTTTGGCA 301  
 QY 5437 AGAGCATGATCTGCTCTTTCAGATGTCAGCGTTCGCGTTGGAGTGTGACTGAGC 5496  
 DB 302 ACAGCATGATCTGCTGCTTTCAGATGTCAGCGTTCGCGTTGGAGTGTGACTGAGC 361  
 QY 5497 CCATTTATCAATGAGAGACATGCGATTCACCCGACGACGACAAAGCTATCC----- 5548  
 DB 362 CTATCTCTTAAATAGGAGCTCCCGAT---TGAGACCTGAAAAGATCATCTGGAAGCT 418  
 QY 5549 -----GGCATTGTGTTCAGGACCGTGTGAATAAGTTCTCTCTCATACCTAG 5601  
 DB 419 CGGTGAAGGAGACTGTGGAAACCATCTGTGGGATTTCTTTTGTGACGACTACATCA 478  
 QY 5602 TTATAGCTTTTGTATGTTATATATATGTCATTTGCTGATCTCGAAGACTATAGTC 5661  
 DB 479 TCATCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538  
 QY 5662 AGGCGACGAGAGAGCTGACAGAGGCTTAAACGACGACGACGACGACGACGACGACG 5721  
 DB 539 TTGCGACAGAGAGAGAGTGCAGAGCTCTGAGTGAAGAGAGCTTGAAGTGTCTAGAG 598  
 QY 5722 TCTGCGACGAATTTGATCTCGAGGCGACCCAGTACATACGCTAGTACGCTGTCGAT 5781  
 DB 599 TCTGCGAGAGATTTGATCTCGAGGCGACCCAGTACATACGCTAGTACGCTGTCGAT 658  
 QY 5782 TCTGCGAGTACGAGGCGCGCTGCGAGATTCACAAACGACGACGACGACGACGACG 5841  
 DB 659 TTGCGAGTACGCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 718  
 QY 5842 CGATGACATACCCATCTGTCGCGGTGACCTCATGCTGCTGCGACATCTCTGACGCGC 5901  
 DB 719 CCAATGACCTGCGACATGCTGAGTGAAGACCGATCACTGCTGACATCTTATTTGCTT 778  
 QY 5902 TTACGAAAGACTTTCTTTCGCGGAAAGGCAATCCGATAGAGAGAGCGGTGAGATTGTG 5961  
 DB 779 TTACAAAGCGGCTCTGCTGCTGAGTGAAGATGATGATGCTCTTCAATCCAGATGAAG 838  
 QY 5962 AG-----ATAGCGCGCGCGCGGATACGAGAGGCTACGAGCCGCTCTCATCAAGCTGT 6015

DB 829 AGCGTTCATGCTCCATCCCTCCAAAGGCTCTCTTATGAGAGCCCATACCAACTCTGA 898  
 QY 6016 GCGCTCAGCGAGAGAGTACGCGCCCGGCTTAATCCAGACGCTCGGGA 6065  
 DB 899 AGCGCAACAAGAGAGGTGTCTGTATTTGATTCACGAGGCTTACAGA 948

## RESULTS

RESULT 10  
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 LOCUS 928 bp mRNA linear EST 16-JUL-2002

## DEFINITION

AGENCOURT 8294886 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6309535

## ACCESSION

BO715936

## VERSION

BO715936.1 GI:21854835

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 928)  
 NIH-MGC <http://mgi.ncl.nih.gov/>.

## AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

## TITLE

Unpublished (1999)

## COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Susan D. Sullivan, Ph.D.  
 cDNA Library Preparation: Resgen, Invitrogen Corp.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/MLML at:  
<http://image.llnl.gov>  
 Plate: LLM13730 row: g column: 08  
 High quality sequence stop: 715.

## FEATURES

source  
 1..928  
 Location/Qualifiers

## ORIGIN

Query Match 4.8%; Score 310.4; DB 5; Length 928;  
 Best Local Similarity 62.5%; Pred. No. 7.3e-69;  
 Matches 507; Conservative 0; Mismatches 292; Indels 12; Gaps 1;

QY 5130 GTAGTGTCAATTTATCATCTTGTACTTGTACTTGTACTTGTACTTGTACTTGTACTTGT 5189  
 DB 1 GTGGGTGATTTCTTCAATTTGAGAAATGTTCTCTGCTGAGTGAAGAAATTTT 60  
 QY 5190 GTGTGCGGACCCCTGCTCCAGTGTGTGCGTGGCGAAGTGGCCGCTGCTTGCAGCTG 5249  
 DB 61 GTGTCTCTTACCTGCTTCCAGTGTATCGCTGCGCCAGATTTGACGAATCTTACGCTG 120  
 QY 5250 GTGAGAGAGCGAAGGCAATTCGACACTGCTCTTCCGCTTGGCCATGCTGCGGCGC 5309  
 DB 121 ATCAAAGCGCGCAAGGGGATCCGACGCTGCTTGTGCTGAGATGATCTCTTCCGCG 180  
 QY 5310 CTGTTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5369  
 DB 181 CTGTTCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
 QY 5370 TCGTTCCTCATGACAGTGAAGAGAGCGGCAATTAACAGAGTCTCAACTTCAAGACC 5429  
 DB 241 TCCAACTTGTGCTATTTAAAGAGGCTGGAATGATGATGATGATGATGATGATGATGAT 300

QY 5430 TTGGGCAAGAGATGATCTCTCTTTTCAGATGTGACGTCACCGGTTGGGATGTGTA 5489  
 DB 301 TTGGGCAAGAGATGATCTCTCTTTTCAGATGTGACGTCACCGGTTGGGATGTGTA 360  
 QY 5490 CTGGAGCCATATATCA-----TGAGGAAGCATGCGATCCACCGGACGAC 5537  
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 DB 421 AGCTCAGTGAAGGAGACGTGTGGAACCCATCTGTGGGATTTCTTTTGTGACATAC 480  
 QY 5598 CTGATATTAAGCTTTTGTGATGTTATTAATGATGATGCTGCTCATCTTCGAGAACTAT 5657  
 DB 481 ATCATATATCTCTCTCTGTTGTGTGATGATGATGATGATGATGATGATGATGATGAT 540  
 QY 5658 AGTCAAGGCCACCGAGACGTGCAAGAGGCTTAACCGACGACGATGATGATGATGATGAT 5717  
 DB 541 AGCGTTGCCACAGAAAGTGAAGGCCCTGAGTGAAGGACGATTTGATGATGATGATGAT 600  
 QY 5718 GAGATCTGGCAGCAATTCATCCGAGGCGACCCAGTACATGCTATGATGATGATGATGAT 5777  
 DB 601 GAGGTCTGGGAGAGTTCGACCCCTGACGCGCACGAGTTCATGAGTTCGACAGCTCTCT 660  
 QY 5778 GAATCTCGAGGATCTGAGGAGCCCGCTGACATGATGATGATGATGATGATGATGATGAT 5837  
 DB 661 GATCTTCGAGCTCCCTGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 720  
 QY 5838 ATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5897  
 DB 721 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780  
 QY 5898 GCCCTTACGAAAGACTTCTTTTGGCGGAGAG 5928  
 DB 781 GCTTTACAAAGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 811

RESULT 11  
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 LOCUS 1700687506664 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone  
 DEFINITION 19600449642363 5', mRNA sequence.  
 ACCESSION BM63126  
 VERSION BM63126.1 GI:18932637  
 KEYWORDS EST.  
 SOURCE Anopheles gambiae (African malaria mosquito)  
 ORGANISM Anopheles gambiae  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
 Anopheles.  
 1 (bases 1 to 502)  
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L.,  
 Charlab,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished (2002)  
 Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
 Plate: NU01004AV7 row: H column: 09  
 Seq primer: M13 Reverse  
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 /clone="19600449642363"  
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FEATURES  
 source

/lab host="DH10b"  
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 cDNA inserts >500 bp cloned directionally into pSport 1.  
 Not 1 site is 3'. Clones available through the Malaria  
 Research and Reference Reagent Resource Center  
 (www.malaria.mr4.org)."

Query Match 4.6%; Score 302; DB 4; Length 502;  
 Best Local Similarity 75.1%; Pred. No. 9.3e-67;  
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QY 4681 TATATTCGATTTTCATCATATTTGATTCCTTTTTCACATCATCTGTCATTTGGTG 4740  
 DB 1 TGTACTTGTGTCTTTATATATCTTTGGTCAATCTTCACGTTGATTCATTCATTTGGTG 60  
 QY 4741 TTATCATGATATTTTATGAGCAAAAGAAAGCAAGTGATCATTTAGAAATGTTCA 4800  
 DB 61 TTTATTTGACAACTTCATGATGACAAAGAAAGCTGTGTGATGCTGATGATGATGATGAT 120  
 QY 4801 TGACAGAGATCAGAAAAAGTACTATATGATGATGATGATGATGATGATGATGATGAT 4860  
 DB 121 TGACAGAGATCAGAAAAAGTACTATATGATGATGATGATGATGATGATGATGATGAT 180  
 QY 4861 TAAAGCCATTTCCAGACCAAGTGTGGCCACCAAGCAATGATCTTGAATATGATACCG 4920  
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 QY 4981 TCGATGTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5040  
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 QY 5041 TCGATGTTATTTTTCAGTTCGATGATGATGATGATGATGATGATGATGATGATGAT 5100  
 DB 361 TCGATGATATTCAGACGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
 QY 5101 TTATGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 5160  
 DB 421 TTATGAGCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480  
 QY 5161 TACTTACGATATTTATCGAGAA 5182  
 DB 481 TTCTTACGATATTCATTTGAAAA 502

RESULT 12  
 CDS01236/c 771 bp DNA linear GSS 26-JUL-1999  
 LOCUS Drosophila melanogaster genome survey sequence SP6 end of BAC  
 DEFINITION BAC070N13 of DrosBAC library from Drosophila melanogaster (fruit  
 fly), genomic survey sequence.  
 ACCESSION AL101052  
 VERSION AL101052.1 GI:5612663  
 KEYWORDS GSS.  
 SOURCE Drosophila melanogaster (fruit fly)  
 ORGANISM Drosophila melanogaster  
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydroidea; Drosophilidae; Drosophila.  
 1 (bases 1 to 771)

REFERENCE  
 AUTHORS Direct Submission  
 TITLE Submitted (23-Jul-1999) Genoscope - Centre National de Sequencage :  
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 COMMENT Determination of this BAC-end sequence was carried out as part of a  
 collaboration with the European Drosophila Genome Project (EDGP) -





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Db      1002 TGAATCTGACGCTGCTCTGCTAAGCGTTCGCGCTAATAGATTCGAGTTGTCATGG 1061
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QY      958 -----GCATCTGA 966
Db      1122 TCACCTCTCTTTAACAATTCATTTGATGGAATGCTACTCTTTAATAGACACTGA 1181
QY      967 CCGACGAACTGAGACTATCACAATGCATAGCTCAATGGTATTCGAGACGAGG 1026
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QY      1087 TGTGCTGACAGGGGTTTGTCGCAATCCGAATTATGCTACACAGCTTCGATTCGTTG 1146
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QY      1147 GATGCGCTTTCCTGTCGCGCTTCGCTGATGACACAGACTTTCGAGAGATCTGTACC 1206
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QY      1267 TAGGTCATCTATCTTGTGAATTTGATTTGGCAATTTGTCATGCTGATGAGAAAT 1326
Db      1479 TGGGCTATTTCTATTAATTAATTTGATCTTGGCTGTGTCGTCATGAGCTTATGAGAA- 1537
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Db      1538 --CAGATCAGGCCACATTTGGAAGAGGCTGACAGAGAGAGC 1578

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RESULT 14
LOCUS   CBS20657 768 bp mRNA linear EST 09-JUL-2003
DEFINITION
  UI-M-G10-cej-n-19-0-UI.r1 NIH BMAP_G10 Mus musculus cDNA clone
  IMAGE:6840500 5', mRNA sequence.
ACCESSION
  CBS20657
  CBS20657.1 GI:29354012
SOURCE
  Mus musculus (house mouse)
  ORGANISM
    Mus musculus
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
    1. (bases 1 to 768)
    NIH-WGC http://mgc.nci.nih.gov/
    National Institutes of Health, Mammalian Gene Collection (MGC)
    Unpublished (1999)
    Contact: Robert Straussberg, Ph.D.
    Email: c9apbs-remail.nih.gov
    Tissue Procurement: Dr. Jim Lin, University of Iowa
    cDNA library preparation: Dr. M. Bento Soares, University of Iowa
    cDNA library Arayed by: Dr. M. Bento Soares, University of Iowa
    DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
    Clone Distribution: Distribution information can be found at
    http://genome.iowa.edu/distribution/mousefl.html
    This clone was contributed by the Brain Molecular Anatomy Project
    (BMAP)

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Seq primer: pYX-5.

FEATURES  
source

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Location/Qualifiers
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/fissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
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/note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I;
Site 2: Not I; The library was constructed according
to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemm Chin, Ph.D.,
program coordinator."

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#### ORIGIN

Query Match 4.4%; Score 288; DB 6; Length 768;  
Best Local Similarity 62.4%; Pred. No. 4,7e-63;  
Matches 472; Conservative 0; Mismatches 272; Indels 12; Gaps 1;

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QY      5036 GAAATTCGATGATTTTCAGTCCGAATGCTATTAATAAATTCGCTTACGATATCA 5095
Db      13 GGTATTCATGCTCTCTTACTGCGAGATTTTCTGCAAGCTCATCTCTCAATACTA 72
QY      5096 CTATTTATTTGACATGAAATTTATTTGATGATGATGATGATGATGATGATGATG 5155
Db      73 CTACTTCACGATTTGGTGGAACATCTTGACTTGTGTGGTGGATCTCTCAATTTGAG 132
QY      5156 TCTTGTACTTACGATATTTATGAGAAGTACTTCTGTGCGGACCTGCTCGAGTGT 5215
Db      133 AATGTCCTTGTGTCGATGATGAGAAGTATTTGTGCTCTCACTCTGTCGAGTCA 192
QY      5216 GCGTGTGCGAAGAGGGCGGTCGCTGCACTGATGAAAGGAGCAAGGCAATTCGGAC 5275
Db      193 CCGCTGACGAGATTTGACGATCTTACGCTGATCAAGGCGCAAGGAGATTCGAC 252
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 1 (bases 1 to 688)  
 Holt R.A., Lin J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,  
 Charlab, R., Collins, P.H., Venter, J.C. and Hoffman, S.L.  
 Celera Anopheles gambiae EST project  
 Unpublished (2002)  
 COMMENT Contact: Holt R.A.  
 Celera Genomics  
 45 W. Gude Dr., Rockville, MD 20850, USA  
 Tel: 2404533151  
 Fax: 2404534580  
 Email: HoltRA@celera.com  
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